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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 01:22:39 ; Search time 3521.68 Seconds  
(without alignments)  
-2011.507 Million cell updates/sec

Title: US-09-361-652-6  
Perfect score: 2333  
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Scoring table: IDENTITY\_NUC  
Searched: 821193 seqs, -1518192014 residues  
Database: GenEmbl:\*  
Word size: 0  
Number of hits that pass the threshold: 1642386

- 1: gb\_dal1\*
- 2: gb\_dal2\*
- 3: gb\_om1\*
- 4: gb\_om2\*
- 5: gb\_om3\*
- 6: gb\_ph1\*
- 7: gb\_ph2\*
- 8: gb\_ph3\*
- 9: gb\_ph4\*
- 10: gb\_ph5\*
- 11: gb\_ph6\*
- 12: gb\_ph7\*
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- 14: gb\_ph9\*
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- 44: gb\_ph39\*
- 45: gb\_ph40\*
- 46: gb\_ph41\*
- 47: gb\_ph42\*
- 48: gb\_ph43\*
- 49: gb\_ph44\*

50: gb\_ph13:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563.6	67.0	2520	12 AF127389	AF127389 Rattus no
2	396.8	17.0	2529	12 AF127390	AF127390 Rattus no
3	266.8	11.4	270	13 G09859	G09859 human STS C
4	205.4	8.8	3106	10 HSHR3501	U45324 Human Krupp
5	143.2	6.1	5249	3 S67307	S67307 Ca(2+)-sens
6	143.2	6.1	5275	5 AR012622	AR012622 Sequence
7	143.2	6.1	5275	5 AR028465	AR028465 Sequence
8	143.2	6.1	5275	5 AR012521	I75051 Sequence 1
9	138.4	5.9	3809	5 AR012524	AR012524 Sequence
10	138.4	5.9	3809	5 AR028467	AR028467 Sequence
11	138.4	5.9	3809	5 I75053	I75053 Sequence 3
12	138.4	5.9	3234	9 HSPCAR1	X81086 H. sapiens
13	138.4	5.9	3234	9 HSPCAR1	D50855 Human mRNA
14	138.4	5.9	3234	10 HSPCAR1	U20759 Human parat
15	138.4	5.9	3234	10 HSPCAR1	S83176 CasR-calcit
16	138.4	5.7	5006	5 AR012623	AR012623 Sequence
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18	132.6	5.7	5006	5 I75052	I75052 Sequence 2
19	132.6	5.7	5009	10 HSPCAR1	U20760 Human extra
20	132.6	5.7	5009	13 G28586	G28586 human STS S
21	132.6	5.5	4550	12 AF110178	AF110178 Mus muscu
22	127.8	5.5	3569	12 AF128842	AF128842 Mus muscu
23	123.4	5.3	4131	5 AR012625	AR012625 Sequence
24	123.4	5.3	4131	5 AR028468	AR028468 Sequence
25	123.4	5.3	4131	5 I75054	I75054 Sequence 4
26	123.4	5.3	4131	12 RNU10354	U10354 Rattus norv
27	123.4	5.3	3761	12 RNU20289	U20289 Rattus norv
28	119.6	5.1	4319	12 AF110179	AF110179 Mus muscu
29	104.4	4.5	2148	5 A73577	A73577 Sequence 1
30	103.4	4.4	798	40 S81755	S81755 calcitum rec
31	102	4.4	4743	4 AB008862	AB008862 Fugu rubr
32	101	4.3	3506	4 AB008857	AB008857 Fugu rubr
33	97.2	4.2	927	4 AB009044	AB009044 Fugu rubr
34	92.6	4.0	2785	4 AF083080	AF083080 Carassius
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36	83.4	3.6	4981	4 AB008859	AB008859 Fugu rubr
37	82	3.5	1786	4 AF083084	AF083084 Carassius
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40	76.8	3.3	761	12 AB027140	AB027140 Mus muscu
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43	76.6	3.3	16570	41 AC011457	AC011457 Homo sap1
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ALIGNMENTS

RESULT	1	AF127389	2520 bp	MRNA	ROD	04-MAR-1999
LOCUS	AF127389					
DEFINITION	Rattus norvegicus putative taste receptor TR1 mRNA, partial cds.					
ACCESSION	AF127389					
VERSION	AF127389.1	GI:4337085				
KEYWORDS						
SOURCE						
ORGANISM	Norway rat.					
	Rattus norvegicus					
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;					
	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1	(bases 1 to 2520)				



AUTHORS	Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J. and Zuker,C.S.
TITLE	Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity
JOURNAL	Cell 96 (4), 541-551 (1999)
MEDLINE	99159821
REFERENCE	2 (bases 1 to 2520)
AUTHORS	Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J.P. and Zuker,C.S.
TITLE	Direct Submission
JOURNAL	Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA
FEATURES	location/qualifiers 1..2520
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BASE COUNT	479 a 749 c 676 g 616 t
ORIGIN	
Query Match	67.0% Score 1563.6; DB 12; Length 2520;
Best Local Similarity	79.9%; Pred. No. 0;
Matches 1866; Conservative	0; Mismatches 464; Indels 4; Gaps 2;
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Dd	187 AGGCCCGACAGCTTAAAGGCCATGGCTAACCACTTCCTCCAGGCATCGGTTCACTGTT 246
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Dd	247 GAGGGAATAAACAACACTCTCGCGCCTGCTGCTCCCAACATCACCTCTGGGTATGAGCTTGAC 306
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Dd	307 GACGtGTGCTCGAATCTGCGCAATGTGATATGCACACCCTGAGAGGTGCTTGCCCTGCAAGG 366
OY	181 caaacacatatagagctccaaggaaaccttctcacatatlcccccagaagtgctgcgca 240
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OY	241 attggagcttgaagacacaacccgtgtctgcacacaaagccgcctgtctgaaccccttct 300
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OY	301 gtf---catattagctatcgcgccagcagcgagacgcctcaagcgtgaagcggcaatccc 357
Dd	487 ATGCCCCGTGTCAGCTTAGAGGCAAGCAACCGTGTACTCAAGTCAAGGCCAAGCTTCCG 546
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O	418	cagaagctcgggtgagaccctggaatctctctctgtgttgcaagcagtgcacatgtagcagcta	477
D	607	CAGAGTTTTGGGTGGGTGGATCTCGTCATTTGGCAGCTACGGATGATTAACGGCAGCTG	666
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D	667	GGTGTGCAGGGGCTGGAGGAGCTGGCCGTGGCCCGGGGAGTGTGGTGGCTTCAAGAGAC	726
O	538	atcaatgccctctctctgcgcaagtggtgcagatgaagaaatgacatgtcctaatgtgcacatg	597
D	727	ATCGTGCCCTTCTCTGTGCCCGGGTGGGTGACCCGAGSAGATCAAGACATGATGACATCTG	786
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D	847	TTTCAGGTCCGGGGTGGCGGCAACCTGTGGAAGTGTGGGTGGCTGCCTCAAMACATCTGG	906
O	748	gccctctccaggacacatcactctgt	777
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D	967	GTGGGCGTCCAGACGAGAACAAAGTCCCTGGGCTTAAGAGATTTGAAGAGTCTTATGTCAGG	1028
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 STS sequence: primer: sequence tagged site.  
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 SOURCE genomic DNA prepared from xv individual of French nationality.  
 ORGANISM Homo sapiens  
 Eukaryota; Eukaryotes; Metazoa; Chordata;  
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopherygii; Choanata;  
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
 Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 270)  
 AUTHORS Murray,J., Sheffield,V., Weber,J.L., Duyk,G. and Bueltow,K.H.  
 TITLE Cooperative Human Linkage Center  
 JOURNAL Unpublished (1995)















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Db 2558 CAGCGCGCTTTGGCATCAGCTGTGCTGTGCATCTGTGCATCTGTGTAACCAAT 2617
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Qy 1830 caaaccacaggtgctgctgcttctgtgtaagtaagcagcagcagcagcagcagc 1889
Db 2675 GGGCTCAACCTGACAGTCTCTGCTGTGCTTCTCTGACACTTCATGACATGTGATCTGT 2734
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RESULT 8
LOCUS 175051 5275 bp DNA PAT 03-APR-1998
DEFINITION Sequence 1 from patent US 5688938.
ACCESSION 175051
VERSION 175051.1 GI:3011192
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 5275)
AUTHORS Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.
TITLE Calcium receptor-active molecules
JOURNAL Patent: US 5688938-A 1 18-NOV-1997;
FEATURES
location/qualifiers
1..5275
BASE COUNT 1277 a 1475 c 1316 g 1207 t
ORIGIN
Query Match 6.1%; Score 143.2; DB 5; Length 5275;
Best Local Similarity 47.3%; Pred. No. 1.5e-21;
Matches 501; Conservative 0; Mismatches 553; Indels 6; Gaps 2;

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RESULT 9
LOCUS AR012624 3809 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5763569.
ACCESSION AR012624
VERSION AR012624.1 GI:3970614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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ACCESSION	175053	Sequence 3 from patent US 5688938.		PAT
VERSION	175053.1	GI:3011194		03-APR-1998
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 3809)			
TITLE	Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.			
JOURNAL	Calcium receptor-active molecules			
FEATURES	Patent: US 5688938-A 3 18-NOV-1997;			
	Location/Qualifiers			
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	/organism="unknown"			
BASE COUNT	910 a	1071 c	979 g	849 t
ORIGIN				

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Best Local Similarity	47.08	Pred. No. 1.7e+20		
Matches 498	Conservative	0	Mismatches 556	Indels 6
				Gaps 2

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Db	2053	TGCTGCTTTTACGTGCTGGAGAGTGTCTCTGATGGGGAGTATGATGAATACAGATGCCAGT	2112
Qy	1410	agatgcacagcttgtagaacaagaaggtgtagactgtagagggagaagcagactgctcccg	1469
Db	2113	GCCTGTACACAGTGGCCCAAGTACCTTCTGTGTCAAATGAAACACACACTCCTGCAATTGCC	2172
Qy	1470	cgcactgtagtgcttttgtagcttgtagcgtgagcaacctcttggtgtgctgtagcagtaac	1529
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Qy	1590	ccgtgtagtgagtcagcagaagggggcgccgtgtctctctatgctgtagctccctgcaagca	1649
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DEFINITION	H. sapiens PCAR1 gene.				
ACCESSION	X81086				
VERSION	X81086.1	GI:599819			















REMARK	COMMENT	FEATURES
GenBank staff at the National Library of Medicine created this entry [NCBI gi158417.1] from the original journal article.	This sequence comes from Fig. 6.	Compare X81086.
	Location/Qualifiers	

BASE COUNT	740 a	930 c	828 g	736 t
ORIGIN				



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 10:28:19 ; Search time 2338.04 seconds  
(without alignments)  
3935.865 Million cell updates/sec

Title: US-09-361-652-6  
Perfect score: 2333  
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Scoring table: IDENTITY\_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:\*

Word size : 0

Number of hits that pass the threshold : 9077268

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- 2: em\_est2:\*
- 3: em\_est3:\*
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- 6: em\_est6:\*
- 7: em\_est7:\*
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- 103: gb\_est14:\*
- 104: gb\_est15:\*
- 105: gb\_est16:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 3	210.4	9.0	525	45	AI390993	AI390993 mb98d01.y
c 4	196.8	8.4	421	46	AI415100	AI415100 mb98d01.x
c 5	178.2	7.6	298	48	AI562167	AI562167 vw73d10.x
c 6	131.6	5.6	247	26	W18663	W18663 mb98d01.r1
c 7	108	4.6	514	105	AO615201	AO615201 HS_5138_B



C	8	85	3.6	468	40	AA937218	AA937218	OK13f08.x
C	9	85	3.6	499	64	AA051287	AA051287	wy83g12.x
C	10	68.6	2.9	732	64	AL040113	AL040113	DEFZp34Cj
C	11	61	2.6	497	70	AM157397	AM157397	au93a09.x
C	12	61	2.6	498	70	AM157806	AM157806	au80f01.x
C	13	60.4	2.6	476	42	AI109009	AI109009	qp28a01.x
C	14	60.4	2.6	438	43	AI2000353	AI2000353	qf98a02.x
C	15	60.4	2.6	488	44	AI283030	AI283030	qms5b04.x
C	16	60.4	2.6	474	47	AI475867	AI475867	tc95b01.x
C	17	60.4	2.6	483	47	AI499186	AI499186	tc08c01.x
C	18	60.4	2.6	479	49	AI623563	AI623563	ly57e12.x
C	19	60.4	2.6	485	50	AI680129	AI680129	tw65b07.x
C	20	60.4	2.6	453	51	AI735731	AI735731	at20g01.x
C	21	60.4	2.6	468	62	AI928061	AI928061	w66f67.x
C	22	60.4	2.6	465	64	AM083336	AM083336	xc01d01.x
C	23	60.4	2.6	495	70	AM156822	AM156822	au89f04.x
C	24	60.4	2.6	510	70	AM157053	AM157053	au91c10.x
C	25	60.4	2.6	418	72	AM161036	AM161036	au78a10.y
C	26	60.4	2.6	445	72	AM161303	AM161303	au80f01.y
C	27	60.4	2.6	466	72	AM162175	AM162175	au89f04.y
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C	32	60.4	2.6	428	72	AM163458	AM163458	au95a09.y
C	33	60.4	2.6	436	72	AM163636	AM163636	au96n03.y
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C	35	58.6	2.5	440	47	AI523924	AI523924	tg98b08.x
C	36	57.8	2.5	386	50	F24619	F24619	HSP01067.H
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 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized  
 libraries were mixed, and ss circles were made in vitro.  
 Following HAP purification, this DNA was used as tracer in  
 a subtractive hybridization reaction. The driver was  
 PCR-amplified cDNAs from pools of 5,000 clones made from  
 the same 5 libraries. The pools consisted of the following  
 libraries and clones: Soares NbHSF pool 1:  
 145032-147339, 133208-325895, Soares Nb2HP pool 1:  
 145032-147339, 147720-148103, 148872-149255, 15002 -  
 150407, 151176-152327 Soares Nb2HR8-9W pool 1:  
 758280-760583, 772104-774407 Soares NbHPA pool 1:  
 304776-306511, 320136-322823, 326280-326653 Soares NbHOT  
 pool 1: 723720-726407, 739080-740999 Subtraction by Bentic  
 Soares and M. Fatima Bernaldo."

```

RESULT      1
AI742401/c

LOCUS       AI742401                562 bp      mRNA
DEFINITION  Wg40e02.x1 Soares_NSt_F8_9d_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:267578 3' similar to TR:093557 093557 PUTATIVE ODORANT
RECEPTOR, mRNA sequence.
ACCESSION   AI742401
VERSION     AI742401.1  GI:5110669
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1130951.
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from GIbc0
High quality sequence stop: 468.
Location/Qualifiers
1..562
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

Db	Accession	Definition	LOCUS	RESULT
Oy	2193	ggttggagcaagccctgagcaccacggcttcggtggaattcttctgcctaagatgctacgtgac	AA853967/c	2
Db	322	GGGCTGACACACTGCTGACACACGGCTTCGGTGGGTATTTTCTGCTAAGTGTCTAGTC		
Oy	2253	ctctgcgcgcccaagacccctcaacagcacagagacattccaggctccatctaaagatacacg		
Db	262	CTCTGCGCGCCAGACCTCAACAGACACAGACATTCTCCAGCGCTCCATTGAGACTACACG		
Oy	2313	aggcgcctgcgcgctccacctga	2333	
Db	202	AGGCGCTGCGGCTCCACTCA	182	
AA853967	496 bp	mRNA	EST	31-DEC-1998
aJ51e10.s1 Soares testis NRT Homo sapiens cDNA clone IMAGE:1393866				
3' similar to SW:CA5R_PAT P48442 EXTRACELLULAR CALCIUM-SENSING				
RECEPTEUR PRECURSOR ; , mRNA sequence.				
AA853967				
AA853967.1	GI:2941505			
EST.				
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
	Euthelia; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 496)			
AUTHORS	NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			















## REFERENCE

304776-306311, 320136-322823, 326280-326663 Soares NbHOT  
pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
Soares and M. Fatima Bonaldo."



AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Dec 20, 1995 this sequence version replaced gi:1134450.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
 Seq primer: -400P from Gldco  
 High quality sequence stop: 440.

## FEATURES

source

```
1..498
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not; Site.2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHR pool 1:
309384-310919, 323208-323895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326653 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 122 a 119 c 135 g 121 t 1 others
ORIGIN
```

## Query Match

Best Local Similarity 53.38; Score 85; DB 64; Length 498;  
 Matches 178; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

```
QY 214 caccattcccttaagcgtgcgcagcagtgattggcctcagcaccacccgctgcacc 273
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 348 CACATTCCTCTACGATGCTGTGTGGAGCACTGGCTCAGCGCTCCACGGCAGTG 289
QY 274 acagccgcccctgtgagcccttctcgtgtacatactgactatgagcgcagcaggaag 333
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 288 GCAAAATCTGCTGGGCTCTTCTACATTCGCCAGTCAAGTTATGCTCTCCACGAGCTC 229
QY 334 ctgaagctgaagcgcagctaccccttctcgtgcagcaccatcccaattgacaagtaac 393
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 CTGAGCAACAAGATCAATTCATCTTCTCTCGAACAATCCCAATGATGAGCACACAG 169
QY 394 gtgagaagcattgtgctgcgtgcctcagaagttcgtgagcactgagactctctcgtggc 453
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 168 GCCACTGCTCCATGGCAGACATCATGAGTATTTCCCTGGAACTGGGTGGCACATTGCA 109
QY 454 agcaagtacagctatggcagcctaggggtgcagcagcacttgagaaaccaagccctgtcag 513
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 108 GGTGATGACGACTATGGCGCGCGGATGAGAAATTCGAGAGGAGAGCGAGAAAGG 49
QY 514 ggcattcgcattgcttccaaggaatcatgcc 546
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 48 GATATCTGATCGACTTCAGTCACTCATCTCTCC 16
```

## RESULT 10

AL040113

LOCUS AL040113 732 bp mRNA EST 28-SEP-1999  
 DEFINITION DKFZ2434C2213\_1 434 (synonym: htes3) Homo sapiens cDNA clone  
 DKFZ2434C2213 5', mRNA sequence.

ACCESSION AL040113  
 VERSION AL040113.2 GI:5935280  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 732)  
 AUTHORS Koehler K., Beyer A., Mewes H.W., Gassenhuber J. and Wiemann S.  
 EST (Koehler, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT On Jul 7, 1999 this sequence version replaced gi:5409080.  
 Contact: Koehler K

## FEATURES

source

```
1..732
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP434C2213"
/clone_lib="434 (synonym: htes3)"
/issue_type="testis"
/development="adult"
/lab_host="DH10B"
/note="Vector: pSPoriT; Site.1: Not; Site.2: SalI"
Am Kioferspitze 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMF within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
```

## BASE COUNT

ORIGIN

```
125 a 245 c 191 g 169 t 2 others
```

## Query Match

Best Local Similarity 45.38; Score 68.6; DB 64; Length 732;  
 Matches 285; Conservative 0; Mismatches 339; Indels 3; Gaps 1;

```
QY 1563 ggcctgttgcctggcaccacacccctgtgtgagcagcagggcgccctgtgc 1622
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19 GGTCCTTTTGGCGCAATGCCACACAGTGTCAAGCCTCAGTCCGGAGCTTCTGC 78
QY 1623 ttcttatgcttgggtctccctgtgagcagcagtgatggcagccctataggctcttgggaa 1682
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 79 TACATCTCTGGGTGTGTGTCTCTCTCTACTGCAATGACCTTCATCTCATTTGCCAAG 138
QY 1683 ccccaagacctgcgtgcttgcagcagcagccctcttgccttggttcacacatctc 1742
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 CCAATCCACGGCAATGTGTACTTACCGCGCTGTGTTGGCACTGGCTTCTCTGTCTGC 198
QY 1743 ctgtccgcctgcagcagtgctcatctccacacatcatcatcttcaagtttccacaaag 1802
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 TACTCAACCTCTGCTACCAAGACCAACCGCATTCGACGCACTTCTGGTGGGCCCGGAG 238
QY 1803 gtacctacatttaccacagcctgtgttccaaacacaggttgcgtgttctgtgatgac 1862
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 GTGTGCCAGCGGCGACGCTTATCATGATCTCTGCTCAAGAGTGGCAATCTCCTGGCACT 318
QY 1863 agctcagcggccctgcttctatctgtctaaccttgcgtgtgtgtgtgtgtgtgtgtgt 1922
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 ATCT--CGGGCCAGCTGCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 375
QY 1923 gctcaggaataaccagcgtctcccccacatctgtgatattcttgagtgacacaggaacttcc 1982
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 GGCAGGAGACAGACCCCGCAACCGCGGAGGTGTGACACTGCGTGCACACCGCGAT 435
QY 1983 ctgggtcttactgtgctctctctacaatgagcctctctctcactcagtgcttctgtctgc 2042
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 GCAAGTATGTTGGCTCGCTGCGCTTCAATGTCTCTCTCATTCGCGCTCTCGACGCTTAT 495
```



QY	2043	agctaccctggggaagagacttgcgcagagactcaacagagcgccaaatgtgtacccttcagc	2102
Db	496	GCCTTCAAGACTCGCAAGTGGCCCGAAAACCTTCAACGAGGCCAAGTTCATTGGCTTCAC	555
QY	2103	ctgcctctcaacttcgtgtctcgtatgcgcctctcttcacacagcgccagcgtctacacagc	2162
Db	556	ATGTACACACACCTGATCATCTGTGGTGGCATTCCTGGCCATCTTGTATGTACCTTCAGT	615
QY	2163	aagctacgtcctgcgcgcacatgatg	2189
Db	616	GACTACCGGTTACAGACCAACCATG	642
RESULT	11		
LOCUS	AM157397/c		
DEFINITION	AM157397 497 bp mRNA EST 04-NOV-1999		
	aus5ad09.31 Schneider fetal brain 00004 Homo sapiens cDNA clone		
	IMAGE:27831992.3 similar to gb:J02984.40S RIBOSOMAL PROTEIN S15		
	(HUMAN); mRNA sequence.		
ACCESSION	AM157397		
VERSION	AM157397.1 GI:6228798		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 497)		
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,		
	Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Matra, M.,		
	Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,		
	Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.		
	WashU-NCI human EST Project		
	Unpublished (1997)		
TITLE	On Dec 20, 1995 this sequence version replaced gi:1135775.		
JOURNAL			
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400p from Glbco High quality sequence stop: 467. Location/Qualifiers 1. 497 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:27831992" /clone_lib="Schneider fetal brain 00004" /sex="male" /tissue.type="frontal lobe" /dev.stage="5 months post-conception" /lab_host="DH10B" /note="Organ: Brain; Vector: pBluescript SK (Stratagene); Site_1: SctI; Site_2: XhoI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-GAGAGAGAGAGAGCTCAGCATCTTAAATTAATATATCCCCCCCCCCC-3' and 3' adaptor sequence: 5'-GAGAGAGAGACTCGAGCTTTTCTTTTCTTTT-3'. The library was size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LMCIB-Area Science Park, Trieste, Italy)." 74 a 151 c 150 g 121 t 1 others		

Query Match	2.6%;	Score 61;	DB 70;	Length 497;
Best Local Similarity	47.4%;	Pred. No. 9.5e-05;		
Matches 181.	Conservative	0;	Mismatches 201;	Indels 0; Gaps 0;

OY	366	gcgcacccatcccccatgatgaagaattaccaggttgtagaacattatgctcgtctcgtcgcagaagt	425
Db	450	ggcgaccttccggcaaatgttacacttaacgccggcggtggacctgcaccagctgctggacatgtc	391
OY	426	cgggtggaactcgtgatctctcgttgttcgacagatfgaacgactatggcctaaagggtfcca	485
Db	390	ctacagacagantgatgcacgctgtracagrgccgcgcagccggcgggcgctgaacccggggcct	331
OY	486	ggcaactgtagaacaccagagcccctgfcacggsggactcgtcattcctttcaagagcatcatgccc	545
Db	330	ggcgccggaaacagcacactctccctgctgaacccctcgcgaagcccaagaaagagccgccccc	271
OY	546	ctctctcgtcccaaggctggcgagatgaagagatgaatgctcactcgtccacactcgtccagagc	605
Db	270	catgagaaagccgggaagtgtgaaagaccacactcggggacatatgatacttaccaggagat	211
OY	606	cggggccacgctcgtgtgtgtgttttttccagccggcgaagtggccaaaggtgttttccagatc	665
Db	210	ggtagggcagcatgtggggcgctctcaaacggcgaacaccttcaaacagggaggaatcaagcc	151
OY	666	cgtagtgtagcacaacctgtagcagaagtgtgggtgcgcccacagaagccgtggccctctc	725
Db	150	cgagatgtatccggccactrctcctggcggaattctccatcactcactcaaacgccctgtaaagcatgg	91
OY	726	caggacatcacactggtggtgcc 747	
Db	90	ccggcccgccgcatccggggccacc 69	

RESULT 12	
AM157806/c	
LOCUS	
DEFINITION	AM157806 498 bp mRNA EST 04-NOV-1999
	aubof01.x1 schneider fetal brain 00004 Homo sapiens cDNA clone
	IMAGE:2782585 3' similar to gb:U02984 40S RIBOSOMAL PROTEIN S15
	(HUMAN); mRNA sequence.
ACCESSION	AM157806
VERSION	AM157806.1 GI:6229207
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
AUTHORS	Eutheria: Primates: Catarrhini: Homnidae: Homo.
TITLE	1 (bases 1 to 498)
JOURNAL	Hillier,L., Allen,M., Bowles,L., Dubugue,T., Gaisel,G., Jost,S.,
COMMENT	Kizman,D., Kucba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Mettin,J., Moore,B., Schellendberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project Unpublished (1997) On May 18, 1998 this sequence version replaced gi:3136531. Other ESTs: aubof01.y1

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from GLDco
High quality sequence stop: 343.
Location/Qualifiers
1..498
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2782585"
/clone_id="schneider fetal brain 00004"
/sex="male"
/tissue_type="frontal lobe"











Oy 726 caggcaccactgggtgcc 747  
| | | | | | | | | |  
Db 96 cggcccgccatcgggccacc 75

Search completed: March 18, 2000, 10:28:32  
Job time: 2317 sec









GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 09:49:55 : Search time 2238.04 seconds  
(without alignments)  
4674.789 Million cell updates/sec

Title: US-09-361-652-4

Perfect score: 2771

Sequence: 1 attcacatcagcgtgtgtct.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY\_NUC

Searched: 4538634 seqs, 1887831982 residues

Database : EST:\*

Word size : 0

Number of hits that pass the threshold : 9077268

1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: em\_est10:\*  
11: em\_est11:\*  
12: em\_est12:\*  
13: em\_est13:\*  
14: em\_est14:\*  
15: em\_est15:\*  
16: em\_est16:\*  
17: em\_est17:\*  
18: em\_est18:\*  
19: em\_est19:\*  
20: qb\_est1:\*  
21: qb\_est2:\*  
22: qb\_est3:\*  
23: qb\_est4:\*  
24: qb\_est5:\*  
25: qb\_est6:\*  
26: qb\_est7:\*  
27: qb\_est8:\*  
28: qb\_est9:\*  
29: qb\_est10:\*  
30: qb\_est11:\*  
31: qb\_est12:\*  
32: qb\_est13:\*  
33: qb\_est14:\*  
34: qb\_est15:\*  
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36: qb\_est17:\*  
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38: qb\_est19:\*  
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41: qb\_est22:\*  
42: qb\_est23:\*  
43: qb\_est24:\*  
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47: qb\_est28:\*  
48: qb\_est29:\*  
49: qb\_est30:\*

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52: em\_est20:\*  
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54: em\_est22:\*  
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56: em\_est24:\*  
57: em\_est25:\*  
58: em\_est26:\*  
59: qb\_est33:\*  
60: qb\_est34:\*  
61: qb\_est35:\*  
62: qb\_est36:\*  
63: qb\_est37:\*  
64: qb\_est38:\*  
65: em\_est27:\*  
66: em\_est28:\*  
67: em\_est29:\*  
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69: qb\_est39:\*  
70: qb\_est40:\*  
71: qb\_est41:\*  
72: qb\_est42:\*  
73: qb\_est43:\*  
74: qb\_est44:\*  
75: em\_est31:\*  
76: em\_est32:\*  
77: em\_est33:\*  
78: em\_est34:\*  
79: qb\_est45:\*  
80: qb\_est46:\*  
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86: em\_est37:\*  
87: qb\_est49:\*  
88: qb\_est50:\*  
89: qb\_est51:\*  
90: qb\_est52:\*  
91: qb\_est53:\*  
92: em\_est38:\*  
93: em\_est39:\*  
94: em\_est40:\*  
95: em\_est41:\*  
96: em\_est42:\*  
97: em\_est43:\*  
98: em\_est44:\*  
99: qb\_est54:\*  
100: qb\_est55:\*  
101: em\_est45:\*  
102: qb\_est56:\*  
103: qb\_est57:\*  
104: qb\_est58:\*  
105: qb\_est59:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	333.6	12.0	421	46	A1415100	A1415100 mb98d01.x
C 2	301.4	10.9	525	45	A1390993	A1390993 mb98d01.y
C 3	294.8	10.6	562	51	A1742401	A1742401 wg40e02.x
C 4	229.2	8.3	298	48	A1552167	A1552167 vw73d10.x
C 5	212.8	7.7	496	39	AA853967	AA853967 aj51e10.s
6	175.6	6.3	247	26	W18663	W18663 mb98d01.r1
7	140.6	5.1	260	71	AV278654	AV278654 AV278654







Source	Organism	Reference Authors	Title Journal Comment
house mouse.	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 525)	Marrin, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuk, R., Riter, E., Kohn, S., Shin, T., Jackson, J., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.		
The Mashu-NCI Mouse EST Project 1999	Unpublished (1999)		
On Jan 17, 1998 this sequence version replaced gi:2044280.	Contact: Marra M/Mashu-NCI Mouse EST Project 1998		
Washington University School of Medicine	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
Tel: 314 286 1800	Fax: 314 286 1810		
Email: mouseest@watson.wustl.edu			
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.			
This read is a RESEQUENCE of a previously sequenced mouse clone			
This read has been verified (found to hit its original self in the correct orientation)			
Seq primer: -40RP from Gibdo			
High quality sequence stop: 481.			
Location/Qualifiers			
1..525			
/organism="Mus musculus"			
/db_xref="taxon:10090"			
/clone="IMAGE:337441"			
/clone_lib="Soares mouse p33MF19.5"			
/dex_stage="19.5 dpc total fetus"			
/lab_host="DR10B (ampicillin resistant)"			
/note="Vector: pT73 (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15', TGTTACCATCTGATGAGTGGAGCGGCCGCGCATTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."			
BASE COUNT	104 a 179 c 102 g 140 t		
ORIGIN			
Query Match	10.9%; Score 301.4; DB 45; Length 525;		
Best Local Similarity	75.5%; Pred. No. 2e-61;		
Matches 443; Conservative 0; Mismatches 31; Indels 113; Gaps 1;			
Y 1944	tcgtctcgtcgtcgaacccctcttctctcgttggttgcacatctctcctcgtcgtgaca	2003	
Db 52	ttctctgtgcgcnacacccctcttctctcgttggttgcacatctctcctcgtcgtgaca	111	
OY 2004	atcgcctctctcaacacgtgcatatcttcaagttttctacaaggtgcgcacattctac	2063	
Db 112	atccccctcttccacactgctatcttcttcaagttttctacaaggtgcgcacattctac	171	
OY 2064	gtacactggcccaaaacacatgctacagttcatctgcatgttaagctccacagttcat	2123	
Db 172	cacactttggcccaaaacacatgctacagttcatctgcatgttaagctccacagttcat	231	
OY 2124	ttgctcatctgctcatcatgctgttctaagttagaccaccaagaccaccaaggaataacag	2183	
Db 232	ttgttctctctgtctca-----	248	
OY 2184	cgtctcccccacatctgtatctctcgaagtcacaagaggtcaaacctcgttagctctctgtg	2243	
Db 248	-----	248	

FEATURES	Source
Journal Comment	Unpublished (1997) On Dec 20, 1995 this sequence version replaced gi:1130951. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400p from Glibco High quality sequence stop: 468.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens
Reference Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 562) NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/nciccap">http://www.ncbi.nlm.nih.gov/nciccap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
Definition	Unpublished (1997)
LOCUS	AI742401 562 bp mRNA EST 21-JUN-1999
Definition	wg00e02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367578 3 similar to TR:093537 093537 PUTATIVE ODORANT RECEPTOR ; mRNA sequence.
Accession	AI742401
Version	AI742401.1
Keywords	EST.
Source	human.
Organism	Homo sapiens</







## COMMENT

On Jan 14, 1998 this sequence version replaced g1:1979381.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrip/image/image.html

## FEATURES

## Source

Possible reversed clone: similarity on wrong strand  
 Insert length: 878 Std Error: 0.00  
 Seq primer: 40ml3 fwd. ET from Amersham  
 High quality sequence stop: 223.

Location/Qualifiers  
 1. 496  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:193866"  
 /clone\_lib="Soares\_testis\_NHT"  
 /sex="male"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech  
 Laboratories, Inc., and primed with a Not I - oligo(dT)  
 primer [5'  
 TGTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3']  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization to Cot5, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 102 a 145 c 148 g 100 t 1 others  
 ORIGIN

## Query Match

Best Local Similarity 7.7%; Score 212.8; DB 39; Length 496;  
 Matches 331; Conservative 0; Mismatches 123; Indels 5; Gaps 4;

2262 ctctctccatcagtaacctgctgctgagctgagctgtaagaaactgcagaaactat 2321  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 493 CTCCTTCCATCAGTGCCTTCCCTGCAGCTACCTGGTAGACTTGCAGAACTAC 434  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2322 aatgaagccaatgtgtaacctgaacctgctcctcaacttgatcttgatcgcttc 2381  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 433 AACGAGGCCAAATGTGTACCTTCAGCCTGTCTTCAAAATTCGTCTGTGATGCTTC 374  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2382 ttcaaccagcagcagcattctccagcagcagcagcagcagcagcagcagcagcagc 2441  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 373 TTCACACGGCCAGGTCTTACGAGGGAAGTA-ANCCTTGGGCCAACATGATGTC-TGG 316  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2442 ctgaccacactgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2501  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 315 CTAGACAGCCTGAGCAGCGGCTTGGTGGATTTTCTGCTAAGTGTCTACGATATCTTC 256  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2502 tggcgcgcagaaactcaaaacacacttccagcagcagcagcagcagcagcagcagcagcagc 2561  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 255 TGGCGGCCAAGCTCAACAGCAGACAGACACTTCCAGGCTTCATTCAGAGACTACAGAGG 196  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2562 cgcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2621  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 195 GCGCGCGCTCCACCTGACAGTGGTGCAGAGGCAAC--GCTGGCAGCTTCTCTGCC 138  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2622 tgcgtgaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2681  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 137 TGAAGGTGGAAGTGCAGAGCGCGGGGGGTGTCCGGGAGAGTCTTTGGG-CATCCGGGTCT 79  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2682 cagctacgataagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2720  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 78 GGGGTTGGACGTGTAGCGCCTGGAGAGCCTAGACCA 40

## RESULT 6

LOCUS W18663 247 bp mRNA EST 10-SEP-1996  
 DEFINITION mb98401.r1 Soares mouse p3NNF19.5 Mus musculus CDNA clone  
 IMAGE:337441 5', mRNA sequence.  
 W18663  
 ACCESSION W18663.1 GI:1294371  
 VERSION EST.  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 247)  
 Maira,N., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.

THE WASHU-HMT MOUSE EST PROJECT  
 Unpublished (1996)  
 On May 9, 1995 this sequence version replaced g1:802427.  
 Contact: Maira N/Mouse EST Project  
 WashU-HMT Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:218841  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 225.

## FEATURES

## Source

Location/Qualifiers

1. 247

/organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:337441"  
 /clone\_lib="Soares mouse p3NNF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Vector: pT73D (Pharmacia) with a modified  
 polylinker; Site\_1: Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGGCCCAATTTTTTTTTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 44 a 89 c 42 g 72 t

## ORIGIN

Query Match 6.3%; Score 175.6; DB 26; Length 247;  
 Best Local Similarity 92.9%; Pred. No. 1.2e-31;  
 Matches 184; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

1944 tgccttgctgcgtcagccctctctctctcgtgggttgcacatctctctctcgcgcagca 2003  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 46 TTCTTGCTGGCTACAGCCCTCTTCTCTGCGTTTGGCCATTTCTCTCTCTGTGACA 105  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2004 atccgcctctccaacacgctcctcagcttccacagagtgccacacatctac 2063  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 106 ATCCGCTCTTCCAACTGATGATCACTTCAAGTTTCTTACCAAGGTACCCACATTTTAA 165  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2064 cgtacctggcccaaaacatggtgcaagtcatactcgtcatctcagctcacaagctcat 2123  
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[illegible]

Contact: Yoshinide Hayashizaki  
Genome Exploration Research Group, Life Science Tsukuba Center,  
Genome Science Laboratory  
The Institute of Physical and Chemical Research (RIKEN), Genomic  
Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel.: +81-298-36-9013  
Fax: +81-298-36-9098  
Email: genome-res@rtc.riken.go.jp,  
URL: <http://genome.rtc.riken.go.jp/>  
Sasaki, N., Izawa, M., Watabiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,  
Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and  
Hayashizaki, Y.  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. *Proc. Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998)  
Itoh, M., Kitsuina, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. *Genome Res.* 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

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FEATURES
SOURCE
    location/Qualifiers
    1. .260
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
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    (DH10B)"
    /sex="male"
    /tissue_type="testis"
    /dev_stage="adult"
    /lab_host="DH10B"
    /note="Site 1: SalI; Site 2: BamHI; cDNA library was
    prepared and sequenced in Mouse Genome Encyclopedia
    Project of genome Exploration Research Group in Riken

```

Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']  
GAGAGAGAGATCTCGAGTTATTAATATATCCCCCCCCCCC 3']. cDNA was prepared by using trehalase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5']  
GAGAGAGAGATCTCGAGTTATTAATATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+ ) after bulk excision from LambdaFLC I. Cloning sites, 5' end: SalI, 3' end: BamHI."

Query Match	5.1%;	Score 140.6;	DB 71;	Length 260;
Best Local Similarity	74.5%;	Pred. No. 2.6e-23;		
Matches 193;	Conservative	0;	Mismatches 59;	Indels 7;
				Gaps 1
QY 2475	ttcccccacaaagtgtatgtatcttcttcgcggtccagaactcaacaatacaaacattt	2534		
DB 5	ttcttttcttaccttacctagatgtattttatcttctgtattttttattacttttaacagttt	64		
QY 2535	cagcgcctcatccagagactacacagagcgtctgcgacactctgtatccactgtgaagaagt	2594		
DB 65	cagcgttccatccatccagagactacacagagcgcgttcgacactctgtattcccttgcgtggtatt	124		
QY 2595	cagaacgggaagaagaacccctctctctctgtcgtgaagtgtgcggttccagtggggccgagag	2654		
DB 125	gagatnaggcagatn-----AGATnaggccttaaaagttgacgtggggccgagag	177		
QY 2655	cttgaagtgctctcggaagagctcccgacaaagcttaccatgtatataaagcacgaggaagaatcc	2714		
DB 178	cttgaagtgctctcggaagagatcaccacagcgcttgcgatgtattataacacacagaaagatcc	237		
QY 2715	agtgcataataaagacggaa	2733		
DB 238	agtgcataataaagacgtgaa	256		

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RESULT      8
AA937218/c

LOCUS
DEFINITION
AA937218      464 bp      mRNA      EST      09-JUN-1998
OK13f08.s1 Scarets_NSF_F8_9M_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:1507719 3' similar to SW:CCSR_HUMAN P41180 EXTRACELLULAR
CACIUM-SENSING RECEPTOR PRECURSOR ;, mRNA sequence.
AA937218
AA937218.1  GI:3095329
EST.

KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 464)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150441.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 1252 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 398.
location/Qualifiers
1..464
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES
SOURCE

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/clone="IMAGE:1507719"
/clone_lib="Soares_NSF_F8_9w_OT_PA_P1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clonesIDs: Soares NBH5F pool 1:
3059384-310919, 333208-325895 Soares NB2HP pool 1:
1450332-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HR8-9w pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
3041776-306311, 320136-332823, 325880-326563 Soares NBHOT
pool 1: 723370-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Boraldo."

```

Query Match	3.0%	Score 84.4	DB 40	Length 464
Best Local Similarity	57.6%	Pred No. 7.7e10		
Matches 151	Conservative 0	Mismatches 111	Indels 0	Gaps 0

Oy	526	tgatggagccttccctctgtagtgcctctgacacctaataagagcagagagtgtaactaagt	585
Db	281	TGCTGGGGCTTTCTACATTCCCAAGTCACTTATGCTCTCTCCAGCAGACTCCTCAGCA	222
Oy	566	ccaagcgaagltccccgctcttccctctcgtaacgtcccccagatgacacagtgtaag	645
Db	221	ACAAAGAAATCAATTAAGTCITTTCTCCGGAACATCCCAATGATGACACAGGCCACTG	162
Oy	646	tcaatgtagcaatctctgtagagagctttagtgtagtgatctcgtctatgttagcactag	705
Db	161	CCATGGCAGACATCATCCAGTATTTCCGCTGGAACTGGGTGGCACAATTGCAAGCTATG	102
Oy	706	gtgattaaagggacaagctgtgtgtatgcaagcgctggaagagctggtccctgccccgggacat	765
Db	101	ACGACTATGGCGCGCGGGGATGAGAAATCCGACGAGAAAGCTGAGAAAGGATATCT	42
Oy	766	ggctgcgcttcaagacatcgt	787
Db	41	GCATCGACTTCAGTGAATCAI	20

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RESULT 9
AM051287/c

LOCUS          AM051287          498 bp          mRNA          EST          20-SEP-1999
DEFINITION     WY3qig12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2555206 3' similar to SW:CAER_HUMAN P41180 EXTRACELLULAR
CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.
ACCESSION      AM051287
VERSION        AM051287.1  GI:5513557
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
               Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 498)
AUTHORS       NCICGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
               Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        On Dec 20, 1995 this sequence version replaced gi:1134450.
               Contact: Robert Strausberg, Ph.D.
               Tel: (301) 496-1550
               Email: Robert.Strausberg@nih.gov
               This clone is available royalty-free through LNL ; contact the
               IMAGE Consortium (Info@image.lnl.gov) for further information.
               Seq primer: -40UP from Gibco

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FEATURES
    source
        High quality sequence stp: 440.
            Location/Qualifiers
                1..498
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2555206"
                    /clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"
                    /lab_host="DH10B"
                    /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco R1;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer
in a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneids: Soares NBHSF pool 1:
309584-310919, 33208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HP8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-332823, 32680-326653 Soares NBHOR
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Boudreau."
222 a 119 c 135 g 121 t 1 others

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Query Match	3.0%	Score 94.4	DB 64	Length 498
Best Local Similarity	57.68	Pred. No. 8e-10		
Matches 151	Conservative	0	Mismatches 111	Indels 0
			Gaps	0

QY	526	ttgttggtgctcttccttcgtgtgccccctgtcaagctatgtgagcaagagagtggttactacgtg	565
Db	281	tctcttgggcctctttctactatttccccagctcatgtatgcttctctccagagactccttcagca	222
QY	586	ccaagcgcgaagttccgcgtcttcttccttcgtacgctcccaagtgaaacgcagtcagtgag	545
Db	221	acaaatgaatcatttatcagctcttctccgaacacatcccacattgatgacacacagccactg	162
QY	646	tcatgtgtcagctcctctgaaagcttttggtgtgtgatactcgtctattgtgcagctacg	705
Db	161	ccatggcagacatcattcagatatttccgctggaaactgggtggcacaattggcacgctcatg	102
QY	706	gtgattacgggcagctgtgtgtgtgcagcgctggaagagctgtgcccgtccccgggcaact	765
Db	101	acgactataggcgccggccgggattatgaatttccagaggaagcgtgacgaagaaggatattct	42
QY	756	ggctgcctctcaagacatgt	787
Db	41	gcattgacctcagtgaaactat	20

RESULT	10			
LOCUS	AO615201/c			
DEFINITION	AO615201	514 bp	DNA	GSS
ACCESSION	HS_5188_B2_C04_SRP61	RPCT-11	Human Male BAC Library	15-JUN-1999
VERSION	AO615201			
KEYWORDS	AO615201.1	GI:5076477		
SOURCE	GSS.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 514)			
AUTHORS	Malatras,G.C., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Kellee,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.			
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome			
JOURNAL	Proc. Natl. Acad. Sci. U. S. A.	96 (17),	9739-9744	(1999)
MEDLINE	99380589			



[illegible]

	sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.					
	No s1 sequence available.					
	This clone is available at the RZPD in Berlin.					
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059y Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.					
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	/dev_stage="adult"					
	/lab_host="DH10B"					
	/note="Vector: pSPori1; Site_1: NotI; Site_2: SalI"					
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ORIGIN	169 t 2 others					
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Best Local Similarity	47.3%; Pred. No. 4.9e-06;					
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OY	1869	tctccatagctgggtttcccgtgcgcgaagttagcttctaagcttcttcgtcgagg	1928			
Dd	79	TACATCTGTGGTGGTGTGTCTTCTCTGTACTGTGATACCTTATCTTATTTCACA	138			
OY	1939	ccccaggtgccgcgtgtctgtcgtcgtcacgcccctcttctcctggyltgcattc	1988			
Dd	139	CCATCCAGGGAGTGTACTTACGAGCGCTGTGGACACTGCTTCTCTGTCTGC	198			
OY	1989	ctctccgtctgtaaatccgcctctctccaacttgtatcatcttc-aagttttacc	2047			
Dd	199	TACTTAGCCCCCTGCTCACCAAGAACCCGATTGACGGATTTGGTGGGCGCGGAG	258			
OY	2048	ggtgcccaattctaccgttacccgtgcgcgaaccaacaatgtgcaggtcatactgt	2107			
Dd	259	GGTGCGCCAGGGCGCACGCTTATCATGCTCTGCTCAG-----GTGGCATCTGCTGC	314			
OY	2108	cagctccaggttccattgtctcatctgtctacatgtctgttaatgtggaaccacg	2167			
Dd	315	ACTTATCTCGGGCCACAGCTGCTCATCGTGGCTGCTGCTGTGAAGGACCGCGAC	374			
OY	2168	caccaaggaataacagcgtctcccccatctgtgtatcttcgaagtgcagaagtt	2227			
Dd	375	AGGCAAGAGAGACACCCCCTCCAMAGGGGGAGGTGTGACATCGCCCTGCACACCGGA	434			
OY	2228	tgttggtctctgtgtgtgtctttaaccacaacatctccctctcatcagtaactgt	2287			
Dd	435	TGCAAGTATGTTGGGCTGCTGCTGCTTACATATGTGCTCTTCATCGCGCTTGAC	494			
OY	2288	cagctacctgtgtgaagaactgtccagagaactaataagaacaaatgtgtcactit	2347			
Dd	495	TGCTTCAAAGCTGCGAAGTGGCCCGAAAACTTCACACGAGGCGCAAGTTCAT	554			
OY	2348	ctgtctaccactgttatctgtatctgcgtcttaccat	2389			
Dd	555	CATGACACCCACTGCATCATCTGCTGGCATCTCGCCCAT	596			
RESULT 12						
AM015382						
LOCUS	AM015382	442 bp	mRNA	EST	10-SEP-1999	
DEFINITION	UI-H-BIO-aat-d-06-0-TI.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone					
IMAGE	IMAGE:22710331 3', mRNA sequence.					
ACCESSION	AM015382					
VERSION	AM015382.1 GI:5864139					
KEYWORDS	EST.					



**SOURCE** human.  
**ORGANISM** Homo sapiens  
**REFERENCE** Eukariota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia; Eutheria: Primates: Catarrhini: Hominoidea: Homo.  
**AUTHORS** 1 (bases 1 to 442)  
**TITLE** NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**JOURNAL** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**COMMENT** Unpublished (1997)  
On May 18, 1998 this sequence version replaced gi:3138688.  
**CONTACT** Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Oligo-dt track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA library preparation: M.B. Soares lab clone distribution: NC1-CGAP clone distribution  
Information can be found through the I.M.A.G.E.T. Consortium/LLNL at: [www-bio.llnl.gov/bdrip/image/image.html](http://www-bio.llnl.gov/bdrip/image/image.html)  
Seq primer: M13 Forward  
POLYA-No.

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1. .442
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/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI-CGAP_Sub1 library is a subtracted library derived from
BI. Bi constitutes a mixture of 21 normalized or
subtracted NCI-CGAP libraries: NCI-CGAP_Col1,
NCI-CGAP_Pr22, NCI-CGAP_Pr28, NCI-CGAP_Col10,
NCI-CGAP_Col16, NCI-CGAP_Kid5, NCI-CGAP_Kid12,
NCI-CGAP_Kid3, NCI-CGAP_Kid11, NCI-CGAP_Lym2,
NCI-CGAP_Pr2, NCI-CGAP_Co8, NCI-CGAP_Chl1, NCI-CGAP_Le12,
NCI-CGAP_Brn23, NCI-CGAP_Lu5, NCI-CGAP_Lu24,
NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_GC6, NCI-CGAP_Brn25.
These 21 libraries were pooled and a single-stranded DNA
preparation of the resulting mixture was used as a tracer
in a subtractive hybridization with a driver whose
composition is detailed below: NCI-CGAP_Kid1 pool 1 L1AM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids
1332376-1323911, 1456008-1456775, 1500552-1502855)
NCI-CGAP_Kid5 pool 1 L1AM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clonoids 1323912-132531, 1471368-1472803,
1452104-1493255) NCI-CGAP_Lu5 pool 1 L1AM 3575-3582,
3681-3854 (IMAGE Clonoids 1414920-1417991,
1520904-1522439) NCI-CGAP_GC4 pool 1 L1AM 3164-3167,
3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,
1459064-1470983, 1475592-1476743) NCI-CGAP_Pr22 pool 1
L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids
985608-986759, 1101192-1101959, 1217928-1220615)
NCI-CGAP_Col10 pool 1 L1AM 2644-2653, 2871-2872 (IMAGE
Clonoids 1057416-1061235, 1145584-1145351) The resulting
subtracted library contained 530,000 recombinants.
Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.
TAG_LIB=NCI CGAP_Le12
TAG_T1TSUF=TelomYosarcoma
TAG_SEQ=AAATCG
118 a 97 c 127 g 100 t

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Query Match      2.13;  Score 58.6;  DB 63;  Length 442;
Best Local Similarity 47.08;  Pred. No. 0.001;
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OY 534 ccttcacgaagcccccgtcagctcatatgagcaagacacgctggtactcagctgccaagcgc 593
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Db	11	CTTTCAACCACTACCTCAGATTGCTTACTCAGACCAACCATCATGATCTTAGTGACAAAGCT	70
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QY	654	cagctgcctgcagagattttgggtgggtgtgtgaattcttcgtcatatggcagcctaegtgatattac	713
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QY	714	ggcgacgtcggtgtgtgcaggcgctggagagctgtgscgtggcccggggagatctgtgtgcc	773
Db	191	GGAGAAATGGGATGGAAGGCTTCAAAGATATGTACAGGAAAGAAAGGATTTGCATGGCC	250
QY	774	ttaagagacatcgtgtcccttctctgcgcgggtgtgtgtaccggaagatgcagacatgagt	833
Db	251	CACCTTTACAAATCTACAGTAAATGCAAGGGAGGACAGACTTGAATAGCTCTGAAAGAG	310
QY	834	cagcatctgtgctcaaggccagagaccagtcgtgtttgtgtctctcttaacgagcaccttgct	893
Db	311	CTCACAACTCATCTTGCCCAAGGCCCGGGTGTGTGGCTACTTCTGTGAGGGCATGACGGTG	370
QY	894	agagtgctcttcacaggtccgtgtgtc	918
Db	371	AGAGGCTGCTGATGGCCATGAGGC	395

## RESULT 13

LOCUS	AI657897	573 bp	MRNA	EST	06-MAY-1999
DEFINITION	fc44h06.y1 zebrafish WASHU MDIMG EST cDNA 5' similar to SM-CAR RAT P48442 EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR				
	; mRNA sequence.				

ACCESSION	AI657897	
VERSION	AI657897.1	GI:4755565
KEYWORDS	EST.	

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Rasbora; Danio.

## REFERENCE AUTHORS

Eddy, S., Hallier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Seepco, M., Theising, B., Allen, K., Ewers, Y.,  
 Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R.,  
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R. and Wilson, R.  
 TITLE  
 JOURNAL  
 Mashu Zebrafish EST Project 1998  
 Unpublished (1998)  
 COMMENT  
 On Jun5, 1998 this sequence version replaced gi:3189663.

Other-ESTs: tcl4h06.x1  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbradish@watson.wustl.edu  
cDNA Library Preparation: Matthew Clark, cDNA Library Arrayed by:  
Matthew Clark, DNA Sequencing by: Washington University Genome  
Sequencing Center Clone distribution: Genome Systems, St. Louis,  
Missouri (web address: [www.genomesystems.com](http://www.genomesystems.com)) (email contact:  
[info@genomesystems.com](mailto:info@genomesystems.com)) and Research Genetics, Huntsville, Alabama  
(web address: [www.resgen.com](http://www.resgen.com)) (email contact: [info@resgen.com](mailto:info@resgen.com)) and  
Ressourcenzentrum rump1: primdatenbank, Berlin, Germany (web address:  
[www.rzpd.de](http://www.rzpd.de))  
Seq primer: T3 ET from Amersham  
High quality sequence stop: 460.

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Db 141 CGGAATCTTTGCCATCTAGGCTCTGACCTAGGACTGCTGGCTGCATCTATGCACCCA 200
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OY 2485 agtctatgctatctctcgcgcgtccagaaactcaacaatcacagaacactt 2533
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Db 201 AGTCTATATATAATTCTCATGANTCAGAAAAGAACACAAAGGAAACACTT 249
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Search completed: March 18, 2000, 10:28:08  
Job time: 2293 sec







\*\*\*\*\*  
 W E S E H  
 \*\*\*\*\* (TM)

Release 3.1A John F. Collins, BioComputing Research Unit.  
 Copyright (c) 1993-1998 University of Edinburgh, U.K.  
 Distribution rights by Oxford Molecular Ltd

Msrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:05:22 2000; Maspar time 113.50 Seconds

Tabular output not generated. 513.137 Million cell updates/sec

Title: >US-09-361-652-1  
 Description: (1-840) from US09361652.pep  
 Perfect Score: 6338

Sequence: 1 MLFWAHLHLISLQLYVCWAF.....NTEHFQASIDYTRCGCT 840

Scoring table: PAM 150  
 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: splrembl12  
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 52.670; Variance 98.786; scale 0.533

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	6338	100.0	840 11	Q920R8	POTATIVE TASTE RECEPTO	0.00e+00
2	2083	32.9	843 11	Q920R7	POTATIVE TASTE RECEPTO	0.00e+00
3	1455	23.0	868 13	Q73636	PEROMONE RECEPTOR.	3.64e-282
4	1422	22.4	848 13	Q93553	POTATIVE ODORANT RECEPTOR	8.57e-275
5	1385	21.9	864 13	Q73637	PEROMONE RECEPTOR.	1.55e-266
6	1371	21.6	940 13	Q73635	CALCIUM2+ SENSING RECEPTOR	2.06e-263
7	1339	21.1	880 13	Q93539	PEROMONE RECEPTOR.	2.79e-256
8	1295	20.4	844 13	Q93552	POTATIVE ODORANT RECEPTOR	1.74e-245
9	1218	19.2	856 13	Q73638	PEROMONE RECEPTOR.	2.25e-229
10	1192	18.8	875 13	Q73640	PEROMONE RECEPTOR.	1.31e-223
11	1170	18.5	912 11	Q70410	POTATIVE PHEROMONE RECEPTOR	9.87e-219
12	1073	16.9	835 11	Q70409	POTATIVE PHEROMONE RECEPTOR	2.75e-197
13	972	15.3	779 11	Q93269	POTATIVE PHEROMONE RECEPTOR	4.63e-175
14	878	13.9	458 13	Q93555	POTATIVE ODORANT RECEPTOR	1.73e-154
15	844	13.3	850 11	Q93189	POTATIVE PHEROMONE RECEPTOR	4.44e-147
16	830	13.1	983 11	Q62915	METABOTROPIC GLUTAMATE RECEPTOR	4.93e-144
17	827	13.0	408 13	Q93558	POTATIVE ODORANT RECEPTOR	2.21e-143
18	808	12.7	866 11	Q93268	POTATIVE PHEROMONE RECEPTOR	2.97e-139
19	799	12.6	908 4	Q95945	METABOTROPIC GLUTAMATE RECEPTOR	2.66e-137
20	795	12.5	803 11	Q95191	POTATIVE PHEROMONE RECEPTOR	1.96e-136

21	755	11.9	667 11	Q95267	POTATIVE PHEROMONE RECEPTOR	8.88e-128
22	746	11.8	429 11	Q70413	POTATIVE PHEROMONE RECEPTOR	7.80e-126
23	718	11.3	350 13	Q93556	POTATIVE ODORANT RECEPTOR	8.45e-120
24	707	11.2	548 11	Q93265	POTATIVE PHEROMONE RECEPTOR	1.96e-117
25	694	10.9	864 11	Q93195	POTATIVE PHEROMONE RECEPTOR	1.22e-114
26	687	10.8	652 11	Q93192	POTATIVE PHEROMONE RECEPTOR	3.87e-113
27	681	10.7	768 11	Q93266	POTATIVE PHEROMONE RECEPTOR	7.48e-112
28	672	10.6	604 11	Q93194	POTATIVE PHEROMONE RECEPTOR	6.34e-110
29	672	10.6	695 11	Q93272	POTATIVE PHEROMONE RECEPTOR	6.34e-110
30	652	10.3	723 11	Q93193	POTATIVE PHEROMONE RECEPTOR	1.20e-105
31	625	9.9	339 11	Q70411	POTATIVE PHEROMONE RECEPTOR	6.84e-100
32	566	8.9	808 11	Q93190	POTATIVE PHEROMONE RECEPTOR	2.16e-87
33	567	8.9	1267 5	Q93564	FSY...4 PROTEIN.	1.33e-87
34	533	8.4	250 13	Q73647	CALCIUM SENSING RECEPTOR	1.87e-80
35	518	8.2	311 11	Q93633	CALCIUM SENSING RECEPTOR	2.57e-77
36	514	8.1	251 13	Q73652	PEROMONE RECEPTOR (FR)	1.76e-76
37	515	8.1	301 11	Q93564	CALCIUM SENSING RECEPTOR	1.09e-76
38	508	8.0	251 13	Q73655	PEROMONE RECEPTOR (FR)	3.15e-75
39	504	8.0	251 13	Q73654	PEROMONE RECEPTOR (FR)	2.15e-74
40	499	7.9	250 13	Q73645	PEROMONE RECEPTOR (FR)	2.36e-73
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43	488	7.7	250 13	Q73649	PEROMONE RECEPTOR (FR)	4.56e-71
44	488	7.7	250 13	Q73646	PEROMONE RECEPTOR (FR)	4.56e-71
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## ALIGNMENTS

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AC Q920R8;				
DT 01-MAY-1999 (TEMBREL. 10, Created)				
DT 01-MAY-1999 (TEMBREL. 10, last sequence update)				
DE 01-MAY-1999 (TEMBREL. 10, last annotation update)				
DE POTATIVE TASTE RECEPTOR TR1 (FRAGMENT).				
OS Rattus norvegicus (Rat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
RN (1)				
RP SEQUENCE FROM N.A.				
RC STRAIN-MISTAR;				
RX MEDLINE: 99159821.				
RA HOON M.A., ADLER E., LINDEMEIER J., BATTLEY J.F., RYBA N.J.P.,				
RA ZUKER C.S.,				
RT "Putative mammalian taste receptors: a class of taste-specific GPCRs				
RT with distinct topographic selectivity."				
RL Cell 96:541-551(1999).				
DR EMBL: AF127389; AAD18069.1; -				
KW Receptor.				
FT NON_TER.	840			
SQ SEQUENCE	840 AA; 93496 MM; B1F5F564 CRC32;			
Query Match	100.0%; Score 6338; DB 11; Length 840;			
Best Local Similarity	100.0%; Pred. No. 0.00e+00;			
Matches	840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	1 XLFWAHLISLQLYVCWAFSCPTSSPGSLP35FLAGSLSGDCIQVHRRLVTS 60			
QY	1 MLFWAHLISLQLYVCWAFSCPTSSPGSLP35FLAGSLSGDCIQVHRRLVTS 60			
Db	61 CDRPDSNGHGVLFPAMRTVEINSSALPNTILGVLVVCESASAVVATIRVAL 120			
QY	61 CDRPDSNGHGVLFPAMRTVEINSSALPNTILGVLVVCESASAVVATIRVAL 120			
Db	121 QGPRHIEIQDLRNHSSKVAFAFGPNTD2AVTTAALGFLMPLVSEASSVLSAKRR 180			
QY	121 QGPRHIEIQDLRNHSSKVAFAFGPNTD2AVTTAALGFLMPLVSEASSVLSAKRR 180			
Db	181 FPFELRIVPSDRHQVEVMVQLOSFGWVSLIGSGIDGVLQVLALELAVRGICVAF 240			
QY	181 FPFELRIVPSDRHQVEVMVQLOSFGWVSLIGSGIDGVLQVLALELAVRGICVAF 240			



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Db 241 KDIVPSARVGDPRMOSMHOHLAARTVYVVSNRHLARVFRSVLANLTGKVMASE 300
Oy 241 KDIVPSARVGDPRMOSMHOHLAARTVYVVSNRHLARVFRSVLANLTGKVMASE 300
Db 301 DVAISITVSYNGIGIGIVLCVAVOQROVPGLKEFEESYRAVYAAASACPEGSWSTN 360
Oy 301 DVAISITVSYNGIGIGIVLCVAVOQROVPGLKEFEESYRAVYAAASACPEGSWSTN 360
Db 361 QLCRECHTFTTRNMPITLAFSMAARYEAVYANABHLLHLLCTSEICSGPVPMOL 420
Oy 361 QLCRECHTFTTRNMPITLAFSMAARYEAVYANABHLLHLLCTSEICSGPVPMOL 420
Db 421 LOOIYKVFLLHENTVAADDNDGLGYDIIAMDNGPEMTFEIIGSASLSPVHLINKT 480
Oy 421 LOOIYKVFLLHENTVAADDNDGLGYDIIAMDNGPEMTFEIIGSASLSPVHLINKT 480
Db 481 KIOHGNKNQVPSVCTTDCLAGHRRVYVSHHCCFECVCEAGTFLNMSLHICOPCGT 540
Oy 481 KIOHGNKNQVPSVCTTDCLAGHRRVYVSHHCCFECVCEAGTFLNMSLHICOPCGT 540
Db 541 EEMAPKESTCEPRTVEFLAMHEPISLVLIANTLLLLVGTAGLFAVHFRTPVVRSG 600
Oy 541 EEMAPKESTCEPRTVEFLAMHEPISLVLIANTLLLLVGTAGLFAVHFRTPVVRSG 600
Db 601 GRCLFELMGLSVAGSCSFYFSGEPYPAQLLQPLFSLGFAITLSCLTIRSFOLVIFK 660
Oy 601 GRCLFELMGLSVAGSCSFYFSGEPYPAQLLQPLFSLGFAITLSCLTIRSFOLVIFK 660
Db 661 FSTRKVPFTYTAQNHGAGLFTVIVSSTVHLICLTWLVMTPRPTREXORPHVILCT 720
Oy 661 FSTRKVPFTYTAQNHGAGLFTVIVSSTVHLICLTWLVMTPRPTREXORPHVILCT 720
Db 721 EVNSVGFLLAFTHNLLISTFVCSYLKELPENNEAKCVTFSLLFVSMIAFTVMS 780
Oy 721 EVNSVGFLLAFTHNLLISTFVCSYLKELPENNEAKCVTFSLLFVSMIAFTVMS 780
Db 781 IYOGSTLPAVNVLAGLITLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRKCGTT 840
Oy 781 IYOGSTLPAVNVLAGLITLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRKCGTT 840

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RESULT 2
ID Q9ZOR7 PRELIMINARY: PRT: 843 AA.
AC Q9ZOR7:
DT 01-MAY-1999 (TREMUREL. 10, Created)
DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)
DT 01-MAY-1999 (TREMUREL. 10, Last annotation update)
DE PUTATIVE TASTE RECEPTOR TR2 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR;
RX MEDLINE: 99159821.
RA HOON M.A., ADLER E., LINDEMEIER J., BATTERY J.F., RYBA N.J.P.,
RA ZUKER C.S.;
RT "Putative mammalian taste receptors: a class of taste-specific GPCRs
RT with distinct topographic selectivity.";
RL Cell 96:541-551(1999).
DR EMBL: AF127390; AAD18070.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 843 AA; 95799 MW; 680A9EE CRC32;

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Query Match 32.9%; Score 2083; DB 11; Length 843;

Best Local Similarity 39.6%; Pred. No. 0.00e+00;

Matches 326; Conservative 188; Mismatches 286; Indels 24; Gaps 22;

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Db 27 NSDFHLADYLLGGLFTLHANYKSISHLYOYPCNLF-TMKYLVGINQAMRFAVEEI 85
Oy 27 NSDFHLADYLLGGLFTLHANYKSISHLYOYPCNLF-TMKYLVGINQAMRFAVEEI 85

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Db 86 NNCSSLPLGVLGYEMVVCYLSNNIHPLGYFLA-QDDDLPLIKDYQYPRVAVIGP 144
Oy 86 NNCSSLPLGVLGYEMVVCYLSNNIHPLGYFLA-QDDDLPLIKDYQYPRVAVIGP 144
Db 145 DMSSEATVNSNLHFLIPOLITSAISDKLDRKHFFSMRTVPSATHTHTEAMVLMVHF 204
Oy 145 DMSSEATVNSNLHFLIPOLITSAISDKLDRKHFFSMRTVPSATHTHTEAMVLMVHF 204
Db 146 DMTDAVATTAALGFLPLVYSASSVSLAKKRFPSFLRTVPSDRHQEVAVOLLQSF 205
Oy 146 DMTDAVATTAALGFLPLVYSASSVSLAKKRFPSFLRTVPSDRHQEVAVOLLQSF 205
Db 205 QMNNVIVLVSDDYGRENSHLISQRLTKTSIDICAFQEVLPJEPSSVYMSSEQRLDNI 264
Oy 205 QMNNVIVLVSDDYGRENSHLISQRLTKTSIDICAFQEVLPJEPSSVYMSSEQRLDNI 264
Db 266 GVMWISLIGSYGDYGOGLVQALBE-LAVPRGICVAFADIVP--SARV-GD-PR-MQSM 258
Oy 266 GVMWISLIGSYGDYGOGLVQALBE-LAVPRGICVAFADIVP--SARV-GD-PR-MQSM 258
Db 265 LDKLRRTSARVYVES-PELSYFHEHEVLRNMTGFVJASMSMAIDVYLHNLTEHRT 323
Oy 265 LDKLRRTSARVYVES-PELSYFHEHEVLRNMTGFVJASMSMAIDVYLHNLTEHRT 323
Db 259 MOHLAARTVYVVSNRHLAR-VFERSVLANLTGKVMASDVAISITVSYNGIGI 317
Oy 259 MOHLAARTVYVVSNRHLAR-VFERSVLANLTGKVMASDVAISITVSYNGIGI 317
Db 324 GTFLGVTIQRVSLPFSQFRNRDRKGYVPVNT-TN-LTTTCNOCDACLN-TTSPNNI 380
Oy 324 GTFLGVTIQRVSLPFSQFRNRDRKGYVPVNT-TN-LTTTCNOCDACLN-TTSPNNI 380
Db 318 GTVGAVAVOORVPGLEKEFEESYRAVYAAASACPEGSWSTNQLCRECHTFTTRNMTL 377
Oy 318 GTVGAVAVOORVPGLEKEFEESYRAVYAAASACPEGSWSTNQLCRECHTFTTRNMTL 377
Db 381 LILGERVYVSYSAYYAAVAHALHLLGCNVRCTKQKYVPQMLREIWHVFTLGNRL 440
Oy 381 LILGERVYVSYSAYYAAVAHALHLLGCNVRCTKQKYVPQMLREIWHVFTLGNRL 440
Db 378 GABS-MSAAYRYEAVYAAVAHGLHLLGCTSEICSGRGPYPQLQIYKVFLLHENTV 436
Oy 378 GABS-MSAAYRYEAVYAAVAHGLHLLGCTSEICSGRGPYPQLQIYKVFLLHENTV 436
Db 441 FPDQGDMPMLDIIQWMDLSQNPFOSTASYSPTSKRL-TYINNVSYTPNNTVPSMC 499
Oy 441 FPDQGDMPMLDIIQWMDLSQNPFOSTASYSPTSKRL-TYINNVSYTPNNTVPSMC 499
Db 437 AFDDNGDGLGYDIIAMDNGPEMTFEIIGSASLSPVHLINKTIOHGNKNQVPSVC 496
Oy 437 AFDDNGDGLGYDIIAMDNGPEMTFEIIGSASLSPVHLINKTIOHGNKNQVPSVC 496
Db 500 SKSCOPGOMKKSGLHPCFCECLDMPGTIYNRSADENCLSCPSGMSYKNDITGFOR 559
Oy 500 SKSCOPGOMKKSGLHPCFCECLDMPGTIYNRSADENCLSCPSGMSYKNDITGFOR 559
Db 497 TTDCLAGHRRVYVSHHCCFECVCEAGTFLNMSLH-COPCGEEMAPKESTCEPRT 555
Oy 497 TTDCLAGHRRVYVSHHCCFECVCEAGTFLNMSLH-COPCGEEMAPKESTCEPRT 555
Db 560 PTFLEHVEPTIVVAILAALGFESTALITF-MRHOTPVRRSAGDPCFVLVPLLA 618
Oy 560 PTFLEHVEPTIVVAILAALGFESTALITF-MRHOTPVRRSAGDPCFVLVPLLA 618
Db 556 VEFLLAMHEPISLVLIANTLLLLVGTAGLFAVHFRTPVVRSGRLFLMGLSVAG 614
Oy 556 VEFLLAMHEPISLVLIANTLLLLVGTAGLFAVHFRTPVVRSGRLFLMGLSVAG 614
Db 619 FGAVPVYGPPTVEFCFROAFVTCISLCTITVVSFOIVCFKMARLPASVPMR 678
Oy 619 FGAVPVYGPPTVEFCFROAFVTCISLCTITVVSFOIVCFKMARLPASVPMR 678
Db 615 SCFSYFSGEPYPAQLLQPLFSLGFAITLSCLTIRSFOLVILFKSTVPFTYTAQNH 674
Oy 615 SCFSYFSGEPYPAQLLQPLFSLGFAITLSCLTIRSFOLVILFKSTVPFTYTAQNH 674
Db 679 YHGPVYVAFITAKVALVGVNMLATINPLGRDPPDPMILSCHPNRNLGNTSM 738
Oy 679 YHGPVYVAFITAKVALVGVNMLATINPLGRDPPDPMILSCHPNRNLGNTSM 738
Db 675 NHGAGLFTVIVSSTVHLICLTWLVMTPRPT-REYOREPVLVILECTEVNSVGFLLAFTH 733
Oy 675 NHGAGLFTVIVSSTVHLICLTWLVMTPRPT-REYOREPVLVILECTEVNSVGFLLAFTH 733
Db 739 DLLSYLGSFSAVNGKELPNYNEAKVITLSMTFSTSSISLCTFMSVHDVGLVTIMDL 798
Oy 739 DLLSYLGSFSAVNGKELPNYNEAKVITLSMTFSTSSISLCTFMSVHDVGLVTIMDL 798
Db 734 NILLSITFVCSYLKELPENNEAKCVTFSLLFVSMIAFTVMSIAFTVMS 793
Oy 734 NILLSITFVCSYLKELPENNEAKCVTFSLLFVSMIAFTVMSIAFTVMS 793
Db 799 VTVNLFLAIGL-GYFGPKCYMILFEYPERNTSAFNSMIGCYMR 841
Oy 799 VTVNLFLAIGL-GYFGPKCYMILFEYPERNTSAFNSMIGCYMR 841
Db 794 AG-LTTLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRR 836
Oy 794 AG-LTTLISGFSGYFLPKCVIILCRELNNTEHFOASIDYTRR 836

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RESULT 3
ID 073636 PRELIMINARY: PRT: 868 AA.
AC 073636:
DT 01-AUG-1998 (TREMUREL. 07, Created)
DT 01-AUG-1998 (TREMUREL. 07, Last sequence update)
DT 01-NOV-1999 (TREMUREL. 12, Last annotation update)
DE PHEROMONE RECEPTOR.
OS CA02.1.
OC Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 98226788.
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,
RA NAKANISHI S., BRENNER S.;
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
RT Fugu.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

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Db 749 VIGYIGLALICFLAFLARLPDNEAKEITFSMLI-FCAYWIAFIPAYVSSPGKFTV 807  
Y 730 AFTHNILLISTFVCSYGLKEPBNENKACVTFSLINFS-WIAFTMASTYQGYLP 788  
Db 808 AVEVFAILASTYGMLEFIFPKCYIILKPKDKSKKL 845  
Y 789 AVNVLAGLTLISGSGYFLPKCYIILCPRELNTEHF 826

RESULT 5  
ID 073637 PRELIMINARY; PRT; 864 AA.  
AC 073637; 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE PHEROMONE RECEPTOR.  
GN CA09.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 98226788.  
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,  
RA NAKANISHI S., BRENNER S.;  
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in  
RT Fugu.";  
RT Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).  
DR EMBL; AB008859; BAA26124.1; -.  
DR PFAM; PF00003; 7tm\_3; 1.  
DR PFAM; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
KW Pheromone.  
SQ SEQUENCE 864 AA; 96216 MW; E26A0114 CRC32;

Query Match 21.9%; Score 1385; DB 13; Length 864;  
Best Local Similarity 30.5%; Pred. No. 1.55e-266;  
Matches 250; Conservative 227; Mismatches 299; Indels 45; Gaps 35;

Db 44 PGVLLGLGFLQVYVSSV-FPEWTFSEPHOPVCTRPDILGFRIAMTAFVQELINKNPD 102  
Y 34 PGVLLGLGFLSLHGDCQVRHRLVTVSCDRPD-S-FNGHGYHLFOARFVEEINNSSL 91  
Db 103 LPMITLIGLYRLDNCALVYFSGALALASQEBALOG-CAGSPVLYIVDSLTFT 161  
Y 92 LPMITLIGLYELDYDCSEBANYATLRYALALOGPRHIEQKLRHSSRYVAFIPDNDHA 151  
Db 162 IASASVGLYKIPMWSTFATCCLTNRQRPSEFRITPSDDFOVRAMITQILKHFMTWG 221  
Y 152 VTAAALGLPFLMLVSEYASVLSAKRKPSEFLRTVPDRHQVEVYVQLQSGFWYMS 211  
Db 222 LLYSDDDYGLHVARSPQSD-LYSGGOCCLAYLEVLPMDNLSNR-R-IYHVIKESTARY 278  
Y 212 LIISYDYGGLGVQALE-ELAVPRGI-CVAFKIVPESARVGPBMQSMQHLAQATTY 269  
Db 279 LMFVASHSHIHL-EEVYRQKTYGLQMLASEAMTGTTFLOTDEPMYLNGLTGLAIRG 337  
Y 270 VVVFNSR-HLARYFPRSVYLANLGKRWASSEDMAISTYITSTVGLIGTIVLGAVQQR 328  
Db 338 EITGLDFLLR-IRPOSSNNTSYDMVQFWEYSFOCKFSGASSAEACTDENIQVDAT 396  
Y 329 QVGLKEFESESYRAV-TAPASACP-EGSM-----CS-TNQLCRE-CHTF-TTRNMP- 376  
Db 397 FLDVSNLRPRYNYKAVYALALDMLQCEPGRGPRSSGSCADIKHLEWQVHYLQHY 426  
Y 377 -LGAFMSAAYRYEAHYAAHGLHLLGC-TS-E-ICS-R-GPVY---PMOQLQOYKYV 427  
Db 457 NETTTFGDOVSPDNGDVLPIYDILMOMLPDGRTOYQVNGEYKRSRGEELQIHEDI 516  
Y 428 NELLH-ENYVAFDNDGLTYDILAMDWNGPEMT-PEITGSASLSYVH---LDINKTKI 482  
Db 517 FWFESNKPVSHVCSSECPGTRMSRKGQPVCCFDCLLCSEGRKISNTDTSMECTSCPD 576

Y 483 QWHGKNNQVPAVSCYCTDCLAGHRRVYVSSH-CCEFCVCEAGTFLNSELHICQPCGE 541  
Db 577 FWSRPRDCHVCRKTEFLSYHEPGLICLTAASLGLVIVSVVGLFIHRRSPVYRANS 636  
Y 542 EWAHPKSTCCPRTVEELFAMHEPISLVLIANTLLELLVGTAGLFAMFHFPPVYSAAG 601  
Db 637 ELSFLLVSLKFLCFLCSLA-FIGRPRLMTQDRLHAFGIFVLCSCIVKTMVYLAVER 695  
Y 602 RUCFLMLGSL-VAGSCSFSEFGEPVPCLLRPLFSIGFAIFLSCLTIRSFOLYIIFK 660  
Y 661 FSTKVPTFFRTM-AQNHGAGLFLVIVSVTHLLICLTLMVMTPRPTREYQRPPLVILEC 719  
Db 755 VVSGTGFVNLSTYGLALISFLAFLARNLPDNEAKLTFSMLI-FCAYWIAFVPA 813  
Y 720 TEVNSVGFLLATFTHNLLISTFVCSYLQELPENENKCVTFSLINFS-WIAFTM 778  
Db 814 YINSPGYADAVEVFAILTSFGLVALFPGKCYIILFPE 854  
Y 779 ASYQSGYLPAVNVLAGLTLISGSGYFLPKCYIILCPRE 819

RESULT 6  
ID 073635 PRELIMINARY; PRT; 940 AA.  
AC 073635; 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE CALCIM2+ SENSING RECEPTOR.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 98226788.  
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,  
RA NAKANISHI S., BRENNER S.;  
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in  
RT Fugu.";  
RT Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).  
DR EMBL; AB008857; BAA26122.1; -.  
DR PFAM; PF00003; 7tm\_3; 1.  
DR PFAM; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
SQ SEQUENCE 940 AA; 105814 MW; 034CB09E CRC32;

Query Match 21.6%; Score 1371; DB 13; Length 940;  
Best Local Similarity 30.8%; Pred. No. 2.06e-263;  
Matches 256; Conservative 237; Mismatches 284; Indels 53; Gaps 35;

Db 29 MNGDILLGLFPIHNG-ISSKDNELAARPESTKCVRFNFRGFRWLQAVYFAIEEINSSS 87  
Y 33 LRGDFLLAGLFLSHGDCQVRHRLVTVSCDRPDS--FNGHGYHLFOARFVEEINNSSA 90  
Db 88 LPMITLIGRIIDTCNTVSKALEATLSEYAKQKIDSLNDEFNCNTDHTPAIAYVGAAG 147  
Y 91 LPMITLIGLYELDYDCSEBANY-ATLRYALALOGPRHIEQK--DLRNHSSKRYAATIGPON 147  
Db 148 SAVSTAVANLISLEVIPOSYASSSRLSNKQYSEMTIPTDEHQATAMADVIEYEPW 207  
Y 148 TDHAYTTALLGLPFLMPLVSYEASSVYLSAKKPFSELTFTVSDRHQVEVYVQLQSGFW 207  
Db 208 MWYIAYASDDYGRGPIEFKEKEKMERDICIHLNELI--SQYFDECEIKALVDRIENST 265  
Y 208 VMSILIGYGDYGLQGVQALELAVPRGICVAFKDIPEPSAVVGPBMQSMQHLAQART 267  
Db 266 KYIYVAFSPDIEPLIKENYRNITDRILWLAESANSSLLAKPEYLDVVBSTIGFVYKA 325  
Y 268 TVVVFNSRHLARVFFRSVYLANLGKRWASSEDMAISTYIT-S--VVGIOG-IGTVL-- 321











ID	AC	RESULT	PRELIMINARY:	PRT:	875 AA.
Db	663	AFIARPRGNTVFCG-VLQRTSVFACI--TLQVVICVLMTLTPRPHPHKATAKRRIT			739
Qy	660	KFTSTKVP--T-FYRMAONHGAFLFVIVSSVTHLLICTLVMVMTPRPREYQRFPLVI			716
Db	740	LECNIGSPVMVWVGVIGTLAVICFILAIFARKLDPDNEAKRTFTPSMLI-FCAAWTF			798
Qy	717	LECTVNSVGLLAFTHHLLISITFTSVSYGKELPEYNNAKCVTTSLLNEFS-WIAF			775
Db	799	IPAVVSPGKFTVAVEIFAIIASSFGLFCIFARCKVYLILPKPKNTKH			848
Qy	776	FTMASIVGGSYLPAAVNVLAGLTLTSGSGSYGFELPKCVYILCRPELNNTEH			825
RESULT	10				
ID	073640		PRELIMINARY:	PRT:	875 AA.
AC	073640:				
DT	01-AUG-1998 (TREMBLrel. 07, Created)				
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	PHEROMONE RECEPTOR.				
GN	CA15.1.				
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;				
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphi;				
OC	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 98226788.				
RA	NATO T., SATO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,				
RA	MAKANISHI S., BENNER S.,				
RT	'Putative pheromone receptors related to the Ca2+-sensing receptor in				
RT	Fugu'.				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).				
DR	EMBL: AB008862; BAA26127.1; .				
DR	PFAM: PF00003; 7tm_3: 1.				
DR	PFAM: PF01094; ANF_Receptor; 1.				
DR	PRINTS: PR00248; GPCRMR.				
DR	Phenome.				
SW	SEQUENCE 875 AA; 94934 MW; 8FC188F2 CRC32;				
Query Match	18.8%;	Score 1192;	DB 13;	Length 875;	
Best Local Similarity	29.4%;	Pred. No. 1,31e-223;			
Matches	251;	Conservative 221;	Mismatches 326;	Indels 55;	Gaps 44.
Db	30	ALTCQWSTPEEQHFCQGHVYVGGLEFNLAHYTPPDIANFQOSHAKACTGLENTPLQYI			89
Qy	19	AFSC-QR-TESPQSGSLDGLFLLAGLPSLHDDCQVRRR-PLVYSCDRPSDFNNGHLE			75
Db	90	YAMVAVEEINHSAALLPRVKLGHYHRSICALHPWTTOTALALVAGDSASCELATPADYS			149
Qy	76	QAMRTVEEINNSSLAPNITLGYELVYDVCESA-NVYATLRVALQOPR-HIDQDLR			133
Db	150	AETSEKKAASVPLDIGASSNAKILGT-LSPILSTYTAACCCLSDRHHYPTFFRTMA			208
Qy	134	NHSS--KYVAETIGPDNDHAATTA-ALLGPRLMP-VSEYASSVYLAKRRFPSEFLTPV			189
Db	209	SDIYAQALALVLEFNTMTIGAVYANDYGHVAKVQEOETOGKGYCLAVEFLQRETI			268
Qy	190	SDRHVEYMGVOLLQSGFWWVSLISGYSDYQOLGVQALEELAVRGICVAKRDLVPPSAR			249
Db	269	VADAVRAARTIQASTAR-VILVFSWYTDVGHLP-RQLQKINVTDROFLASEANSTSEVL			325
Qy	250	VGDPRMQSMOHLQARFTTVVYVES-NRHLARVFFRSVVALNTLGKVVASDEMAISTYI			308
Db	326	LKDPDTISVAGGVGVVALIASOHIGDFELGLMLPSLRSPSKFTQEFMEEFQCSPPSPS			385
Qy	309	TSVIGTIGIGT-VLGVAAYOOROVPLKEF--E-ESYVR-A--VTA--APS-AC-PGSGW			356
Db	386	SETSGDLNAASLPPCGASLEEGVQHPFDTSILRTVYVYLAIVAAANALSHLSCPIHN			445
Qy	357	CSTN-QL--C-RECHTFTT-RNMP-TLCAFS-MSAAVYVYLAIVAAVAGHLQHLIGC----			405
Db	446	SPSGTSHCTSPKGIITTELLQHLKSVNFTTPOGKHLLYFRGADIPAWYDLINWQ-SGTDGT			504

QY	406	T-SET	-CSRG	-PYPMQOLLOQIYKVFLELHENTVAFDDNGDGLGYDDIAMDNGEPWT	461		
Db	505	LQLVIGAVAGFQDLQNESEIEMGAXXNOYVSYSCSCDPTGRKARKGEPJLCCFDCIP	564	505	LQLVIGAVAGFQDLQNESEIEMGAXXNOYVSYSCSCDPTGRKARKGEPJLCCFDCIP		
QY	462	FEIISASLSVYHLDINKTKIOMHGKKNNOYVSYCTICDCLAGHRRVYV	GSHECCFECVP	520	462	FEIISASLSVYHLDINKTKIOMHGKKNNOYVSYCTICDCLAGHRRVYV	
Db	565	CADGEISNTSGSLQ	-CDRCPPPEFMSNDGRTACVPROJDLFSNETLIGVALLTAVAVSAYV	623	565	CADGEISNTSGSLQ	
QY	521	CEAGFELNMSE	-LHICCCGCTEEMAPKRESTCPFRTEVFLAMHEPISLVLIAANTLILL	579	521	CEAGFELNMSE	
Db	624	TTATVAVVFL	-HYKATPMVRANNSLSLSLJSLKCLCSL	-VFIGRPSWSCRFOOAF	661	624	TTATVAVVFL
QY	580	LVGTAGLEAMFH	-RTPVRSAGSLCFLMLGSL	-VAGSCSFYSFEPFEPVACILRQPLF	637	580	LVGTAGLEAMFH
Db	682	GISFLVLCSCQVOTIYVLAFRSARGAGLAKMWPESQORGSVCFTCVQARVICV	741	682	GISFLVLCSCQVOTIYVLAFRSARGAGLAKMWPESQORGSVCFTCVQARVICV		
QY	638	SLGRFIFLISCLTITSFQVLIIFKSTVPTFRFTW	-AONHGAG	-LEVIVSSTVHLLCLT	655	638	SLGRFIFLISCLTITSFQVLIIFKSTVPTFRFTW
Db	742	WLSISPPVQADLD	-VPGLOVTECAMASVGSFSLVGYGLACTOLLALFLARKLPDN	800	742	WLSISPPVQADLD	
QY	696	MLVMMTPRTPREYORPFL	-VILDETEVNSGFLPLATIHLLISIFVGSYLGKLEPEN	754	696	MLVMMTPRTPREYORPFL	
Db	801	FNEAKLTFSKLT	-FCAYMAVFPAYITSSPGKSVAVEIFAILASSYGLLFCIFAPKCFI	829	801	FNEAKLTFSKLT	
QY	755	YNEAKCVTFSLLENFVS	-WIAFETMASIYOGSYLPAVNLVAGLTLTSSGSGFYLPXCV	813	755	YNEAKCVTFSLLENFVS	
Db	860	ILPREKTKKHL	872	860	ILPREKTKKHL		
QY	814	ILCRELNNTHEF	826	814	ILCRELNNTHEF		
RESULT	11	PRELIMINARY;	PRT;	912	AA.		
ID	070410						
AC	070410						
DT	01-AUG-1998	(Tremblrel_07, Created)					
DT	01-AUG-1998	(Tremblrel_07, Last sequence update)					
DT	01-NOV-1999	(Tremblrel_12, Last annotation update)					
DE	PUTATIVE PHEROMONE RECEPTOR V2R2.						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;						
CC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
RN	(1)						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=VOMERONASAL NEURONS;						
RX	MEDLINE: 97436753.						
RA	RYBA N.J., TRINDELLI R.,						
RT	"A new multigene family of putative pheromone receptors."						
RL	Neuron 19:371-379(1997).						
RN	(2)						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=VOMERONASAL NEURONS;						
RA	RYBA N.J.P., TRINDELLI R.,						
DR	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.						
DR	EMBL: AF053986; AAC08413.1; -						
PFAM:	PF00003; 7tm_3; 1.						
DR	PFAM: PF01094; ANF_receptor; 1.						
DR	PRINTS: PR00248; GPCRMR.						
SO	SEQUENCE 912 AA; 102348 MW; 35AEF35A CRC32;						
Query Match	18.5%;	Score 1170;	DB 11;	Length 912;			
Best Local Similarity	29.6%;	Pred. No. 9,87e-219;					
Matches 248;	Conservative 229;	Mismatches 300;	Indels 62;	Gaps 46;			
Db	50	LVYAGLPFHSRITPVDEALILEPSPMCCEGFRNGEFMMKMTIMHTIKETINERKDIPLNHT	109	50	LVYAGLPFHSRITPVDEALILEPSPMCCEGFRNGEFMMKMTIMHTIKETINERKDIPLNHT		
QY	37	FLNGLFSLHDCQVRRRLPVTSQDBPSDFNGHYFLFOAMRTEVIEINNSALLPNIT	96	37	FLNGLFSLHDCQVRRRLPVTSQDBPSDFNGHYFLFOAMRTEVIEINNSALLPNIT		
Db	110	LGYOIFDCVYITSKAMESSL-VF-LTG	-OEEFKPNRSTGSLIALVSGSSSLVA	165	110	LGYOIFDCVYITSKAMESSL-VF-LTG	
QY	97	LGEYELDYVC	-SESANVATRLVLAQSPRHIEIOKDLRNN	-SKVAFAFICPDNTDAVTT	154	97	LGEYELDYVC
Db	166	SRILGLYMPGVGYTSSCSILSDKFOEPSYLRVLPSDNIQSEALVNLIKHFGWVGATA	225	166	SRILGLYMPGVGYTSSCSILSDKFOEPSYLRVLPSDNIQSEALVNLIKHFGWVGATA		



Oy	155	AALIGPFILPLVSVASSVVLISAKRKPPSFLRTPYPSDRHGYEVWVVLQDSGWMISLIG	21.4
Db	226	ADDYGGKGVKTEFKKMSANLCAVFSSTIP-KV-YSEKKQKAVKAVKSTAKVLYLT	283
Oy	215	SYGDGGQGLGVALAEELAVPRGICVAEFKQIVFESARVGGPRQSMQMLAARTVVVF-	273
Db	284	SDIDS-LFVLEMIHNHTDRITMEAMITFASALAKREYPRYGGIGFATPPSVJGL	34.2
Oy	274	SNRHLARFPFRSVYLANLGLKGVWASEDMALSTYTITSTYGIGTGYLGVAVQGRVPL	33.33
Db	343	KEFLYDVHPNKDPNDVLTIEFWQAFNCTWPNSSVYVNDHRVNMTKEDRLYDMSDLC	40.2
Oy	334	KEFE-ESYV-R-A--V-TAA--PSA-C--DEGS-WCSTNO--LC-RECHTFTRN-MP	37.57
Db	403	TGEERLEDLKNYLDTSOLRLITKCKKAVVVAIANGDHLSTSCQGGQGFPGNQCAIPT	46.3
Oy	376	T---LGAP--S-MSAA-YRV--Y-EAVYVAHGHLHOLLCT-SE--TCSRGP-VY-P-	41.7
Db	463	FDFWOLATYMEKEIKKESHEDKMWVILDDNGDLKNGHYDVLNMHLDDEGHISFVTVGRENFR	52.22
Oy	418	WQLDGOIT-K-VNPLHEMT-VAFDDNGD-TLGYDILADMDMGP-EMPEIIGSASLS	47.17
Db	523	STNFEVLVPTNSTIPWNTESSRRPDSFCTQVCPPTKRGKRGOCPTCFDCIPADSVS	56.2
Oy	472	PVHLD-I-TNKTIKIMGRKNNOVPVSYCTTCLGHNHVVVSHH-CCFEVCPCEAGTFL	52.2
Db	583	EKSGOREDDPCGEDMSNAGSKCVPKLYEFLAVGEALGFTLVLSIFGALVLAIVVY	64.2
Oy	528	NKSELHICQPCGTBEMAKESTCTCPRIYVELANHEPISLVLIANLILLILLVGTAGLF	58.7
Db	643	VIHHTPLVKANDRELSTLQMSLVITVLSLFTIGKPCNMSCARQITLALGFCICLSS	70.2
Oy	588	AMHEFTPVVRSAGRGICLIMGLSVAGSCSFSEFGEPTVPACILRLOPESLGAIFLSC	64.7
Db	703	ILGKISLFEPYRIVSVKTRLI-S-MHIFPKLYLVVCGEIVCGAAYVLEBPRMFKN	76.6
Oy	648	LTIRSFQVLIIFKSTKVPPTTYRTAONHGAGLFYIVSSVYHLICLTLVLMVMTPTRE	70.7
Db	761	IE-IQNVAKIIFECNE-GSVEFLCSIFGFDVLRALLCELTTPVARQLPDNYEKGICITFGM	81.8
Oy	708	YORPFL-VILECTEVNSVGL-LAFTHNILLISTFVCSYLGKELDENVEACVTFSL	76.5
Db	819	LVFFIWMISFPAYISTGKRKRVAVETPAIIASSVGLLGLCFDPKCFIILPRKRNDE	87.7
Oy	766	LINFWSIAFTMASIYGSTPLPAVNLALGLTISGGSGYFLPKCYVILCRPELNTE	82.4
RESULT	12		
ID	070409	PRELIMINARY:	PRT: 855 AA.
AC	070409		
DT	01-AUG-1998	(TREMBLrel. 07, Created)	
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)	
DT	01-MAY-1999	(TREMBLrel. 10, last annotation update)	
OS		Mus musculus (Mouse).	
OC		Eutaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia;	
NC		Eutheria, Rodentia; Sciurognathi, Muridae; Murinae; Mus.	
RC		[1]	
RP		SEQUENCE FROM N.A.	
RC		TISSUE=VOMERONASAL NEURONS:	
RA		RYBA N.J., TIRINDELLI R.,	
RL		Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.	
DR		EMBL, AF053985, AAC08412.1.	
DR		PFAM; PF00003; 7tm_3; 1.	
DR		PFAM; PF01094; ANF_receptor; 1.	

Seq	SEQUENCE	855 AA;	96215 MW;	C8389B1C CRC32;			
Query Match	16.9%;	Score 1073;	DB 11;	Length 855;			
Best Local Similarity	28.5%;	Fred. No. 2.75e-197;					
Matches 237;	Conservative 234;	Mismatches 301;	Indels 59;	Gaps 51.			
Db	29 AASGYODADVADVIGLPEFLRYTDGDTFISGSVDTESHIAEYVCGSIKRYQHILAVFA 88						
Qy	27 SSGPSLPGDFLLAGLGLSLH-GDGLQYRHRRLV-TGCDRPD-SRNGH-GY-HLFGAARFT 81						
Db	89 IEKINKDPNILLFNKSLGFFLEFNNFIEKKAEGSMALLGESP-IPNYSCKPEKTDKLV 147						
Qy	82 VEEINNSALLPNITLIGLEYDYVC-SESANYATLRVALALOGPHRIEIODLRNHSKVV 140						
Db	148 AVIGGISISISIQSRVLSLYTNQIASAPDQDILGRVLOQSRYQESMHTAA-LYQYIG 206						
Qy	141 AFIGDNDHAVTTAALLGPFMLVLEYEASSVYLSAKRRFPS-FLTYTSDRHQVYVMV 199						
Db	207 QLLLYFTYVWGLVVPDDMRBELYLRDITKEMISHGICFAEAKVTEYSSMDITNNMH-F 265						
Qy	200 QLLGSGFWWVWISLIGSYDYGQLGVQALEELAVPRGICVAFKIDIV-FSARVGDPRMQSM 258						
Db	266 MERLLLT-PVLIYGDTHSLRLIYV-FVIFNLSGNWITTSMPYITTFPEQULYTH- 322						
Qy	259 MOHLAQATTVVAVFNSNHLARVFRSVLANLIGKXWASDEMAIST-YITSVTGIQG 316						
Db	323 FGGGSEFSEFHNDEILGFEDELFRSQPRKRYPDIDIRHWMSLSEFCGPHYOHRMLDSQCE 382						
Qy	317 IGTVLGVAVAQROVPGIAKEF--E-ES--YYRAV-TA-A-PS-ACPRGSMCTNQLOCR-E 365						
Db	383 PNGSLSTPPLAMDMNTSPSYKYAAVYATACALHELSIRVGGSSNKCLDAPL-PW 441						
Qy	366 CH-FTTNMPTLTGAFSAASAYRYEYEVAVAHGLHQ-L-L--GCSTELCS-RGPYYPW 418						
Db	442 KLHPQOAKQGRSTINEENTYKREVSAAIKLIDIFYOSIQ-SGTE-AHYKGEFVDSHSV 499						
Qy	419 QL-LQQLYKKNFLHE-NIYAFPDNDGDTLGYDIIAMDNKNGPMTTEIIGSASL-S-PV 473						
Db	500 QHLSLNDKIITW-GKHSQCPPLSVCSQSCPEFSGSKTAVESGPFCCFDCVPCPDGEIANKT 558						
Qy	474 -HLDINKTKIOMHGKN-NQVPSVCTIDCAGHHRVAV-GSHCCCFCEVCPEAGTFINMS 530						
Db	559 DMHQCINCPEDQYNNKORNOCLPKIILFIAMHEDLGVIVYLSAISLAFSAMLIGLICY 618						
Qy	531 ELHIQCPQGTETEMAPKESTCTFPRTEVLAMHEPISLVLANTLTLLLVAGTAGLRAWH 590						
Db	619 RETPIVRANNNLSYLLISLKLQCFCSLI-FIQOPRTVCVLRLQIFGIYFISVISAII 677						
Qy	591 FHTPVRSAGRIQCFIMGLS-VAGSCSFSFSEPEFVPACLLNQPLFSIGFAIFLSCLT 649						
Db	678 AKTILVVVAEF-AIKPGSILKMGWTRLSNAIYCCGSILOYICAVWLGLIYPPPDVDM 736						
Qy	650 IRSPQVLIIFKFSKVPFRTFMQNGAGLFYVSSIVHLLICLTVLVMVTPRPREYQ 709						
Db	737 SEFGQ-IILMONESTIAFYCVLGLY-LGFLASLSLI-AFLARLPSFNEAKITTFEML 793						
Qy	710 R-FRLHVLLECTEVNSGF-LLAFTHIILISITFPCSYIGKRLPENYENAKVYTSLL 766						
Db	794 V-FCGSWISFVPAYLSKGTMAVEILSILAS-SAGLIGCIFLPCKYVIL 842						
Qy	767 INFVS-WIAFPTMASIYQGSYLPANVNLAGITLISGGSFGY-FLPKCYVIL 815						
RESULT	13						
ID	035269	PRELIMINARY;	PRT;	779 AA.			
AC	035269;						
DT	01-JAN-1998 (TIREMBLrel. 05, Created)						
DT	01-JAN-1998 (TIREMBLrel. 05, Last sequence update)						
DT	01-MAY-1999 (TIREMBLrel. 10, Last annotation update)						
DE	PUTATIVE PHENOMONE RECEPTOR.						
GN	GO-VN5.						
OS	Rattus norvegicus (Rat).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;						











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 WISE (TM)  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Fri Mar 17 13:03:18 2000; MasPar time 44.06 Seconds  
 569.357 Million cell updates/sec  
 Tabular output not generated.

Title: >US-09-361-652-1  
 Description: (1-840) from US09361652.pep  
 Perfect Score: 6338  
 Sequence: 1 MFMMAHLLLSQLVYCNMF.....NNTERRQASIDYTRCGTT 840

Scoring table:  
 GAP 11  
 PAM 150

Searched: 82229 seqs, 29854866 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 54.039; Variance 93.294; scale 0.579

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1311	20.7	1085	1	CASR_BOVIN EXTRACELLULAR CALCIUM-	3.56e-271
2	1290	20.4	1078	1	CASR_HUMAN EXTRACELLULAR CALCIUM-	4.19e-265
3	1285	20.3	1079	1	CASR_RAT EXTRACELLULAR CALCIUM-	6.74e-265
4	873	13.8	1203	1	MGR5_RAT METABOTROPIC GLUTAMATE	2.46e-165
5	870	13.7	1212	1	MGR5_HUMAN METABOTROPIC GLUTAMATE	1.26e-165
6	847	13.4	872	1	MGR2_RAT METABOTROPIC GLUTAMATE	3.43e-160
7	843	13.3	912	1	MGR4_RAT METABOTROPIC GLUTAMATE	3.01e-159
8	837	13.2	912	1	MGR4_HUMAN METABOTROPIC GLUTAMATE	7.84e-158
9	821	13.0	1199	1	MGR1_RAT METABOTROPIC GLUTAMATE	4.63e-154
10	819	12.9	872	1	MGR2_HUMAN METABOTROPIC GLUTAMATE	1.37e-153
11	812	12.8	1194	1	MGR1_HUMAN METABOTROPIC GLUTAMATE	6.10e-152
12	808	12.7	877	1	MGR3_HUMAN METABOTROPIC GLUTAMATE	5.33e-151
13	808	12.7	908	1	MGR8_RAT METABOTROPIC GLUTAMATE	5.33e-151
14	806	12.7	908	1	MGR8_MOUSE METABOTROPIC GLUTAMATE	1.57e-150
15	800	12.6	908	1	MGR8_HUMAN METABOTROPIC GLUTAMATE	4.06e-149
16	793	12.5	879	1	MGR3_RAT METABOTROPIC GLUTAMATE	1.79e-147
17	779	12.3	877	1	MGR6_HUMAN METABOTROPIC GLUTAMATE	3.48e-144
18	772	12.2	871	1	MGR5_RAT METABOTROPIC GLUTAMATE	1.53e-142
19	760	12.0	915	1	MGR7_HUMAN METABOTROPIC GLUTAMATE	9.94e-140
20	755	11.9	915	1	MGR7_RAT METABOTROPIC GLUTAMATE	1.47e-138
21	561	8.9	976	1	MGR_DOMO METABOTROPIC GLUTAMATE	1.18e-93
22	372	5.9	999	1	MGR1_CAEL PROBABLE METABOTROPIC	1.72e-51
23	145	2.3	938	1	NM21_HUMAN GLUTAMATE [NMDA] RECP	1.16e-06

24	144	2.3	938	1	NM21_RAT GLUTAMATE [NMDA] RECP	1.68e-06
25	148	2.3	1233	1	NM23_HUMAN GLUTAMATE [NMDA] RECP	3.75e-07
26	145	2.3	1237	1	NM23_RAT GLUTAMATE [NMDA] RECP	1.16e-06
27	145	2.3	1239	1	NM23_MOUSE GLUTAMATE [NMDA] RECP	1.16e-06
28	142	2.2	938	1	NM21_MOUSE GLUTAMATE [NMDA] RECP	3.54e-06
29	130	2.1	1125	1	CYGS_STRUP SPRACT RECEPTOR PRECU	2.68e-04
30	125	2.0	986	1	CYGR_ARBP RESACT RECEPTOR PRECU	1.52e-03
31	126	2.0	1323	1	NM24_MOUSE GLUTAMATE [NMDA] RECP	1.08e-03
32	123	1.9	1464	1	NM21_MOUSE GLUTAMATE [NMDA] RECP	2.99e-03
33	123	1.9	1464	1	NM21_RAT GLUTAMATE [NMDA] RECP	2.99e-03
34	120	1.9	1482	1	NM22_MOUSE GLUTAMATE [NMDA] RECP	8.19e-03
35	120	1.9	1482	1	NM22_RAT GLUTAMATE [NMDA] RECP	8.19e-03
36	112	1.8	434	1	VG05_VARY PROTEIN G5	1.10e-01
37	111	1.8	434	1	VG05_HELPY PROTEIN G5	1.10e-01
38	113	1.8	532	1	YB37_YEAST HYPOPHYSICAL 61.2 KD P	8.00e-02
39	117	1.8	842	1	YB37_TREPA TRANSLATION INITIATION	2.20e-02
40	117	1.8	1108	1	CYGF_RAT RETINAL GRANULYL CYCLA	2.20e-02
41	111	1.8	1108	1	CYGF_HUMAN RETINAL GRANULYL CYCLA	1.50e-01
42	115	1.8	2749	1	IP3R_MOUSE INOSITOL 1,4,5-TRISPHO	4.21e-02
43	109	1.7	360	1	CKR4_MOUSE C-C CHEMOKINE RECEPTOR	2.80e-01
44	109	1.7	434	1	VG05_VACCC PROTEIN G5	2.80e-01
45	110	1.7	444	1	CEFG_CEPAC ACETYL-COA--DEACETYLCE	2.06e-01

## ALIGNMENTS

RESULT	1	STANDARD:	PRT:	1085 AA.
ID	CASR_BOVIN			
AC	P35384;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).			
DE	CASR OR PCAR.			
GN	Bos taurus (Bovine).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;			
OC	Bovinae; Bos.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PARATHYROID;			
RX	MEDLINE; 94077182.			
RA	BROWN E.M., GAYDA G., RICCARDI D., LOWARDI M., BUTTERS R., KIFOR O., SUN A., HEDIGER M.A., LYTTON J., HERBERT S.C.;			
RT	"Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid."			
RL	Nature 366:575-580(1993).			
CC	-1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	*****			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	*****			
DR	EMBL; S67307; AAB29171.1; ..			
DR	PIR; S40476; S40476.			
DR	GCRRB; GCR_0900; ..			
DR	PROSITE; PS00979; G-PROTEIN_RECP_F3_1; 1.			
DR	PROSITE; PS00980; G-PROTEIN_RECP_F3_2; 1.			
DR	PROSITE; PS00981; G-PROTEIN_RECP_F3_3; 1.			
DR	PFAM; PF00003; 7tm_3; 1.			
DR	PFAM; PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL 1 19			







RX MEDLINE: 95179179.  
 RA POLLAK M.R., BROWN E.M., ESTEP H.L., MCILAIN P.N., KIFOR O., PARK J.,  
 RA HERBERT S.C., SEIDMAN C.E., SEIDMAN J.G.:  
 RT "Autosomal dominant hypocalcemia caused by a Ca(2+)-sensing receptor  
 RT gene mutation.";  
 RL Nat. Genet. 8:303-307(1994).  
 RN [7]  
 RP VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.  
 RX MEDLINE: 95243223.  
 RA CHOU Y.-H.W., POLLAK M.R., BRANDI M.L., TOSS G., ARNOVIST H.,  
 RA ATKINSON A.B., PAPADOPOULOS S.E., MARK S., BROWN E.M., SEIDMAN J.G.,  
 RA SEIDMAN C.E.:  
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause  
 RT familial hypocalcemic hypocalcemia.";  
 RL Am. J. Hum. Genet. 56:1075-1079(1995).  
 RN [8]  
 RP SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.  
 RX MEDLINE: 95403641.  
 RA AIDA K., KOISHI S., INOUE M., NAKAZATO M., TAMATA M., ONAYA T.:  
 RT "Familial hypocalcemic hypocalcemia associated with mutation in the  
 RT human Ca(2+)-sensing receptor gene.";  
 RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).  
 RN [9]  
 RP VARIANTS NSHPT LEU-227 AND TYR-598.  
 RX MEDLINE: 96292293.  
 RA PEARCE S.H.S., TROMP D., WOODING C., BESSER G.M., CHEW S.L.,  
 RA GRANT D.B., HEATH D.A., HUGHES I.A., PATERSON C.R., WHITE M.P.,  
 RA THAKKER R.V.:  
 RT "Calcium-sensing receptor mutations in familial benign hypocalcemia  
 RT and neonatal hyperparathyroidism.";  
 RL J. Clin. Invest. 96:2683-2692(1995).  
 RN [10]  
 RP VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.  
 RX MEDLINE: 96311554.  
 RA BARON J., WINER K.K., YANOVSKI J.A., CUNNINGHAM A.W., LAUE L.,  
 RA ZIMMERMAN D., CUTLER G.B. JR.:  
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal  
 RT dominant and sporadic hyperparathyroidism.";  
 RL Hum. Mol. Genet. 5:601-606(1996).  
 RN [11]  
 RP VARIANT FHH ARG-174.  
 RX MEDLINE: 97442275.  
 RA WARD B.R., STUCKEY B.G.A., GUTTERIDGE D.H., LAING N.G., PULLAN P.T.,  
 RA RATAJCZAK T.:  
 RT "A novel mutation (L174R) in the Ca2+-sensing receptor gene  
 RT associated with familial hypocalcemic hypocalcemia.";  
 RL Hum. Mutat. 10:233-235(1997).  
 CC -1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF  
 CC CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A  
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND  
 CC MESSENGER SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS SEEM TO BE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: FOUND IN KIDNEY, BUT NOT IN BRAIN, LUNG,  
 CC LIVER, HEART, SKELETAL MUSCLE, OR PLACENTA.  
 CC -1- DISEASE: DEFECTS IN CASR ARE A CAUSE OF FAMILIAL HYPOCALCEMIC  
 CC HYPERCALCEMIA (FHH) AND NEONATAL SEVERE HYPERPARATHYROIDISM  
 CC (NSHPT); TWO INHERITED CONDITIONS CHARACTERIZED BY ALTERED CALCIUM  
 CC HOMOEOSTASIS. THE MUTATIONS REDUCE THE ACTIVITY OF THE RECEPTOR.  
 CC FHH AFFECTED INDIVIDUALS EXHIBIT MILD OR MODEST HYPERCALCEMIA,  
 CC RELATIVE HYPOCALCEMIA, AND INAPPROPRIATELY NORMAL PTH LEVELS. IN  
 CC CONTRAST, NSHPT IS A RARE AUTOSOMAL RECESSIVE LIFE-THREATENING  
 CC DISORDER CHARACTERIZED BY VERY HIGH SERUM CALCIUM CONCENTRATIONS,  
 CC SKELETAL DENSITRIFICATION, AND PARATHYROID HYPERTROPHY. IN SOME  
 CC INSTANCES NSHPT HAS BEEN DEMONSTRATED TO BE THE HOMOZYGOUS FORM OF  
 CC FHH.  
 CC -1- DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT  
 CC HYPOCALCEMIA (ADH) IN WHICH THE RECEPTOR IS ACTIVATED AT SUBNORMAL  
 CC CA(2+) LEVELS.  
 CC -1- DISEASE: DEFECTS IN PCAR1 ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT  
 CC HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCEMIA  
 CC AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID

CC HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 DR EMBL: X81086; CAA56990.1; -  
 DR EMBL: U20759; AAB6503.1; -  
 DR EMBL: U20760; AAB6504.1; -  
 DR EMBL: D50855; AAB09453.1; -  
 DR EMBL: S83176; AAB46873.1; -  
 DR EMBL: S79217; AAB35262.1; -  
 DR EMBL: S68032; AAB29413.1; -  
 DR EMBL: S68033; AAB29414.1; -  
 DR EMBL: S68036; AAB29415.1; -  
 DR GCRDB: GCR\_1337; -  
 DR GCRDB: GCR\_1874; -  
 DR GCRDB: GCR\_2012; -  
 DR GCRDB: GCR\_2013; -  
 DR GCRDB: GCR\_2696; -  
 DR GCRDB: GCR\_2697; -  
 DR MTM: 601199; -  
 DR MTM: 145980; -  
 DR MTM: 601198; -  
 DR PROSITE: PS00979; G-PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE: PS00980; G-PROTEIN\_RECEP\_F3\_2; 1.  
 DR PROSITE: PS00981; G-PROTEIN\_RECEP\_F3\_3; 1.  
 DR PFAM: PF00003; 7tm3.3; 1.  
 DR PFAM: PF01094; ANF\_receptor; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Disease mutation; Alternative splicing; Polymorphism.  
 FT SIGNAL 1 19  
 FT CHAIN 20 1078  
 FT DOMAIN 20 612  
 FT TRANSMEM 613 635  
 FT DOMAIN 638 649  
 FT TRANSMEM 650 670  
 FT DOMAIN 671 681  
 FT TRANSMEM 682 700  
 FT DOMAIN 701 724  
 FT TRANSMEM 725 745  
 FT DOMAIN 746 769  
 FT TRANSMEM 770 792  
 FT DOMAIN 793 805  
 FT TRANSMEM 806 828  
 FT DOMAIN 829 836  
 FT TRANSMEM 837 862  
 FT DOMAIN 863 1078  
 FT CARBOHYD 90 90  
 FT CARBOHYD 130 130  
 FT CARBOHYD 261 261  
 FT CARBOHYD 287 287  
 FT CARBOHYD 386 386  
 FT CARBOHYD 400 400  
 FT CARBOHYD 446 446  
 FT CARBOHYD 468 468  
 FT CARBOHYD 488 488  
 FT CARBOHYD 541 541  
 FT CARBOHYD 594 594  
 FT CARBOHYD 536 536  
 FT VARSPLIC 39 39  
 FT VARIANT 62 62  
 FT VARIANT 66 66  
 FT VARIANT 116 116  
 FT VARIANT 116 116  
 R -> C (IN FHH).  
 R -> M (IN WILD FHH AND NSHPT).  
 R -> A (IN FHH).  
 R -> T (IN ADHP).  
 /FTId-VAR\_003586.  
 /FTId-VAR\_003587.  
 /FTId-VAR\_003588.







FT CARBOHYD 488 488 POTENTIAL.  
 FT CARBOHYD 541 541 POTENTIAL.  
 FT CARBOHYD 594 594 POTENTIAL.  
 SO SEQUENCE 1079 AA; 120867 MW; 34118BE9 CRC32;

Query Match 20.3%; Score 1285; DB 1; Length 1079;  
 Best Local Similarity 31.6%; Pred. No. 6.74e-265;  
 Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

Db 30 GDILGLGFPPIHFG-VAAKDDDKSRPESVECIIRYNFRGLQAMIFAIIEINSSPLL 88  
 QY 35 GDFLLAGLFSHGDCLOVHRHPLVITSCDRPDS--FNGHGHLDFQAMRFTVEINNSSL 92  
 Db 89 PNMTGLYIFPTCNTVSKALEATLSFVAONKIDSLNDFECSCSHISTIIWVATQSG 148  
 QY 93 PNITGLYILVDCSESANVY-ATLEVLALQGRHIEIOK--DLRHHSSKVVAFFIPDNTD 149  
 Db 149 VSTAVANLLGLFYIPQVYASSSSRLSNKNOYKSFRTIPNDEQATAMADIEYFRNMW 208  
 QY 150 HAVITTAALLGFFLMPVSEYASSVYLSAKRKFPSEFLRTVPDRHQVEVYVQLQSGFWW 209  
 Db 209 VGTIADDDYGRPGIEKREAEEDIDIDSELI--SOYSEEDIQOVVEYIQTAKV 266  
 QY 210 ISLIGSYDYGQDGVQALEELAVPRGICVAFEDIVFSAVGDPMQSMOHLAQARTTV 269  
 Db 267 IVFSSGDPLEPLI-KEIYRNRITGRIMVLASEPAMASSLIAMPEYFHVGGTIGFGLKAG 325  
 QY 270 VVVSFN-RHLARVFRFRVYLANLTKVAVASEDMA----IS-T-YITSYTG-IQ-GI--G 318  
 Db 336 QIPGREFRLQVHPRKSVHNGFAKEWEETFNCHLOEGAKGPLPVDFVRSHEGGRNL 385  
 QY 319 TVLG---VA-VQORQ-VP-GI-KEF-EESY---VR-AVTA-A-P-S-A-CPE--GSM-- 356  
 Db 386 NSSTFRRLCTGDEINSEVETPYKMEYHRLISYNYLAVYSTAHALODITYCLPRGFLT 445  
 QY 357 -CSTN-Q-LCECHTFTTRNMTLGFASMSAYRYEAVYAAHGLHOL--L-CC--I 406  
 Db 446 NGSCADIKKVAOYLKRLHLNFTNNMGEOYFDECGDLVGNYSIIMWHSPEGSIVF 505  
 QY 407 SEICS-RBPVYPMOLLOOYKYNFLH-ENTVAFDNDGDTLGYIILAMDKNPE-WI-F 462  
 Db 506 KEVGYNYVYAKGERLFTNEKILWSGFSREVPFNSCRDCAQTRKGIIEGEPTCCFEC 565  
 QY 463 EIIG--SA-SLSPVHLINKTKIQWGHKNNOYPAVCTTDCIAGHRRVY--GSHHCCEC 518  
 Db 506 VECPRGEISGETDASACKCPDDEFNSNHNHSCIAKEIEFLAMTPFGIALTLFVVLGIF 625  
 QY 519 VPCEAGTILNSELHICQPCGIEEWAPKESTCPRIVEFLAMHEPISLVLIANTLILL 578  
 Db 626 LTAFLVGFYI-KFRNTPYKATNRELSTYLLFSLLCFSSSLF-FIGEPDMTCRLQPA 683  
 QY 579 LTVAGTAFANHH-TIPVRSAGRLCLMLQSLVAG-SCSFYSFGEFTYPACLLRPL 636  
 Db 684 FGISFVLCISILVKNFVLLVFE--AKIPTSFHRKMWGLNLOFLVLCFTMOLICII 741  
 QY 637 FSLGHAIFLSCLTRISFOLVIEFKSTKVPY-FYRTWAQNHGAGLFVYVSSVHLLICLT 695  
 Db 742 WLYTAPPSYNNHLEDDIITTCHEGSLMAGSLIGTC-LLAACIFF-AFKRKRLPE 799  
 QY 696 WLVMVTPRTREYORFPPLVILECEEVN--SVGFLLAFTHNLLISITFVCSYLKELPE 753  
 Db 800 NENEAKFTFEMLIFFIYVIFIPAYASTY-GKEVSAVEVIALLAASGLLACIFENNVY 858  
 QY 754 NYNEKACTESLILNFVWIAFFTM-ASIIQGSYLPVAVNLAGLTLTSGSGSYFLPKCY 812  
 Db 859 IILKPSRNTIEEVRSSTAHA 880  
 QY 813 VILCRPELNTHEQASIQDYT 834

RESULT 4  
 ID MGRS\_RAT STANDARD; PRT: 1203 AA.  
 AC P31424;

DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.  
 GN GRM5 OR MGLUR5.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN:  
 RX MEDLINE: 92317054.  
 RT "Molecular characterization of a novel metabotropic glutamate receptor mglur5 coupled to inositol phosphate/Ca<sup>2+</sup> signal transduction."  
 RL J. Biol. Chem. 267:13361-13368(1992).  
 RN [2]  
 RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE-BRAIN:  
 RX MEDLINE: 93343913.  
 RT "A variant of metabotropic glutamate receptor subtype 5: an evolutionally conserved insertion with no termination codon."  
 RL Biochem. Biophys. Res. Commun. 194:622-627(1993).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED CHLORIDE CURRENT.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL, MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: 5A (SHOWN HERE) AND 5B; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF 32 RESIDUES.  
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE CENTRAL NERVOUS SYSTEM.  
 CC -1- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE > TRANS-1-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST, TO MGLUR1.  
 CC -----  
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 CC -----  
 DR EMBL: D10891; NOT ANNOTATED\_CDS.  
 DR EMBL: S64315; AB27666.1; -.  
 DR PIR: A42916; A42916.  
 DR GCRDB: GCR\_0444; -.  
 DR GCRDB: GCR\_0760; -.  
 DR PROSITE: PS00979; G-PROTEIN\_RECP\_F3\_1; 1.  
 DR PROSITE: PS00980; G-PROTEIN\_RECP\_F3\_2; 1.  
 DR PROSITE: PS00981; G-PROTEIN\_RECP\_F3\_3; 1.  
 DR PFM; PF00003; 7tm\_3; 1.  
 DR PFM; PF01094; ANF\_receptor; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; signal; Multigene family; Alternative splicing.  
 FT SIGNAL 1  
 FT CHAIN 21 1203  
 FT DOMAIN 22 578  
 FT TRANSMEM 579 601  
 FT TRANSMEM 602 615  
 FT TRANSMEM 616 636  
 FT TRANSMEM 637 647  
 FT TRANSMEM 648 666  
 FT TRANSMEM 667 692  
 FT TRANSMEM 693 713  
 FT TRANSMEM 714 736  
 FT TRANSMEM 737 758  
 FT DOMAIN 759 771  
 FT CYTOPLASMIC (POTENTIAL).  
 FT METABOTROPIC GLUTAMATE RECEPTOR 5.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT I (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT II (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT III (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IV (POTENTIAL).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT V (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).



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FT TRANSMEM 772 794 VI (POTENTIAL).
FT DOMAIN 795 800 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 801 826 VII (POTENTIAL).
FT DOMAIN 827 1203 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 209 209 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 381 381 POTENTIAL.
FT CARBOHYD 444 444 POTENTIAL.
FT CARBOHYD 733 733 POTENTIAL.
FT YANSPIC 876 907 MISSING (IN ISOFORM 5A).
SO SEQUENCE 1203 AA; 131885 MW; 2935EA33 CRC32.

Query Match 13.8%; Score 873; DB 1; Length 1203;
Best Local Similarity 27.7%; Pred. No. 2,46e-166;
Matches 231; Conservative 215; Mismatches 325; Indels 64; Gaps 56;

Db 31 MGDIIIGALFVHOP-TV-DVHERKCG-AVR-EQYIGQVEMALHTLERINDPTLL 86
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
33 LPGDFLAGLFLHSGDCLQVRRHPLVTSQDRPDSFGHGYHFLQAMRFVEEINSSALL 92
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
87 PHTIGCEIRDCMWSAVALDESIERIRDSLISSEEBGLVACVDSGSSFRKKPIYGI 146
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
93 PHTIGELYLDVCSANVYA-TLR-VL-ALOGPRHTE--IQ-KD-LRN-HSKK-VVAET 143
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
147 GPGSSVAIQVONLLQLENIPOIAYSATSMDLSDKTLFEKFRVPPSDAQARAVDIK 206
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
144 GPDNDHVAITALLGPFMLPLVSEASSVVSJAKRKFSPFLRTYPSDHOVENVQLQ 203
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
207 RYNTVYSAVHTEGNGESGMEAFKDMASKESICIAHSYKI-YSN-AGEOSFDLKKIR 264
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
204 SFGWAMISLIGSYGQGOGLVOALEBELAPRGICVAFKDIIVFSEVAPDRMQSMQHL- 262
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
265 SMLPARVACCEGTVTGILAMBRGLAGEPFLLSGSGMA-DRYDT-DSGY-REAV 321
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
263 AO-ARTVYVSNRHLAVFRFSVLANLFGK-VWASEDMAISTYITVTGIGIGTV 320
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
322 GGIITKL-OSPDVKWFDDYLLKRPETNLNPMFQEFNHRQCRLEGFAOENSKYKTK 380
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
321 LGVAOQORQVPLKFESEYV--RAVTAAPSACPEGSW-----CSINOACRCHFT-TR 372
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
381 NSSLRLRHVODSKMGVINAISMAVGLHNMOMSLCGVGLCDAMKPIDGRKILDSL 440
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
373 NMP-FLGAFMSAAAYRV--EAVYVAHGLHOL-LG-CTS-E-IC-SRGPYPMWLQOI 424
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
441 MNTNTGSGMDLFDENDSPGREIMNFKEMKDY-FDYINSGMDGELKMDDEV- 498
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
425 YKVNFL-LHENTVAFDDNDGLGYIDILAMDNMGPEWTFEILGSASLSVPHLDINTKIQ 483
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
499 WSKKNNIIR-SVCSPECEKGOIKVIRKEVSCWCTCPCKENEDYV-FDE-YTCKACOLGS 555
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
484 WGRKNNOVAVSCTIDCLAGHHRVYV-GSHHCCFECVPEADGTFPLMSLHICQCGTBE 542
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
556 WFTDGLGCDLIPVQYLRMGDEPPIAAVFAAGLGLATLV-TVPIIYR-DTPVYKSS 613
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
543 WAPKESTICFPTVFLAM-H-EPISTLVIANANTLLVLLVSTAGLFAHFTPTPVYRSAG 600
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
614 RELCYIIAGLIGLCTFC-LIAKPKOYLICLORIGLISPAWSAIVTNTNRIARL 672
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601 GRLCLMLGSLVAGS-CSYFSFGEPTVACILROPFLSLGFRILFSLCLTINSFOLVIF 659
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
673 AGSKRKICR-KPRMSACQVIAFIIICILGIIIVAFIIEPPDIIMHYSIRE-VYL 730
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
660 KFSKR-VPEFYRTAQNHRAGLFV-IVSSTVLLICLTVMVMPRTPEYGRPHLVIL 717
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
721 ICNTN-IGVTPPLGYNGLIISCTF-YAFKRRNPANFNKAIFYATMYTCIILWAF- 787
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
718 ECTEVNSVGFLLAFTHNLLIS-TEVCSYGLKELEPENENAKCTVFSLLNFVSIWAF 776
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
788 -VP-IYFSGNYIIMCFVS-LSATVALGCMFVPRVYIILAKPRENVASATTS 839
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
777 TMASITYGSLPAVNLVAGLTLISGGS-GY-FLPCVYILCRPELNTHEFOAS 829
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RESULT 5
ID MGR5 HUMAN STANDARD; PRT; 1212 AA.
AC P41594.1
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGLUR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE; 94197696.
RA MINAKAWI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;
RT "Molecular cloning and the functional expression of two isoforms of
RT human metabotropic glutamate receptor subtype 5."
RL Biochem. Biophys. Res. Commun. 199;1136-1143(1994).
RN [2]
RP REVISIONS.
RA KATSUKI F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 860-952 FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE; 93343913.
RA MINAKAWI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon."
RL Biochem. Biophys. Res. Commun. 194;622-627(1993).
CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC - ALTERNATIVE PRODUCTS: TWO ISOFORMS: 5A (SHOWN HERE) AND 5B. ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC - SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR1.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D28538; BAA05891.1; -
DR EMBL; D28539; BAA05892.1; -
DR EMBL; S64316; AAD13954.1; -
DR GCRDB; GCR_0761; -
DR GCRDB; GCR_1002; -
DR GCRDB; GCR_1003; -
DR GCRDB; GCR_1317; -
DR MIM; 604102; -
DR PROSITE; PS00979; G_PROTEIN_REC_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_REC_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_REC_F3_3; 1.
DR PFAM; PF00003; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1212 METABOTROPIC GLUTAMATE RECEPTOR 5.
FT DOMAIN 22 579
FT TRANSMEM 580 602 I (POTENTIAL).
FT DOMAIN 603 616 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 617 637 II (POTENTIAL).

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FT DOMAIN 638 648 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 649 667 III (POTENTIAL).
FT DOMAIN 668 693 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 694 714 IV (POTENTIAL).
FT DOMAIN 715 737 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 738 759 V (POTENTIAL).
FT DOMAIN 760 772 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 773 795 VI (POTENTIAL).
FT DOMAIN 796 801 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 802 827 VII (POTENTIAL).
FT DOMAIN 828 1212 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 210 210 POTENTIAL.
FT CARBOHYD 378 378 POTENTIAL.
FT CARBOHYD 382 382 POTENTIAL.
FT CARBOHYD 445 445 POTENTIAL.
FT CARBOHYD 734 734 POTENTIAL.
FT VARSPLIC 877 908 MISSING (IN ISOFORM 5A).
SQ SEQUENCE 1212 AA: 132468 MW: 1681574 CRC32;

```

Query Match 13.7%; Score 870; DB 1; Length 1212;

Best Local Similarity 27.6%; Pred. No. 1,256-165; Indels 65; Gaps 55;

Matches 231; Conservative 214; Mismatches 326; Indels 65; Gaps 55;

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Db 31 MGDIIIGALFVHOP-TV-DKVERKCG-AVR-EQYGIQVEMAMHTLERINSDPTLL 86
OY 33 LPGFLLAGLFSLHGDCLQVNRHRLVTSODRPFNGHGLFLPAMRTVEINSSALL 92
Db 87 PNITLGEINDSCWMSVALEOSTIEFRDLSISEEEGLRCYDGGSSFSRKKPIVGV 146
OY 93 PNITLGEYELDVCSANVYA-TLR-VL-ALQGRHIE-IQ-KDLRHS--SK-VYAF 142
Db 147 IGPSSSSVAIOVOMLLOLNFPIAISTMSDLSKTLFKFMVAVPSDAQAAAMDIV 206
OY 143 IGPNTAHAVITALLPFLPMLPVYEAASSVLSAKRPFSLRTVPSDRQVEVMQQL 202
Db 207 KRYMNTVSAVHTEGNYESGEMAEFKMSAKEGICIAHSYKI-NSN-AGEOSFYLKTL 264
OY 203 QSPFWWISLIGSYGDYGOLOVQLLEAVRGICVAFKDLVPPSARQDPRMSKMOHL 262
Db 265 TSHLPKARVAVCFEGMTVRGLLAMRRLGAGEFLLLGSDGMA-DRYDVT-DEYO-REA 321
OY 263 A-Q-ARTVVVVVFNRHLARVFEFRSVLANLTGK-VWVASEDMAISTYITSVTGIGIGIT 319
Db 322 VGGITLIL-QSPDKVMFDDYLYLKRPEINRNPFOEFMORFQCRLEGFOENSKYIKT 380
OY 320 VLGVAVOORVPGLEKEEESYRAVTAAPSACP--EGSW-----CSTNQLRECHTFP-T 371
Db 381 CNSLTLKTHVODSKMGFEVINALIYSMAVGLHNMOMSLCPGYAGLADAMKPIDGRKILES 440
OY 372 RNMP-TLGAFMSAAHYRY--EANYAAVAGHOL-LG-CTS-E-IC-SRGVYFWMOLLQO 423
Db 441 LMKTNFTGVSDDILLFDENGDSRGYEIMNEKMGKDY-PDYINVSGDNGLKMDDEV 499
OY 424 IYKVNFL-LHENTVAFDNDGDTLGYDILAWDMGPEWTEFIISASLSYPHLINKIKI 482
Db 500 -WKSXSNIR-SVCSPECEKQIVIRKGEVSCCTCTPCKENEYV-FDE-YTKACOLG 555
OY 483 QWHRKNNOVPVSVCTTCLAGHHRVV-GSHHCCFECVPCAGCTFLNNSLHIDPOCOTE 541
Db 556 SWPDDLTGCDLIPOYLRMGDPEPIAAVPAAGLLATLLEV-TVVFIIYR-DTPVYXS 613
OY 542 EMARESTTCPRIVEFLAW-H-EPISLVLIANNTLLLLLVAGLAFAMFHFHPVYRSA 599
Db 614 SRELGYIILAGLICGLYCTFC-LIAKPKQIYCYDORIGIGLSPAMSSYALVTIKRIARI 672
OY 600 GGRCLCFMLGSLVAGS-CSFYSEFGEPTVPACLLRQPLFSIGAFILFSLCTIRSFOLYI 658
Db 673 LAGSKKIKCR-KRPFMSACQOLVIAFILIOIGIIVALEFIMPPDLMHYPISIRE-VY 730
OY 659 KFEFTK-VPIFYRIWAOHGGLFV-IVSSIVHLLICITFWLVMTPPRETRVQORPHLYI 716
Db 731 LICNTTN-LGVVPLGYNGLLILSCTF-YAFKTRNVNPNANEAKYIAFTMTTCIIMLAF 788

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OY 717 LCEVNSVGLLAFTHNILLIS-TEVCYLKELDENENKACVFFSLLNFVSIKIAF 775
Db 789 --VP-ITFGSNYKIIITCFYSV-LSATVALGCMFVPVYIILLAKPENNVSAFTS 840
OY 776 FIVASIVOSGYLPAVNLAGLIT-SSGFS-GY-FLPKCYVILCRPELNTEHFOAS 829

RESULT 6
ID MGR2-RAT STANDARD; PRT; 872 AA.
AC P31421;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GN GRM2 OR MGLUR2.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MDLINE; 92110002.
RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
RT "A family of metabotropic glutamate receptors."
RL Neuron 8:169-179(1992).
CC -FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
CC SYNAPTONEGENESIS OR SYNAPTIC STABILIZATION.
CC -SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
CC EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME
CC PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
CC -SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR3.
CC -----
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CC -----
DR EMBL; M92075; -; NOT_ANNOTATED; CDS.
DR PIR; JH0561; JH0561.
DR HSSP; P06612; 1ECL.
DR GCRDB; GCR 0361; -.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PFAM; PF01093; 7tm_3; 1.
DR PFAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 872
FT DOMAIN 19 567 METABOTROPIC GLUTAMATE RECEPTOR 2.
FT TRANSSEM 568 590 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 591 604 I (POTENTIAL).
FT TRANSSEM 605 625 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 626 637 II (POTENTIAL).
FT TRANSSEM 637 655 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 656 679 III (POTENTIAL).
FT TRANSSEM 680 700 IV (POTENTIAL).
FT TRANSSEM 701 725 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 726 747 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 748 760 V (POTENTIAL).
FT TRANSSEM 761 783 VI (POTENTIAL).
FT TRANSSEM 784 793 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 794 819 VII (POTENTIAL).
FT TRANSSEM 820 872 CYTOPLASMIC (POTENTIAL).

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Query Match 13.4% Score 847; DB 1; Length 872;  
 Best Local Similarity 26.6%; Pred. No. 3,436-160;  
 Matches 227; Conservative 222; Mismatches 341; Indels 62; Gaps 51;

FT	CARBOHYD	203	203	POTENTIAL.
FT	CARBOHYD	286	286	POTENTIAL.
FT	CARBOHYD	338	338	POTENTIAL.
FT	CARBOHYD	402	402	POTENTIAL.
FT	CARBOHYD	547	547	POTENTIAL.
FT	SEQUENCE	872 AA;	95773 MM;	C3C34676 CRC32;

DB 4 LIGFLALLLMG-AVAGSPAKVLTLEBDLVGLGFLPH---Q-KGSP-AEECG-PVN-54  
 9 LLS-LQVYCAAFSCORTESPGLSPEDFLAGLFLSHGGLVRRHPLVTSQDRPSE 67  
 55 EHRGIRLEALFALDRINRPHLLPGVRLAHILDSKDTLHLEQALDVPASLSGA 114  
 68 NGHGYLFOARKFTVEELINSSALUPITLIGELYDVCESANYA-TL--RV-LA--L 120  
 115 DGRHICPDGSYATHSDAPAVTGVIGGSYSVSIQVNLRLPQIPQISYASTAKLSD 174  
 121 QGPHIEIQKDLRNHS-S-KVYA-FIGPDNDHATVTTALLGFLMPLVSEASSVLSA 177  
 175 KSRDVFARKYPPDFQAKAMAEILRFNWYVSTVASEGDTGTAFLERARNIC 234  
 178 KRKPSFLRTVPSDRHOVEVVOQLQSGWWSIGSYGQGLQVQALBELAVPRGIC 237  
 235 VATEKRG-RA-MSRAAFEGVVRALLOKPSARVAVLFRSDARELLAATQRLN-ASPTW 291  
 238 VAFMDIYFPAKRVDPKRMQMOHLQART-VVVFNSRHLARFERSVVLNLTGKVM 296  
 292 VASDGMALLESVAGSERAAEGAL-TIELASPISDASYPOSIDPMNNSHNPFRFWE 350  
 297 VASDGMALISTVTSVIGIGTGVAVQORVPGLKEFESEY-VRAVTAAPSACP--E 353  
 351 ERFCSERQ-RDCAHSLRAVP-FEDSK-IMFYV-NAVYAMAHALNNHRLACPNTH 405  
 354 GSW-CSTNQLRECHTFTTRMPTLGAESMAARYEAVAHAGLQDL-G-C--TSE 408  
 406 LCDAMPVNGRRLKDFLANKFDAPFRADTDEVRDGRDGIGRNITTYLRAGSGR 465  
 409 IC-SRGFYVQQLAQ-Q-ITYKNF-L-LH-ENT--VAFDNGDTLIGYDITLAMPNGPEW 460  
 466 -YRY-QKGVYAEGLTDTSPFIPWASPSAGPLPASRSEPCLONEVKSQGEVOCWLCI 523  
 461 TFEIIGSASISLPHLDIKTKIQWNG-KNNGVPVSVCTDCLAGHRRVYVSHHOCFECV 519  
 524 PCQYER-RUDEP-TCADCGIGY-PNASLTGCELPQETIRMGDANAAGVYTTACIGAL 580  
 520 PCEAGTFLNMSELICQPCGTEEMAPKES-TTCEPRIVEFLAMEHPISLVLIANTLILL 578  
 581 ATLEVLGVFVHNMPYKASGREICYLLGGLVLCYCMTEVFETAKPSTACTARLIG 640  
 579 LLVOTAGLFAWHFTPVKRSAGRLCFMLSLVAGSCSFSEGEFVVPACLRQPLS 638  
 641 TAFSVCSALTCTNRIARIG-GAREGA-ORPRISPAVOALALISQILLIVAML 698  
 639 LGFAIFLSCULIRSFQVILFKFSKVPTEFRTAQNNGALFIVS-STVHLILCLTML 697  
 699 VVEAPGTGKETAPRREYVTLRCNHRDA-SMUGSLAVVLLIACLT-YAFKTRCPENF 756  
 698 VMMPRPTREVORPH-LVILECTEVNSVGLAFTHNILL-SISTEFCYSYLGKELPENY 755  
 757 NEAKFIFTMTTCTIIMLAFPIYVNSDYRVQTTMCVSVSIVGLCLAPKLI 816  
 756 NEACVTFSLINFSWIAFTMASITOGSYLPAVNVLAGLTTISGGRS-GY-FLPKCYV 813  
 DB 817 ILFOPKVVSH 828  
 QY 814 ILCRPELNTEH 825  
 RESULT 7

ID	MGR4_RAT	STANDARD;	PRT;	912 AA.
AC	P31423;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.			
GN	GRM4 OR MGLUR4.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RC	TISSUE-BRAIN;			
RA	TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;			
RT	"A family of metabotropic glutamate receptors."			
RL	Neuron 8:169-179(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RC	MEDLINE: 93332699.			
RA	O'HARA P.J., SHEPPARD P.O., THOGERSEN H., VENEZIA D., HALDEMAN B.A.;			
RT	"The ligand-binding domain in metabotropic glutamate receptors is related to bacterial periplasmic binding proteins."			
RL	Neuron 11:41-52(1993).			
CC	- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.			
CC	- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST, TO MGLUR6.			
CC	-----			
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CC	-----			
DR	EMBL; M92077; -; NOT ANNOTATED; CDS.			
DR	EMBL; M90518; AAA3190.1; -			
DR	PIR; JH0563; JH0563.			
DR	GCRDB; GCR_0352; -			
DR	GCRDB; GCR_0363; -			
DR	PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.			
DR	PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.			
DR	PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.			
DR	PFAM; PF00003; 7tm_3; 1.			
DR	PFAM; PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;			
KW	Multigene family.			
FT	CHAIN	1	32	POTENTIAL.
FT	DOMAIN	33	912	METABOTROPIC GLUTAMATE RECEPTOR 4.
FT	TRANSSEM	588	610	I (POTENTIAL).
FT	DOMAIN	611	624	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	625	645	II (POTENTIAL).
FT	DOMAIN	646	656	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	657	675	III (POTENTIAL).
FT	DOMAIN	676	699	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	700	720	IV (POTENTIAL).
FT	DOMAIN	721	750	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	751	772	V (POTENTIAL).
FT	DOMAIN	773	785	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	786	808	VI (POTENTIAL).
FT	DOMAIN	809	821	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	822	847	VII (POTENTIAL).
FT	DOMAIN	848	912	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	98	98	POTENTIAL.







FT TRANSMEM 751 772 V (POTENTIAL).  
 FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 786 808 VI (POTENTIAL).  
 FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 822 847 VII (POTENTIAL).  
 FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 98 98 POTENTIAL.  
 FT CARBOHYD 301 301 POTENTIAL.  
 FT CARBOHYD 454 454 POTENTIAL.  
 FT CARBOHYD 484 484 POTENTIAL.  
 FT CARBOHYD 569 569 POTENTIAL.  
 SQ SEQUENCE 912 AA: 101867 MW: 740D9054 CRC32;

Query Match 13.28; Score 837; DB 1; Length 912;  
 Best Local Similarity 26.5%; Pred. No. 7,84e-158;  
 Matches 211; Conservative 222; Mismatches 300; Indels 63; Gaps 50;

75 GHRLEAMLEALDRINNDPDLNLTGARIIDTCSRDHALBOSLTFOALIKDGTGV 134  
 71 GYLFQAMRTVEINSSALPNITLITGLDYCESANVA-TLR-VLAL-Q-GP-- 123  
 135 RCGSGPPIITKERVYVIGASGSSVIMVANIILFKIPQISYASTADLSDSRYDF 194  
 124 RHEIOKDRNHSKVVAFEPNDTHAVTTALLGPFILMPLVSYASSVLSAKRPPS 183  
 195 FSRVPSDYYQAMVDIYALKMNVSTVASEGSGESGVEAFLOKSRDEGVCAOSV 254  
 184 FLRTVPSDHQVEVMYOLLSFGVWISLIGSYGDGQGLQVQALBELAVPRG-ICVAFKD 242  
 255 KIPREKAGE--FDKIRRLLETSNARAVIIFANEDJIRVLEAARRANONGHFPMGSD 312  
 243 IVPFSARVDDPRMSQMOQLAQART-VVVFSSNHLAVERFSYVALNLGKV-WVASE 300  
 313 SWG-SK-IAPVHLBEVANG-AVTLIPKMS-VRGFDRTFSRTLDNNRNIMFAEFMED 368  
 301 DVAISTYITSTVGIOGIGVAVVQOORVPGIKFEESYV-RAVTAAPSAC--PE--G 354  
 369 NFHCLSRHALKKGSHVKCTNRERIGODSAEKGXQVYIDANYANGHALHAMHRDLC 428  
 355 SW-CS-TNQ-LORECHT--FTTRNPTL-GAFSMSAAYR-YEAVYAVAHGHOLL-G-C 405  
 429 PGRVGLCPRMDDVDTOLIKYIRANVFSGLAGNPTVENGDAGRGYDIYQOLRNSA- 487  
 406 TSEI--CSR-GPVYPMQLLOQYIKVNF-LHNVTAFPDNDDTLGYDILMD-WNGPEW 460  
 488 EYKVGSWT-DHLHRIER--MHWPSSGOQPRISCSLPQCPGGERKTKVGMPCWCEP 544  
 461 TFEIIGSASLSVHLDKTKTKIOMHGKNNVPSVCTTDCLAGHRRVYVSGSHCCFECVP 520  
 545 C-TG-YOYVDRYCTCKCPYDMRPTENRTGCRPIPIIKLEWSPMAVLPFLAVVGIAT 602  
 521 CEAGTFILMSLHICOPCGTEEMAPKRESTICFPRTVEFLANHEP-ISLVL-IAANTLLL 578  
 603 LEVYIT--FVKNPTPIYKASGRELSYVLAGIFLCATATFPLMAEDLTGCSLRITLG 660  
 579 LVTAGTGAFAHFTPVARSAGRLCLMLGSLVAGSCSFSEFGEPTVPACLLRQLFS 638  
 661 LGMISYAAALTKTNRIYRIPEOGKRSVAPRISPAQSALATPSLS--LQLLGIV-W 717  
 639 LGFALIFSLCLIRSFQVLIIFKESTKPTPYR-TWQNHGGLGVIVYSSVTHLL-ICLLW 696  
 718 FVYDPSISVVDQDRTLDPRFARGVLC-DISDLSLCLIGYSMLMAMCTVYAIKTRG 776  
 697 LVMTPTPTREYQ--R-F-PHLV--ILECTEVNSVGLFLAFTHNILLISTEPCSYLGE 750  
 777 VPENENAKRIGTMTYTTCIYMAFIPIFGTOSADKLYIOTTTLVSVSLASVSLG 836  
 751 LPEYVNAKCVTSLINFSWIAFTMA-SIYQSY-L-PAVNVLAGLITLSGGS-G- 805  
 837 LYMKVYIILFHEON 852  
 806 YFLPKVYIILCREPN 821

RESULT 9  
 ID MGR1\_RAT STANDARD; PRT: 1199 AA.  
 AC P23385;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.  
 GN GRI1 OR MGLUR1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPAGUE-DAWLEY; TISSUE-BRAIN;  
 RX MEDLINE; 91156047.  
 RA MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO R., NAKANISHI S.;  
 RT "Sequence and expression of a metabotropic glutamate receptor.";  
 RL Nature 349:760-765(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 92022526.  
 RA HOUAMED K.M., KUIJPER J.L., GILBERT T.L., HALDEMAN B.A., O'HARA P.J.,  
 RT MDLVIRHILL E.R., ALMERS W., HAGEN F.S.;  
 RT "Cloning, expression, and gene structure of a G protein-coupled  
 glutamate receptor from rat brain.";  
 RL Science 252:1318-1321(1991).  
 RN [3]  
 RP ALTERNATIVE SPLICING (1B).  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 92110002.  
 RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;  
 RT "A family of metabotropic glutamate receptors.";  
 RL Neuron 8:169-179(1992).  
 RN [4]  
 RP ALTERNATIVE SPLICING (1C).  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 93066232.  
 RA PIN J.-P., WAEBER C., PREZENTU L., BOCKAERT J., HEINEMANN S.F.;  
 RT "Alternative splicing generates metabotropic glutamate receptors  
 inducing different patterns of calcium release in Xenopus oocytes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS  
 MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
 CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL  
 ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN  
 THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY  
 TRUNCATED FORMS OF 1A.  
 CC -1- TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR  
 PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND  
 MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.  
 CC -1- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE >  
 TRANS-1-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY  
 2-AMINO-3-PHOSPHONOPROPIONATE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGLUR5.  
 CC  
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 CC  
 CC EMBL; X57569; CAA40799.1; -  
 CC DR EMBL; M61099; AAA19497.1; -  
 CC DR EMBL; S48085; AAB24138.1; -  
 CC PIR; S15362; S15362.



DR	PIR: A41939; A41939.
DR	GCRDB: GCR0216; -.
DR	PROSITE: PS00979; G_PROTEIN_RECPE_F3_1; 1.
DR	PROSITE: PS00980; G_PROTEIN_RECPE_F3_2; 1.
DR	PROSITE: PS00981; G_PROTEIN_RECPE_F3_3; 1.
DR	PFAM: PF00003; 7tm_3; 1.
DR	PFAM: PF01094; ANF_receptor; 1.
KW	G-protein coupled receptor; Transmembrane; glycoprotein; signal;
KW	Multigene family; Alternative splicing.
FT	SIGNAL 1 18
FT	CHAIN 19 1199
FT	DOMAIN 19 592
FT	TRANSMEM 593 615
FT	DOMAIN 616 629
FT	TRANSMEM 630 650
FT	DOMAIN 651 661
FT	TRANSMEM 662 680
FT	DOMAIN 681 705
FT	TRANSMEM 707 727
FT	DOMAIN 728 750
FT	TRANSMEM 751 772
FT	DOMAIN 773 785
FT	TRANSMEM 786 808
FT	DOMAIN 809 814
FT	TRANSMEM 815 840
FT	DOMAIN 841 1199
FT	DOMAIN 1014 1034
FT	DOMAIN 1074 1080
FT	DOMAIN 1126 1135
FT	DOMAIN 1140 1199
FT	CARBOHYD 98 98
FT	CARBOHYD 223 223
FT	CARBOHYD 397 397
FT	CARBOHYD 515 515
FT	VARSPHYC 887 906
FT	
FT	VARSPHYC 907 1199
FT	VARSPHYC 888 897
FT	VARSPHYC 898 1199
FT	
FT	SEQUENCE 1199 AA; 13335 MM; D5E211AF2 C8C32; .

Query Match	13.0%;	Score 821;	DB 1;	Length 1199;
Best Local Similarity	26.9%;	Pred. No. 4.63e-154;		
Matches	213;	Conservative	209;	Mismatches 314;
				Indels 56;
				Gaps 47;

Db	80	EA MHHTLDKINADVLLPNITLIGSEIRDSCHSHSVALEQSIETFRBDSLISIRBCKDCLNR	1399
OY	76	QAMREYVEEINNSSSALLPNITLIGELYDYCESA-NY-AT-UR-VL-ALOGPRH-IE-	1277
Db	140	CLPDGOTLPGRTRKPKPIAGVIGPSSSAIDOVOMLOLEDPQIAYSATSIDSDKTLX	199
OY	128	-IQK-D-LR-NHSSKYVA-FLGPONTBHAVTALLGPFLLMPLVSYASSVYSAAKKFP	182
Db	200	YFLRVVPDILQARAMLDIYKRYNMTYVASVHTEGNYESGOMAFKELAAEGICIAHD	259
OY	183	SELRTPSPDRHQYEVWVOLLOSFQWVWISLIGSYGDYGOIQALJEBELAVPRGICVAFK	242
Db	260	KI-YSN-AGESEPRBLRKLRELPKARYVYCEEGATVQGLLSAMRGLGVEFSLIGS	317
OY	243	IYPSFARVGDPRMOSMMOHL-AQ-ARTIVVYFENRHLARFFFSVYLANLTGVW-VAS	299
Db	318	DGMADRDVEVIGYEVEANGCI-TIKLOSPEVRSDDYFLK-LTRDTRNMPPE-FMOH	374
OY	300	EDMAITITITSVTIGIGTIGYLVGAIVOQROVPGLKEFEESYRVAVTVAAPSA-CPEGWC	358
Db	375	RFQ-CLEPGLLENDPNEFKVCTGNESSLEENYVODSKGFYIMAIYAHAGLQNNHHALC	433
OY	359	TNOLCR-ECHFTITRNMPTL--GAFSSMAAY---RV-Y-EAVYVAHGHQHL-C-CT	406
Db	434	GHVGLCDMAKRIIDGRKLLDFILKSFYGVSGSEELVPEDEKDAPOBRYIMNLQOTENR-Y	422
OY	407	SEI--C-SRGVYPMOLLQOIKYKNFLEHNTVAFGDNGDTLQYDIIMADWNGEPMTF	462

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Db 493 DYVHVGTHGEGVLYNDIKYO-MAKSGMYR-SVCSFPCXGOIVIRKGEVSCCMIC1AC 550
Oy 463 ELIGSAS:SPYHLIDINKTKIQWGRKNNOVPVSYTCICLGHNRHVW-GSHHCCFCEVCPC 521
Db 551 KENEVVO-DEF-TORACDGLGWWPAELETGCEPPVRYLWMSDIESIIAIFSCGILVTL 608
Oy 522 EAGTILNANSELHICOPCCTEBMAKRESTITCPRIVEFLANHEPISLVLIANTLITLVLV 561
Db 609 FYTLIFVLYRDTPVVKSSRSRELCYIILAGIFLGYVCPF-TLIAKPTTSCYLORLVLGVS 667
Oy 582 GJAGLEFAWHEHTPVVRSAGRLCFLMLGSLVAG-SCFYSFSEFPPTVACLLRQPLESLG 640
Db 668 SAMCSALVTTNTRARIARLASSKKKCTKRRKREVSANAOYIIASILISVOLTVLITIM 727
Oy 641 FAIFLSCTIIRSFOLVIFFKFSTK-VPEFVRTMAONAGLFLVVSSTVHLICLTMLVM 699
Db 728 EPPMELIYSRSIKE-VYLIC-NTSNLGVAVPVGNYGLIMSCYR-YAFKRRRNPANENEA 784
Oy 700 WTPRRTREXQAFPHVILIEC:EVSXSVGLFLAFTNTLISIS-IFVCGYLKELPENTANEA 758
Db 785 KYAIFATMYITCIWIAF-VB-IVEGNSYKIIITCFEAVS-SVTVALOCMFTPKMYIIIAK 841
Oy 759 KCVETSLNLNVSNIAPFTMASIVOGS-YLPBAAVNLAGJTLTSLGSGFGYFLPKCYVILCR 81,718
Db 842 PERANRASAFTTS 853
Oy 818 PELNANTEHOAS 829

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RESULT 10
ID MG92_HUMAN STANDARD: PRI: 872 AA.
AC Q14416;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DI 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.
GN GRM2 OR MGLUR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RA SEQUENCE FROM N.A.
RX MEDLINE: 95346007.
RA FLOR P.J., LINDAUER K., PUTTNER I., RUEGG D., LUKIC S., KNOPFEL T.,
RA KUHN R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 2."
RL Eur. J. Neurosci. 7:622-629(1995).
CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC MAY IMMEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN
CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE
CC ADULT BRAIN AS WELL AS IN FETAL BRAIN.
CC - SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR3.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L35318; AAA76855.1; -
DR CCDB: GCR 1846; -
DR MIM: 604099; -
DR PROSITE: PS00979; G_PROTEIN_REC_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_REC_F2_1; 1.
DR PROSITE: PS00981; G_PROTEIN_REC_F3_3; 1.

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DR PFAM: PF00003; 7tm\_3; 1.  
 DR PFAM: PF01094; ANF\_receptor; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KM Multigene family.  
 FT SIGNAL 1 18  
 FT CHAIN 19 872  
 FT DOMAIN 19 567  
 FT TRANSSEM 568 590  
 FT DOMAIN 591 604  
 FT TRANSSEM 605 625  
 FT DOMAIN 626 636  
 FT TRANSSEM 637 655  
 FT DOMAIN 656 679  
 FT TRANSSEM 680 700  
 FT DOMAIN 701 725  
 FT TRANSSEM 726 747  
 FT DOMAIN 748 760  
 FT TRANSSEM 761 783  
 FT DOMAIN 784 793  
 FT TRANSSEM 794 819  
 FT DOMAIN 820 872  
 FT CARBOHYD 203 203  
 FT CARBOHYD 286 286  
 FT CARBOHYD 338 338  
 FT CARBOHYD 402 402  
 FT CARBOHYD 547 547  
 SQ SEQUENCE 872 AA; 95507 MM; 9369084C CRC32;

Query Match 12.9%; Score 819; DB 1; Length 872;  
 Best Local Similarity 26.3%; Pred. No. 1.37e-153;  
 Matches 224; Conservative 227; Mismatches 339; Indels 63; Gaps 51;

4 LIALALLPLWG-AVAEGPARKVLTLEGLVGLGFLFVH---Q-KGGP-AEDCG-PVN-54  
 8 LLSLGLVYCAFCSCQRESSPGSLPEDFLAGLFLSHGCLQVRRHPLVTSQDRDSE 67;  
 55 EHRCIQRLKAMFLADLRINDPHLLPGVRLGAILLDSCKTALKEQALDFVRLSLRGA 114  
 68 NGHGHFLFOAMRFVEELINSSALLPNTLGLYELDYWCSESANYA-TL--RV-LA--L 120  
 115 DGSRLICPDGSYATHGAPTLITGVIGSSYDVSIOVANLLRLPQIPQISVYASATLSD 174  
 121 QGPRHT--ETQKDLRNHSSKYVA-FIGDNDHVTTRALLGPTLMPVSTYESSVLSA 177  
 175 KSRDYFARTVPDPFOAKAMAEILREFNMVYSTESEGDYGTGLAEFLERARNIC 234  
 178 KRKPSRLRTVPDRHQYEVWVQLQSGWVWISLISGYGLQVGLAEFLAVPRGIC 237  
 235 VAISEKVG-RA-MSRAPFEGVYVRLALQKPSARVAVLFTRESDARELLAASORLN-ASFTW 291  
 238 VAFEDIVPFSARVQDPRQSMQHLAQRRT-VVVVFESNRHLARVFRSVVLANLTGKVM 296  
 292 VASGMALESVAVSGSGAAE-GAI-TIELASPISDPASFQSLDPNNNSRNWFRFW 349  
 297 VASDMD-AISTYITTSVTGIGIGIVLGAOVOQROVPGLEKEEST-VRAVTAASACP-- 352  
 350 EORFCSFRQ--RDCAASHLRAVP-FEESK-IMEVV-NAVYAAHALLHNNHRLCEPTT 404  
 353 EGS-WGCTNQLCRCHFTTRNNMPTLGAFSMAAYRYEAYAAHGHQLL-G-C--TS 407  
 405 RLCDAMPVNGRLIKYKQFVLNFKDAPPRADTHNEVFRDFGIGIGIRNYFTYLRAGSG 464  
 408 EIC-SRGPVPMWLOO-IYKVF-L-LH--E--NTVAFDNGDGLIYYDIADWNGPE 459  
 465 R-YKX-QKVGWAGGLLUDSLIPWASPSAGPLAASRSECDLNEVKSQVPGVCCMLC 522  
 460 WTEFISASISPVHLIDINKRIQMGH-KNNQVNVSVCTDCLGHHRVVGVSHCCFEC 518  
 523 IPCOPYEY-RLDER-TCADGIGYV-PNASLTCGFELPOEYIRRGDANAVPYTIACGA 579  
 519 VPCAGTFLNMSSELHICQPCSTEMAPKES-TTCFPRVYELAHHPISLVLIANLTL 577  
 580 LATFLVGLVFNHNAFVYKASGRELCTILGVSFLCYCMTFFIFANPSTAVCTLRIGL 639

QY 578 LLVAGTAGLAWHFTHPVYRASAGRGFLCFLMGLSLVAGSCSFYFCEPVPADLLKQPLF 637  
 DB 640 GTAFSVYSAALKTNRIARFG-GAREGA-ORPRFISPAQVAILALISGLLIVAM 697  
 QY 638 SLGFAITLSCLLTRSDRIIFEFSTKVPFTYRTMONGAGLFLVYS-STVALLCLTW 696  
 DB 698 LVYEPATGKETAPEREVYTLRCNHRDA-SMUGSLAYNVLIALCTL-YAFNTRKCPEN 755  
 QY 697 LVWMTPTREYQRPFR-LVILECTEYNSVGFLLATHNLL-SISTFVCSYIGKELPEN 754  
 DB 756 FNEAKFIQFTMYTCIIWALLPIFYVTSDDYVQTTMCVSVLSGSSVGLCLAPKHA 815  
 QY 755 YNEAKCTFSLILNFMSWIAFTMASIYOGSYLPAVNVLAGLTLTSGGS-GY-FLPKCY 812  
 DB 816 IILFOPKQNVSH 828  
 QY 813 VILCRPELNTHE 825

RESULT 11  
 ID MGR1.HUMAN STANDARD: PRT: 1194 AA.  
 AC 013255; 013256; 014757; 014758;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.  
 GN GRM1 OR MGUR1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 96029774.  
 RA DESAI M.A., BURBENT J.P., MAYNE N.G., SCHOEPP D.D.;  
 RT "Cloning and expression of a human metabotropic glutamate receptor 1  
 alpha: enhanced coupling on co-transfection with a glutamate  
 transporter.";  
 RT Mol. Pharmacol. 48:648-657(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97231349.  
 RA STEPHAN D., BON C., HOLZWARTH J.A., GALVAN M., PRUSS R.M.;  
 RT "Human metabotropic glutamate receptor 1: mRNA distribution,  
 RT chromosome localization and functional expression of two splice  
 variants.";  
 RL Neuropharmacology 35:1649-1660(1996).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL  
 CC ACTION OF GLUTAMATE IN THE CNS. SUCH AS LONG-TERM POTENTIATION IN  
 CC THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: ALPHA (SHOWN HERE) AND BETA;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGUR5.  
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 CC \*\*\*\*\*  
 CC EMBL: U31215; AAA87843.1; -  
 CC EMBL: U31216; AAA87844.1; -  
 CC EMBL: U76627; AAB05337.1; -  
 CC EMBL: U76631; AAB05338.1; -  
 CC GCRDB: GCR\_1825; -  
 CC GCRDB: GCR\_1826; -  
 CC GCRDB: GCR\_1827; -  
 CC GCRDB: GCR\_1828; -



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DR GCRDB: GCR_1983;
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 1194
FT DOMAIN 19 592
FT TRANSMEM 593 615
FT TRANSMEM 616 629
FT TRANSMEM 630 650
FT DOMAIN 651 661
FT TRANSMEM 662 680
FT DOMAIN 681 706
FT TRANSMEM 707 727
FT DOMAIN 728 750
FT TRANSMEM 751 772
FT TRANSMEM 773 785
FT TRANSMEM 786 808
FT DOMAIN 809 814
FT TRANSMEM 815 840
FT DOMAIN 841 1194
FT DOMAIN 1014 1035
FT DOMAIN 1067 1081
FT DOMAIN 1095 1130
FT DOMAIN 1142 1194
FT CARBOHYD 98 98
FT CARBOHYD 223 223
FT CARBOHYD 397 397
FT CARBOHYD 515 515
FT VARSPLIC 887 906
FT VARSPLIC 907 1194
FT VARSPLIC 887 906
FT CONFLICT 593 593
FT SEQUENCE 1194 AA; 132376 MW; 6ACDFEC3 CRC32;

Query Match
Best Local Similarity 26.6%; Pred. No. 6,10e-152;
Matches 211; Conservative 210; Mismatches 315; Indels 56; Gaps 48;

Db 80 EAMFHLIDKINADVLPPLNTLCSFIRDSQWSSVALDSIFRSLISIRKQICINR 139
QY 76 QAMRFIVEEINSSALLPNTLTGLYDVCSESA-VNY-AT-LR-VL-ALQPRH-IE- 127
Db 140 CLPDGSLPPGRTKRPDIAGVIGPSSSSVAIOVNLQLEDPQIAYSATSIDSKTLTK 199
QY 128 -I-Q-KDLR-NHSSKYYA-FIGPDNDHATVTTALLGLPFLMPLVSEASSVLSAKRPF 182
Db 200 YELRVVPSDTLQARALDIYKRYNMTVSAVHTEGNYESGMDAFKELAAQEGCIAHSD 259
QY 183 SFELRTYPSRHOVEYVWQLQSGFWWISLIGSYGQGLQVQALBELAVPRGICVAFKD 242
Db 260 KTYSN-AEKSVDRLKRLKRLPRKRVVVCCEGMIVAGLSAKRRLGVCEPFLIGS 317
QY 243 IYFESRVADDPWQSMOH-AQ-ARTIVVYFSNRHLAEFRSVYLANLTCKW-VAS 299
Db 318 DGMADREVEIEGVEVANGCI-TIKLOSPEVRSFDYFLK-LRLDNTNRMPPE-FWQH 374
QY 300 EDMAITVITSTGTIGTIGLVANQOQVPLKKEFEESYVAAYAAPSA-CPESSWCS 358
Db 375 RFO-CRLPGHLENNPKFKICTGNESLEENYVODSKGEVINAIVAMHGLQNMHALCP 433
QY 359 TNLQCR-ECHITFTTR-MPT-LGAFMSAAY---RV-Y--EAVYVAHGLHQLL-G-CT 406
Db 434 GHVGLCDAAKPIDGSKLLDFLTKSSFIGVSGEYVWDEKDGADGRDIMLQTEANR-Y 492
QY 407 SET--C-SHGPAVPMQLLOQIKVNF-LHENTVAADDNDGLTYDYDIAMWNGGEWTF 462

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Db 493 DYVHWGTWEEGVLNIDYKIO-YNKSQVVR-SVCSPECLKGOIKVIRKGEVSCQWICAC 550
QY 453 ELIGSSLSLEPHDIKIKTIQWGNKNQVPSVCTICDLAGHRRVY-GSHHCPCPCVC 521
Db 551 KENEIVQ-DEF-TCKACDIDGMWPNADLTGCEPIPVARYLEMSNIEPIAIAFSCGLIVTL 608
QY 522 EAGTFLNMSLEHICQPCGEEMAPKRESTICFPRTVEFLMHEPISLIVIANLTLLILLV 581
Db 609 FYLLIVLRDPPVYKSSSRELCTIILAGIFLYVQCF-TLAKPTTSCYIQRLLVGS 667
QY 582 GTGLAFMHPHPVVSAGGRLOFLMGLSVAG-SCSEYVSFEPEVPVACILRQPLFSIG 640
Db 668 SAMCYALVTKTRIRIARIAGSKKICTRKPSPMSAAQVIAIISILYQVLFVTLIM 727
QY 641 FAFPLSCLIRSQVLIIRKFSK-VPTFYRMAQNHGAGLYVSVTHLLICLTWLV 699
Db 728 EPPMPLSPSKE-VYLIC-NTSNIGVAPLQVNGLIMSCY-YAEFRVNPANFNA 784
QY 700 WTRPRTREVQRFPHVILCTEYNSVGFLLAETHN-TLSIS-TFVCSYLKELPENYND 758
Db 785 KYIAFMVYTCIIWAF--VP-IYFSNKKIITTCVAVSLSTVALGCMFTPRMIIIAK 841
QY 759 KCVTSLLINFEVSWIAFFTMASTYQGS-YLZAVNVLAGJTLUSGFSYFLPCVILCR 817
Db 842 PERNVRSATTS 853
QY 818 PELNTEHFOAS 829

RESULT 12
ID MGR3_HUMAN STANDARD; PRT; 877 AA.
AC Q14832;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
GN GRM3 OR MGLUR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 96437205.
RA MAKOFF A., VOLPE F., LELCHUK R., HARRINGTON K., EYSON P.;
RT "Molecular characterization and localization of human metabotropic
RL glutamate receptor type 3."
RC Brain Res. Mol. Brain Res. 40:55-63(1996).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR2.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X77748; CAAS4796.1; -.
DR GCRDB: GCR_2070; -.
DR MIM: 601115; -.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.

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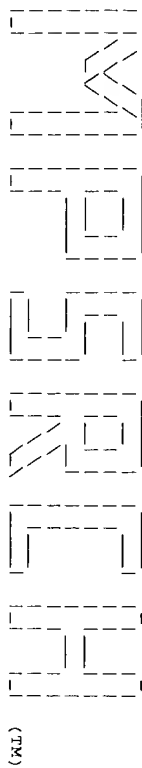
QY 71 GYHLFOAMRFTVEEINNSSALLPNTIGELYLVCS-ESANYATLR-VIAL-Q-GPRHI 126  
DB 132 KCANGDPPIFKDRIKSGVIGAAASVSIMVANILRLFKIPQISYASTAPELSDNTRYDE 191  
QY 127 ELOK-D-LRNHSSKYVAIFGPNTDHAVTIALLPFLPLVSYEASSVLSAKRRFPS 183  
DB 192 FSRVVPDSDYQAOAMVDIYALGMYVSTLASENGYSGEVEAFIQISREIGVCIAQSQ 251  
QY 184 FLRTVPSDRHQVEVMVQLOSFQWVWISLIGSYGDYQGLGVQALELAVPRG-ICVAFKD 242  
DB 252 KIPREPRGE--FEKIKRLLETPNARAVIMFANEDDIRILEAKKLNOGHFLIGSD 309  
QY 243 IVPFSARVGDPRQSMOHLAQART-VYVVFNSRLARVFRSVLANLTGR-VWVASE 300  
DB 310 SWG-SK-IAPVYQOEIEIAG-AVTILPKR-ASIDGFRYFRSRTLANNRRNWFAEFW-E 364  
QY 301 DMAISTYITSVIGIQIGIVLGAOVOOYOPGLKEFEEST-VRAVTAAPSAC-PEGSWCS 358  
DB 365 ENFGCKLGHGRKRNHKKCTGLERJARDSVYOEKGVOFVIDAVYSMAAYALHMHKDLQ 424  
QY 359 TNOLOCR-ECH-TETTR-NMPT-LGAFSMAAY---RV-Y--EAYVAVAHGLHQLL-G-C 405  
DB 425 PGYIGLCPKMSITDCKELLCYTRAVNFNGSAGTPVTFNENGDAFGXYDIPQOITNKSTE 484  
QY 406 TSEI--CSR-GPYWPOLLQOIKYKNFLHENT-VAFDNGDTLGYDIIAMDMNGPEWT 461  
DB 485 YKVIQWMT-NOLHXVED--MOMAHREHTHPASVCSLPCPKGERKKTGVGPCMHCERC 541  
QY 462 FELIGSASLSPVHLIDINKRKIONHGKKNNOVPVSVCTDCLAGHHRVVGSHCCFECVPC 521  
DB 542 EGVNY-QVDELS-CELCPLDQRPNNMRTGCOLIPIIKLEHSPMAVVPYVAILIGIATY 599  
QY 522 EAGTEFLMSELHICQCGTEEMAPKRESTICFPRTVEFLAMHEPISLVLIANTLILLLV 581  
DB 600 FYIVTVRINDPIYVASGRELSTVLTGIFLCYSTFL-MIAPDTIICSEFRVFLG 658  
QY 582 GTAGLEFAMHFTPVVASAGRLCFML-GSLVAGSCSFYSFGEPTVPACLLRQPLFSIG 640  
DB 659 MCFSAALLTKINRIHRIFEQKKSVTA-PKEI-SPASQVITFSLISVOLLGVFWFVY 716  
QY 641 FAIFLSCLTIRSFOLVIRKFSKVPFTFRIMQONHAGLFVIVS-STVHLILCLTLVW 699  
DB 717 DPPHIIIDYGEORTLDPEKARGVLC-DISDLSLCSLGSYLIMVTCVYANKTRGVPE 775  
QY 700 WTPRPRTREY--QR-F-PHLY--ILECTEVNSVGLAFTHNILLSTSTFCVSLGKELPE 753  
DB 776 TENEAPRTGFTMYTTCIIMLAFIPFFGTAQSAEKMYIOTTLTVSKS--LSASVSLGMLY 834  
QY 754 NYNEACVTFSLINFSWIAFFTMA-SIYOGS--YLPVAVNLAGITLISGGFS-G-YF 807  
DB 835 MPKVYIIIFHPEON 848  
QY 808 LPRCIVILCRPELN 821

Search completed: Fri Mar 17 13:05:03 2000  
Job time : 105 secs.









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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Fri Mar 17 13:02:07 2000; Maspar time 35.36 Seconds  
Tabular output not generated. 951,981 Million cell updates/sec

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Description: (1-840) from US09361652.pep  
Perfect Score: 6338  
Sequence: 1 MFMMAHLLLSQLVYCNMF.....NNTHEHQASIQYTRRCGT 840

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r62  
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 52.607; Variance 107.685; scale 0.489

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1311	20.7	1085	2	S40476	Ca(2+)-sensing recept
2	1293	20.4	1078	2	S49341	calcium-sensing recep
3	1290	20.4	1078	2	A56715	calcium receptor (clo
4	1285	20.3	1079	2	159362	calcium/polyvalent ca
5	1198	18.9	1088	2	B56715	calcium receptor (clo
6	873	13.6	1171	2	A42916	metabotropic glutamat
7	870	13.7	1180	2	JC2132	metabotropic glutamat
8	870	13.7	1212	2	UC2131	metabotropic glutamat
9	847	13.4	872	2	JH0561	metabotropic glutamat
10	843	13.3	912	2	JH0563	metabotropic glutamat
11	841	13.3	912	2	158149	metabotropic glutamat
12	840	13.3	1218	2	171376	metabotropic glutamat
13	821	13.0	1199	2	A41939	glutamate receptor ho
14	806	12.7	908	2	149142	G protein-coupled glu
15	793	12.5	879	2	A00562	metabotropic glutatu
16	772	12.2	871	2	A46742	metabotropic glutamat
17	755	11.9	915	2	A49874	metabotropic glutamat
18	208	3.3	958	2	T02741	probable ligand-gated
19	196	3.1	1005	2	S33525	guanylate cyclase (EC
20	177	2.8	940	2	T02740	probable ligand-gated
21	166	2.6	938	2	T01809	hypothetical protein
22	162	2.6	960	2	JE0356	gamma-aminobutylic ac
23	163	2.6	965	2	151244	N-methyl-D-aspartate

24	149	2.4	934	2	T02742	probable ligand-gated
25	145	2.3	885	2	A47551	N-methyl-D-aspartate
26	144	2.3	885	2	JN0339	N-methyl-D-aspartate
27	144	2.3	901	2	JN0337	N-methyl-D-aspartate
28	144	2.3	922	2	JN0338	N-methyl-D-aspartate
29	145	2.3	938	2	A46612	N-methyl-D-aspartate
30	144	2.3	938	2	C19710	N-methyl-D-aspartate
31	144	2.3	962	2	C43274	N-methyl-D-aspartate
32	144	2.3	997	2	S33754	glutamate receptor -
33	145	2.3	1203	2	155466	N-methyl-D-aspartate
34	145	2.3	1239	2	149705	glutamate receptor ch
35	144	2.3	1250	2	B45219	N-methyl-D-aspartate
36	142	2.2	1125	1	0YURCP	spectact receptor prec
37	130	2.1	986	1	0YURCA	spectact receptor prec
38	125	2.0	1323	2	S27224	N-methyl-D-aspartate
39	126	2.0	1323	2	S27224	N-methyl-D-aspartate
40	126	2.0	1356	2	C45219	N-methyl-D-aspartate
41	127	2.0	1464	2	S47555	N-methyl-D-aspartate
42	122	1.9	1323	2	178557	N-methyl-D-aspartate
43	123	1.9	1454	2	S29159	glutamate receptor, N
44	123	1.9	1464	2	A43274	N-methyl D-aspartate
45	120	1.9	1482	2	149704	glutamate receptor ch

ALIGNMENTS

RESULT 1  
ENRI S40476 #type complete  
TITLE Ca(2+)-sensing receptor - bovine  
ORGANISM #formal\_name Bos primigenius taurus #common\_name cattle  
DATE 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999

ACCESSIONS S40476  
REFERENCE S40476  
#authors Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kilfor, O.; Sun, A.; Hediger, M.A.; Lytton, J.; Hebert, S.C.

#journal Nature (1993) 365:575-580  
#title Cloning and characterization of an extracellular Ca  
(2+)-sensing receptor from bovine parathyroid.  
#cross-references MIMD:94077182  
#accession S40476  
#status preliminary  
##molecule\_type mRNA  
##residues 1-1085 #label BRO

SUMMARY  
Query Match 20.7%; Score 1311; DB 2; Length 1085;  
Best Local Similarity 31.9%; Pred. No. 3,226-229;  
Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;

Db	31	GDIILGIFPIHFG-VAVKODLKSREPSEVCIRYNGFRFWLQAMTFAIEINSSPALL	89
Oy	35	GDPLAGIFSLHGDCLOVRHRLVTSIDRPS--FNGHGHLFOAMFTVEEINSSALL	92
Db	90	PNNLTGRIPTCTVSKALPATISFAVONKIDSLN--DECCNGSEH--PTIAVVGARGSG	149
Oy	93	PNITLGEIYDVCSESNVY-ATLRVALDGPRIETOK--DLRNHSSKVVAIFGPNITD	149
Db	150	ISTAVANLGLFYIPQVSYASSRLSNKQFKSLRTINDEHQARADIIIEYFMMW	209
Oy	150	HAVTVALIGFLFPLIVSYEASSVYLAKRKFPLFTVSDRQVEMVQGLLOFQMW	209
Db	210	VGTIADDDIGRPGIEKFRFAEERDIDFSELI--SQSDEKIQOQVEIVONSTAKV	267
Oy	210	ISLIGSYGDVGOLEVALLEELAVPRGICVAFKDIIPVSARVGDPMQSMHQLQARTV	269
Db	268	IIVSSSGDLEPLT-KETVRRNTGRVLAASEMAASSITAMPYFHVVGITIFGLKAG	326
Oy	270	VWVFSN-RHLARVFRSVLANLTGKVVASEDA---IS-T-YITSVG-ID-GI--G	318
Db	327	QIPGFRFLQVHPKRSVHNGFAKEFEETFNCHLQAGANGPLVPDFFLGHHEGGRALS	386



QY 319 TVLG---VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P-S--ACPEG-SW-C 357

Db NSPTAFRLCTGEENISSEVENPYMDYTHLRISYNYVLAIVASIAHALODIYICBGRGLFT 446

QY 358 -S-IN-Q-LCECHFTTRNPTLTAFSMSAAYRYEYAVAHGLDGLGCTG--I-- 409

Db 447 NGSCADIKKVEAMQVLKHLRLNFTSNMGEOVTEDECDLGNYSIIMHLSPEDEGSIVF 506

QY 410 --CS-RGPVYPMQLDQIYKYNFLH-ENTVAFDDNGDITGYDIIAMDMNGPE-WT-F 462

Db 507 KEVGYVNYAKKGERLFINDEKILMSGFSREVPSCSRDCLAGTRKGIIEGEPTCCFEC 566

QY 463 EIIQ--SA-SLSPVHLIDNKTIRIOMHGKNNQVPSVCTDCLAGHRRVY-GSHHCPEC 518

Db 567 VECPDGEYSDTDASACKCPDDDFWSNENHTSCAKIEFLSWTEPFGIALTLFAVLGIF 626

QY 519 VPCEAGTFLNNSLHICPCGTEBAPKESITTCPRIVYEFLLAMHPEISLVLIANTLLL 578

Db 627 LTAFLVLGVFI-KFRNTPIVAKTNRELSTYLLFSLCCFSSSLF-FIGBPDWTCRLRQPA 684

QY 579 LTVGAGLFAWHFH-TPVVRSAGRLCFMLGSLVAG-SCSFYSFSGEPYVACULRQPL 636

Db 685 FGISFVLCISCIIVKTNVLLVEF--AKIPTSFHRKMGMLNQLVFLVCTFMQIVICAI 742

QY 637 FSLGFAIFLSCLTIRSFQVLIIFKSTKVPF-FYRTWAQNHGAGLFAIVSSVTHLLICLT 695

Db 743 WLNTAPSSYNHLEDEIFITCHEGSLMALGLIGYTC-LLAICEFF-AFKSRKLE 800

QY 696 WLWMTPTPEYORFPLVILIECTEVN--SVGFLATTHNLLISITFVCSYKLEPE 753

Db 801 NFNEAKFTFSMLJEFIWISFIPAYASTY-GKEVSAVEVIAIILASGLLACIFENKY 859

QY 754 NYNEAKCVTFSLNLFVSWIAFETW-ASIVOGSYLPAVNVLAGLTLTSGSGYFLPCY 812

Db 860 IILFKPSKNTIE 871

QY 813 VILCRPELNTE 824

RESULT 2

ENTRY S49341 #type complete

TITLE calcium-sensing receptor - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 03-Aug-1995

ACCESSIONS S49341; A49419; B49419; C49419

REFERENCE S49341

#authors Pearce, S.H.S.; Thakker, R.V.

#submission submitted to the EMBL Data Library, August 1994

#accession S49341

#status preliminary

#molecule\_type DNA

#residues 1-1078 #label PEA

#cross-references EMBL:X81086

REFERENCE A49419

#authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levl, T.; Seidman, C.E.; Seidman, J.G.

#journal Cell (1993) 75:1297-1303

#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism.

#cross-references MUID:94094324

#accession A49419

#status preliminary

#molecule\_type DNA

#residues 178-180, 'K', 182-192 #label POL

#experimental\_source family N

#note sequence inconsistent with nucleotide translation

#note sequence modified after extraction from NCBI backbone

#note 186-Arg mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism

#note sequence extracted from NCBI backbone (NCBIN:142453)

#accession B49419

#status preliminary

#molecule\_type DNA

#residues 289-303 #label P02

#experimental\_source family E

#note sequence modified after extraction from NCBI backbone

#note 298-Lys mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism

#note sequence extracted from NCBI backbone (NCBIN:142455)

#accession C49419

#status preliminary

#molecule\_type DNA

#residues 788-802 #label P03

#experimental\_source family J

#note sequence modified after extraction from NCBI backbone

#note 796-Tyr mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism

#note sequence extracted from NCBI backbone (NCBIN:142457)

SUMMARY

##note

##length 1078 #molecular\_weight 120672 #checksum 8159

Query Match 20.4%; Score 1293; DB 2; Length 1078;

Best Local Similarity 32.0%; Pred. No. 1,51e-225;

Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

Db 30 GDIIILGHPFHHC-VAAKODLKSRESVEICIRYNERGFRWIOAMFAIEINSSPAL 88

QY 35 GDFLLAGLFSJHGDCLOVRHPLVTSRDPDS--FNGGHYLRQAMFTVEIINSSALL 92

Db 89 PNLLIGRIEDTCTVSKALEATLSFYAONKIDSLNDEFNCSEHPISTAVVAGSG 148

QY 93 PNILIGELVDGSESNVY-ATLRVALAQPRNIEIQK--DLRNHSSKYVAFIGPNTD 149

Db 149 VSTAVANLGLFPIPVYSSSSRLSKNNOFGLTIRPDEHQATAMADIIYFPMW 208

QY 150 HAVTTAALLGFLMPLIVSYSAKRSVLSAKRKFSEFLTRVPSDRQVEMVOLLQSFWM 209

Db 209 VGTIAADDYGRPGIEKFEAREEDICIDFSELI--SQSDEEIOHVVVEIONSRKY 266

QY 210 ISLIGSGDGLQVQLLEELAVPRGICVAFKDIVPSARVGDPRMOSMQLAQATTV 269

Db 267 IVFSSGPDLLEPLI-KEIVRNITGKIWLASEAWASSLIAMPQFVVGGTIGFALKAG 325

QY 270 VVVFSSN-RHLARVFRSVLVANLQKVAWSBDA----IS-T-YLISVG-IG-GI-G 318

Db 326 QIPGFREFLKVHPKRSVHNGFAKEWETFNCHLOGAGPLVDFTFLGHESGDRFS 385

QY 319 TVLG---VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P-S--ACPE-GSM-- 356

Db 386 NSTAFRLCTGDENISSEVENPYDTHLRISYNYVLAIVASIAHALODIYICBGRGLFT 445

QY 357 -CSIN-Q-LCECHFTTRNPTLTAFSMSAAYRYEYAVAHGLDGLGCTG--I-- 406

Db 446 NGSCADIKKVEAMQVLKHLRLNFTSNMGEOVTEDECDLGNYSIIMHLSPEDEGSIVF 505

QY 407 SEIS-RGPVYPMQLDQIYKYNFLH-ENTVAFDDNGDITGYDIIAMDMNGPE-WT-F 462

Db 506 KEVGYVNYAKKGERLFINDEKILMSGFSREVPSCSRDCLAGTRKGIIEGEPTCCFEC 565

QY 463 EIIQ--SA-SLSPVHLIDNKTIRIOMHGKNNQVPSVCTDCLAGHRRVY-GSHHCPEC 518

Db 566 VECPDGEYSDTDASACNKKCPDDDFWSNENHTSCAKIEFLSWTEPFGIALTLFAVLGIF 625

QY 519 VPCEAGTFLNNSLHICPCGTEBAPKESITTCPRIVYEFLLAMHPEISLVLIANTLLL 578

Db 626 LTAFLVLGVFI-KFRNTPIVAKTNRELSTYLLFSLCCFSSSLF-FIEBPDWTCRLRQPA 683

QY 579 LTVGAGLFAWHFH-TPVVRSAGRLCFMLGSLVAG-SCSFYSFSGEPYVACULRQPL 636

Db 684 FGISFVLCISCIIVKTNVLLVEF--AKIPTSFHRKMGMLNQLVFLVCTFMQIVICAI 741

QY 637 FSLGFAIFLSCLTIRSFQVLIIFKSTKVPF-FYRTWAQNHGAGLFAIVSSVTHLLICLT 695



DB	742	WYTRPSSYSNOELEDLIIITTCHEGSLMGLIYTC-LLAICOFF-ARKSKULE	799
QY	666	WLVMMTPPRITREYQFPPHLVILLECTEVN--SVGFLLAFTHNLLISTSTFCSTYGLKELE	753
Db	800	NENAKFTTESLFIIFWISFIPAVASTY-GKFSVAVEVIALIILASFGIACIFFNKTY	858
QY	754	NNENAKCFTFLLNFVSWIAFFIM-ASIVGSLPRAVNNLAGITLISGFSOIFPKCY	812
Db	859	ILFKFSRNRTIE 870	
QY	813	VILCRPELNTTE 824	
RESULT	3		
ENTRY	A56715	#type complete	
TITLE	calcium receptor (clone p1pCa4.0) - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999		
ACCESSIONS	A56715		
REFERENCE	A56715		
authors	Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.		
#journal	Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F.		
#title	J. Biol. Chem. (1995) 270:12919-12925		
#cross-references	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.		
#accession	M01D:95279439		
#status	A56715		
#molecule_type	preliminary		
##residues	1-1078 ##label GAR		
##cross-references	GB:U20759; NID:G683744; PID:G683745		
KEYWORDS	glycoprotein; receptor; transmembrane protein		
SUMMARY	glycophorin 1078 #molecular_weight 120537 #checksum 7868		
Query Match	20.4%; Score 1290; DB 2; Length 1078;		
Best Local Similarity	32.0%; Pred. No. 6,16e-225;		
Matches	273; Conservative 230; Mismatches 276; Indels 73; Gaps 45;		
Db	30	GDIIIGLFPPIHFC-VAAKDODLKSREPSEVCIRYNERGRFWMQAMIFALIEITNSPALL	88
QY	35	GDPLAGLFSLHGCOLQYRHRPRLVTSDDRPS--FNGHGHLQOAMFTVEEINNSALL	92
Db	89	PMLTIGYIPEDNTNVSKALEATISFAQKIDSLNDECCNSEHPIPIAVAGATGG	148
QY	93	PNITIGIYLVCSASAVY-ATLRVATLQGPRIETQK--DLRNSKVVATIGDNTD	149
Db	149	VSTAVANLGLFIPOVSYASSRLLSNKNOFKSLTIPNDEHOATAMADIEFRMM	208
QY	150	HAVTAALGLFLMPDIVSYEASSVYLAKRFPRLFTVSDRHOVEYVMQVLLSGCW	209
Db	209	VGTIADDDYRPGIEKREFAERDIDCFSELI--SQYSEDEIOHVEVIONSTAKV	266
QY	210	ISLISSYDYQOLQVQALEELAVRGICVAFKDIIVPSASVGPDRMQSMOHIQAQRTIV	269
Db	267	IIVFSSGDEPLLI-KEIVRENTIKIMLASEMAVSSLLAMPQYEVVGGIIGFALKAG	325
QY	270	VVPSN-RHLRAVFRSRVLANITGKVAVSEDM-----IS-T-YITVSTG-IQ-GI-G	318
Db	326	QIPGREFLKVHPRKSYHNGFAKEFEETFNCHLOGAGPLPVDTFLRGHEESGDRS	385
QY	319	TVLG---VA-VQORQ-VP-GL-KEF-EESY---VR-AVRIA-P-S---ACE-GSW--	356
Db	386	NSTAFRLCTGDENISSVEPIYDTHLRKSYNYLAVVISIAHALODITYCLPGGLT	445
QY	357	-CSTN-Q-LCEECHFTTRNMPITGASMSAAVYDAVYAVALHGHOL--L-GC--T	406
Db	446	NGSCADIKKVAAMQIKLRILNTNNNGEVTDECGDVGKYSIIMHLSSEDSIYE	505
QY	407	SEIC-SRPPYVPMQLOOIKYKNLLH-ENTVAARDNGDITGLYDITIAMDNQPE-WT-F	462
Db	506	KEVGVYNAKGERLPIINEKILMSGFSREVPNSRCDLAGTRKGIIEGPTCCFEC	565

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QY      463 ELIG--SA-SLSPVHLJDINKRKIQWGHKNNOVPVSVCTTDLCLAGHHRVY--GSHHCCFEC 518
Db      566 VECPDGEYSDETDASACNKKCPDDFWSENHNTSCIJAKIEFLSWTEPPGIALTFFAVLGI 625
QY      519 VPCGAGTFLNSELHICQPCGTSEEMAPKRESITCPRVVEFLAMHEPISIVLIANTLLLL 578
Db      626 LIAFLVGLVFT-KFRNPTEVXKATNDELSTLLLSLLCCFSSSLF-FIEPDMDTCRLRQPA 663
QY      579 LLYGTAGFLAMFH-FTPVARSAGRLCFLMGLSGSLVAG-SCSFYSFECEPVPACLLRQPL 636
Db      684 FGISVLCISCLVYKTNVLLVFE--AKIPISPHRKMGSLNGLFVLELCTFMQIVCVI 741
QY      637 FSLGRHFLSCLTISFSLVLIIEFTSTVPF-FRIRAKNGAGLFLVIVSVHLLCLT 695
Db      742 WETAPSPSRNOEDEDIEITTCHEGSLMAGFLIYVTC-LLAALICFF-AFRSKRLPE 799
QY      696 WLVMPTPRTRRYQAFPLVILLECTEVN--SVGFLAFTHNLLISITFVCSYLGKRLPE 753
Db      800 NNEAKFTFSKLIFFIYIWISFIPPAVASTY-GKRVASVEVYAIILAAISFGLLACIFENKIY 858
QY      754 NYNEAKCVTFSELLENFWSIAFFTM-ASIVGSLYLPVNVYLAGLTLLSGFSGYFLPKCY 812
Db      859 ILTFPSRNTIE 870
QY      813 VILCRPELNTE 824

RESULT      4
ENTRY      159362      #type complete
TITLE      calcium/polyvalent cation-sensing receptor precursor - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE      02-Jul-1996 #sequence_revision 02-Jul-1996 #-ext_change
            01-May-1998
REFERENCES
#authors   Kuwat, M.; Kolliver, M.E.; Snowman, A.M.; Snyder, S.H.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165
#title     Calcium sensing receptor: molecular cloning in rat and
            localization to nerve terminals.
#cross-references MUID:95241465
#accession I59362
#status     translated from GB/EMBL/DBU
#molecule-type mRNA
#residues  1-1079 #label RES
#cross-references EMBL:C20289; NID:g790578; PID:g790579
REFERENCE
#authors   Ricciard, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.;
            Hebert, S.C.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135
#title     Cloning and functional expression of a rat kidney
            extracellular calcium/polyvalent cation-sensing receptor.
#cross-references MUID:95116508
#accession A55594
#molecule-type mRNA
#residues  1-133, 'X', 135-1079 #label RIC
#cross-references GB:u10354
##experimental_source kidney
KEYWORDS    calcium; glycoprotein; phosphoprotein; transmembrane protein
FEATURE
1-20      #domain signal sequence #status predicted #label SIG\
187-212   #region hydrophobic\
613-635   #domain transmembrane #status predicted #label TM1\
650-670   #domain transmembrane #status predicted #label TM2\
683-700   #domain transmembrane #status predicted #label TM3\
725-744   #domain transmembrane #status predicted #label TM4\
770-790   #domain transmembrane #status predicted #label TM5\
806-828   #domain transmembrane #status predicted #label TM6\
841-860   #domain transmembrane #status predicted #label TM7\
90,261,,267,386,468,
488,594,893,1005 #binding_site carbohydrate (Asn) (covalent) #status
predicted\

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D	b		207	KRYNLTYSAVTTEGNYGGSGMEAFEDMSAKRGICIAHSYKTL-YSN-AEGSFFDLTKLTK	264
Oy			203	OSFGWMTSLISSTGYGLGVQLVEELVAPRGICAFQDIOPFYSRKYSDPPRMQSOMHL	262
D	b		265	TSHLRKARYAACFCGCMGTGRGLMMRRRLIGLAGEFLLGSDDMA-DRYDVT-DGYO-REA	321
Oy			263	A-Q-ARTTVVVVFNSRHRLARVEFRSVLVLANLGK-VWVASDEMALITYITSTVGIOGIST	319
D	b		322	VGGITIKL-QSPDVYWFEDDYLYKLRPETNRHPWFQEFQHRPOCHRSCEPDENSKYNT	380
Oy			320	VLGVAVOORQVPGTLKEFEESYVRATYAAPSAC--EGSW-----CSTNOLCRECHFT-T	371
D	b		381	CNSSLTLEKTHHODSMGCVINAIYASMAGLNNMOSLSGPRAGCDAAKPIDGRKLIES	440
Oy			372	RMP-TLGFASFSAAYRY--EAYIVAHGLIOL-LG-CTS-E-IC-SNGPYPMOLLQ	423
D	b		441	LMKTNETGVSGDTILFEDENGDSRGREYINFKEMGRDY-FDIYNVSMDNGELKMDDEV	499
Oy			424	IKYVMFL-LHEHTVAFDONGDLTGYYDILAMNMNGEWTFELLIGSSLSPLHLDINKTI	482
D	b		500	-WSKSNIIR-SYGSEPCERGOIKVIYRKGEVSCWTCPCKENEYV-FDE-YTCACQLG	555
Oy			483	QMHGKNNOVPVSYCTCDLAGHHRVV-GSHRCCECVACEAGTELINMSELHCOPCGTE	541
D	b		556	SMPDDLGLGCDLIPOYLWMGSRPEPIAAYVFPCLGIATLFV-TVFIILYR-DTPVKKSS	613
Oy			542	EAPKEPSTCCPRTYEFLAM-H-EPISTVLANTALLLLVLGTAGLFMHHTPVVRA	599
D	b		614	SRELCTYIIILAGICLYLCTFC-LIAKPKOICYLORIGIGLSPAMSYSALVTKTNRIARI	672
Oy			600	GGRLOCFIMGLSVAS-CSFYSPFGSPPTACLLRPLSLSPALFSLCSLTRSQVLII	658
D	b		673	LAGSKKICTK-KPRMSACADLVAFILICIQGLIYALFTMEPPDINHDPISIRE-VY	730
Oy			659	FKFSTR-VPTFERTMAONHAGLIFV-IYSTVHLICTLTMWMPTRPREYORPFHLVI	716
D	b		721	LICNTNT-LGVYTPGLGNLLLSICF-YAFKTRNPANFNPAKTYAFMTYTICIWLAF	788
Oy			717	LECTEVNSVGLIATFHNLISLS-TEVCSTYGLKELPENYNEAKCYTFSLLINPFWIAF	775
D	b		789	--VP-IYFGSNKIITMCFSVS-ISATVALGCMFYPKVYIIIAKPERNARSFAFTS	840
Oy			776	FTMASIYGSYSLPANVNLAGLTTLSGGS-GY-PLPKCVIILCRBELNTEHFQAS	829
RESULT			8		
ENTRY		JC2131	#type complete		
TITLE			metabotropic glutamate receptor 5 B - human		
ORGANISM			#formal_name Homo sapiens #common_name man		
DATE			28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change		
			05-Jan-1996		
ACCESSIONS		JC2131			
REFERENCE		JC2131			
#authors			Minekami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;		
			Sugiyama, H.		
#journal			Biochem. Biophys. Res. Commun. (1994) 199:1136-1143		
#file			Molecular cloning and the functional expression of two		
			isoforms of human metabotropic glutamate receptor subtype		
			5.		
			#cross-references MUID:94197696		
			#accession JC2131		
			#molecule_type RNA		
COMMENT			##residues 1-1212 ##label MIN		
KEYWORDS			This protein is coupled to guanine nucleotide binding proteins.		
			glycoprotein; neurotransmitter; receptor; transmembrane		
			protein		
FEATURE					
			560-604	#domain transmembrane #status predicted #label TM1\	
			617-637	#domain transmembrane #status predicted #label TM2\	
			644-664	#domain transmembrane #status predicted #label TM3\	
			694-714	#domain transmembrane #status predicted #label TM4\	
			738-759	#domain transmembrane #status predicted #label TM5\	
			773-794	#domain transmembrane #status predicted #label TM6\	

[illegible]



DB	524	PCQRYE- RUDF- TCADGCLGW- PNASITGCFELPCTYIMGDMANVPYTIACAL	580
OY	520	PCBAGTEUNSESLICOPCGTEEMAPRES- TIOFPRVTEFLMHEPISLVLNAATLLIL	578
Db	581	ATLEVLGEVHNNAEPVKASGRELICYILLGGVFLCYCTEFVIAKPSAVTTLRLIG	640
OY	579	LLVGTAGLFANHFTEPVRSAGRLCFLMGSLVAGSCFFYFEGEPYPAQLLQPLFS	638
Db	641	TAFVCSALLTKTNRIARIFG- GABEGA- QRPRTISPAOVAICLALISGLLIYAAM	698
OY	639	LGPAIFLSCLTIRFQCVLIFKSTKVPFEYFRTMAQNGAGLFVYS- STVHLLICLTML	697
Db	639	VVEAPGICKETAPRRCVTLRCNHDA- SMGSLAVNVLALCTL- YAEFTRCPENF	756
OY	698	VMMPRPTREVRQRP- LVILLETVNSGFLAFPHNLL- SIFPVCSYSGKRLPENY	755
Db	757	NEAKFIGTWTTCIIMLAFLEFYVSSDYRQOTITMCVSLSGSVYGLGFLPKLHI	816
OY	756	NEAKCVTFSLTNVSMIAFTMASTYQGSYLPAVAVLAGLTLLSGFS- GR- FLPKCY	813
Db	817	TLFOPQKNVSH 828	
OY	814	ILCRPELNTEH 825	
RESULT	10		
ENTRY	JH0563	#type complete	
TITLE	metabotropic glutamate receptor 4 precursor - rat		
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat		
DATE	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998		
ACCESSIONS	JH0563		
REFERENCE	JH0561		
authors	Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.		
#journal	Neuron (1992) 8:169-179		
#title	A family of metabotropic glutamate receptors.		
#cross-references	MIMD:92110002		
#accession	JH0563		
##molecule-type	mRNA		
##residues	1-912	##label	TAN
##experimental-source	brain		
COMMENT	This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.		
CLASSIFICATION	#superfamily metabotropic glutamate receptor 4		
KEYWORDS	G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein		
FEATURE			
1-32	#domain signal sequence #status predicted #label SIG\		
33-912	#product metabotropic glutamate receptor 4 #status predicted #label MET\		
588-620	#domain transmembrane #status predicted #label TR\		
625-645	#domain transmembrane #status predicted #label TR\		
657-675	#domain transmembrane #status predicted #label TR\		
700-720	#domain transmembrane #status predicted #label TR\		
751-772	#domain transmembrane #status predicted #label TR\		
766-807	#domain transmembrane #status predicted #label TR\		
822-847	#domain transmembrane #status predicted #label TR\		
96,301,454,484,	#binding-site carboxylate (Asn) (covalent) #status predicted\		
569	#binding-site carboxylate (Asn) (covalent) #status predicted\		
621,689,695,859,	#binding-site phosphate (Ser) (covalent) #status predicted		
870	#binding-site phosphate (Ser) (covalent) #status predicted		
SUMMARY	#length 912 #molecular-weight 101818 #checksum 808		
Query Match	13.3%:	Score 843:	DB 2; Length 912;
Best Local Similarity	26.5%:	Score No. 1,19e-134;	
Matches	211; Conservative	222; Mismatches	301; Indels 61; Gaps 49;
Db	75	GIRHEMLAFALDRINDPDLNITLIGARILDTCGRDTHALFOSITFYQALIKNDGIV	134
OY	71	GTHLGFQARFVEINSSALLNITLIGELVDYCESANVYA- TLR- VLAH- Q- -GP- -	123



GENETICS	GL004	
#gene	#superfamily	metabotropic glutamate receptor 4
CLASSIFICATION	#neurotransmitter	receptor
KEYWORDS	#length	912
SUMMARY	#molecular_weight	101846
	#checksum	818
Query Match	13.38;	Score 841; DB 2; Length 912;
Best Local Similarity	26.58;	Pred. No. 2,97e-134;
Matches	211;	Conservative 222; Mismatches 301; Indels 61; Gaps
Db	75	GHHLEAMLFALDINDNDPLLNITLGGARILDTGSRDTHALEQSLITFYRALIENDGTREV 13
Qy	71	GHHLEAMLFALDINDNDPLLNITLGGARILDTGSRDTHALEQSLITFYRALIENDGTREV 13
Db	135	RCGGGEPITTKERVVGVYASGSSSVSYIMVNIILFKIPQISYASTAPDSDSRDF 19
Qy	124	RHIEIQDLKNNHSSKVVAFIGPDNDTHATTAALLGPIFLMPLVSYEASSVYLAKRKP 18
Db	195	FSRVVSDITVQAQAMDYVRLALKANVSTLASEGSGYGEAFIQRKRENGVCIASV 25
Qy	184	FLRVVSDITVQAQAMDYVRLALKANVSTLASEGSGYGEAFIQRKRENGVCIASV 25
Db	255	KIRREPTEGEFDK-IIRKLETSNAGNIIFPNEDIDRYVLEAARAGQTHFFMMSDS 31
Qy	243	IYVPSANVGPBRQSMQGLAQARTVYVVENRILAKYFRSRYLALTKV-VWASED 30
Db	314	WG-SK-SAPVLRLEEVAAES-AVTIIPKEMS-VRGEDRYFSRTLDNNRNITWFAEFEDN 36
Qy	302	WALSTYITSTVGLOGIGVLGVAQVQRPGLKEFEESYV-RAVTAAPSAC--PE---GS 35
Db	370	FHCKLSRHALKSKSHIKCTNERNIGDQSAVEQEKQGVFIDAYYAGMHLAHNRDLP 42
Qy	356	W-CS-TNQ-LCEBCH--FTTNMPTL-GAISMASANY-VYEAVYAAHGHOLL-G-CT 40
Db	430	GRVGLCPMDPVDGSQLKYIRNVNFSGIAGNPYTFENGGDAPERYDIYQYOLRNGSA-E 48
Qy	407	SEI--CSR-GPYRPMQLQOIKYKVF-LHENTYAFDNDGSLGYDIIAMD-WNGEPT 46
Db	489	YKYGWMT-DHILRIER--KQMPSSGQDLPRISCSLPCPQGERKKTVMKMACWCHEPC 54
Qy	462	FELISGASISPYHLDINKTKIQMGKNQNVASCTIDCLAGHRRVYVSGSHCCFECVPC 52
Db	546	-TG-YOYVDRTATCTCPYCDKAPTEENRTSCQPIYKLEWDSPAVLYPLAVANGIATL 60
Qy	522	EAGTFLNMSSELIHQPGCTEDMAKRESTITCPRIYVELANHEP-ISLVL-TAANTILLIL 57
Db	604	FVVV--FYRYNDPIYVASSRELSYLLAGIFCYATFIMTAEPDLGTSRRIFLGL 66
Qy	580	LVTGLGDPAMHEHHPVVASAGRCFLMTGLSVAGSCFYSFGEPYVPCILRLPLFSL 63
Db	662	GMSISYAAALIKRNIRIYIFQGRKRSVADRFISPAQOLITILIS--LQILGIV-WF 71
Qy	640	GAAILLSCLITRSQOLVITTFEISKVPYFR-TWAQNHGGLGVIVSSVTHIL-TCLTL 69
Db	719	VVDSHVSVPDQDRTDLPFRFAGVLKC-DISDLSTLCGLGSMMLAVTCYVATIKRGV 77
Qy	698	VMMTPRPREYO--R-F-Phly--ILECTEYNSGVFLATFTHILISIFVOSYIGKTL 75
Db	778	PETFEAKPISEFTMYTTCIWMIAFIPPIFPGTSSADKLYIQTTLLVSYSLASVSLGML 83
Qy	752	PENYEAACVTFSLILNFVSWIAFTWA-SITYGSY-L-PAVVVLAGITLLSGGFS-G-Y 80
Db	838	YMPKVIYIILFHEON 852
Qy	807	FLPKCYVILCRPELN 821
RESULT	12	
ENTRY	S71376	#type complete
TITLE	glutamate receptor homolog - cherry salmon	
ORGANISM	formal name Oncorhynchus masou #common_name cherry salmon	
DATE	11-Mar-1998	#sequence_revision 17-Apr-1998 #text_change 01-Mar-1998



Accessions	751376
REFERENCE	751376
Authors	Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
Journal	EES Lett. (1995) 392:71-76
Title	Cloning and characterization of a bifunctional metabotropic receptor activated by both extracellular calcium and glutamate.
cross-references	MUID:96354880
Accession	571376
Status	not compared with conceptual translation
molecule_type	mRNA
residues	1-1218 #label KUB
KEYWORDS	glycoprotein; phosphoprotein
FEATURE	
603-625	#domain transmembrane #status predicted #label TM1\
640-660	#domain transmembrane #status predicted #label TM2\
672-690	#domain transmembrane #status predicted #label TM3\
717-737	#domain transmembrane #status predicted #label TM4\
761-782	#domain transmembrane #status predicted #label TM5\
796-817	#domain transmembrane #status predicted #label TM6\
826-850	#domain transmembrane #status predicted #label TM7\
104,233,403,525,575	#binding-site carbohydrate (Asn) (covalent) #status predicted\
636,699,961	#binding-site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\
705	#binding-site phosphate (Thr) (covalent) (by protein kinase C) #status predicted\
892	#binding-site phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
SUMMARY	#length 1218 #molecular-weight 136838 #checksum 1674
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Best Local Similarity	27.5%; Pred. No. 4,70e-134;
Matches	198; Conservative 197; Mismatches 274; Indels 51; Gaps 38
D	166 IAGVIGPSSSVAYQVONLQVLFNIPQIAYATSIDSDKTLFFYFRVPSDTLQARAI 225
Q	139 VVAEIGPNDTHAATTAALLGPFLMPLFVSYASSSVLSAKKRPFSFRTVPSDRHQYEM 198
D	226 LDIVKRYWTVVSAVHTPEGNGYGESGMFEKFLASQEGICINHSKI-YSN-AGCKHEDR 283
Q	199 VQLLOSGFWWISLIGSGIDGIGQVQLAEFLAVPRGICVAFKQITVPSARVGSPRQSM 258
D	284 LRKLERLRPKARVAVCEFGMTVGLILMAKRLVAVGFEILLIGSDGADRDEVEGEYEOE 343
Q	259 MQHL-AQ-ARTTVVVFNSRLNAVFPFSVVLNLGTG-VWVASBDAISYIIVSICIQ 315
D	344 AVGGI-IVKHLSEVTSDDYFLK-LRLNITRNMPERPE-FWQHRFO-CRIPIGHLENNM 399
Q	316 GIGTIVLGVAVOORVPGIKFEFEESYVRAVTAAPSA-CREGSWSCTNDCRECH-ITFTRN 373
D	400 YRKNGSGESLEDNYVQDSKMGFIINATYMAOGILHDSHSLCGNHGLCKAMPIDISQ 459
Y	374 MPLT-GAF-SKSAAY---RV-Y-EAAYAAHGCHOLG--CSEI-C-SRQVYPMQ 419
D	460 LLEFLMRTSFTGVSGEDVYFDENGDTGRGVINMLQYVEP-AEDYINVSGWEHGOQLSID 518
Q	420 LLOQIYKYNEL-LHENYVAFDNDODLTGYDILIAMDMKNPMTTEIIGSASLSVYHLDIN 478
D	519 DYMAQ-INRSDMY-LSVSCFPCSQGEIKVIRKGEVSCWICGTACKDNEIYO-DEF-TCQA 574
Q	479 KTKIOMHKKNOVPSVCTTCLGLGHHRVVY-GSHHCCFECEVPCAGTFLMSELSHICP 537
D	575 CDLGMPPELEGEPIRLRYLMEGNPESIQVVFACGLIVTSFVFIFLYLADTPYVK 634
Q	538 CGTEWMAKESTTGPFRVFERLAHEPISLILIANNTLLLELLVGTGLGFWHEHTVVR 597
D	635 SSSRELICYIILAGIFLIGICPF-LLIAQPIYASCYLQRLVLSATQCYASLAKTRIA 693
Q	598 SAGSLGICLMLGSLVAG-SCSFYSFSGFPYTPACLLNQPLPFLSGLAFLSCLTIRSQLY 656
D	654 RILAGSKKICITKRPRENSAQAQVIAGL-LVS-VQVILEVTLIILEPMPVKSYPSTI 749

QY	1F-----KSTKVPPTTFRKMAONRGAGLFVIVSSVHELICITLWVMTPTPTPTRYQAF	711
Db	750 RE-VELIC-NTSGVWAPLGYNGLLIMSCY-YAFKXINSPANFANAKYIAFTMYTTCI	806
QY	712 PHVLTECEVNSVGLFLAFTNHTLLIS-TFVCSYLGLELDENNENACVFFSLNLNV	770
Db	807 IWLAF--VP-IYGSNKKITTFSSVSLVAYALGCMSPKRIIITLAKERNVRSAFTTS	863
QY	771 SWIFFETMASIYOGS-YLPAVNVLAGLITLGGFSCYFKPCYVILICRELNTNTEHFQAS	829
RESULT	13	
ENTRY	A41939	#type complete
TITLE	G protein-coupled glutamate receptor - rat	
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat	
DATE	04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998	
ACCESSIONS	A41939; S15362	
REFERENCE	A41939	
#authors	Houamed, K.M.; Kujiper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, E.R.; Almers, W.; Hagen, F.S.	
#journal	Science (1991) 252:1318-1321	
#title	Cloning, expression, and gene structure of a G protein-coupled glutamate receptor from rat brain.	
#cross-references	MOID:92022526	
#accession	A41939	
#status	preliminary: not compared with conceptual translation	
##molecule_type	nucleic acid	
##residues	1-1199 ##label HOU	
##cross-references	GB:M61099; NID:g397805; PID:g204460	
##experimental_source	cerebellum	
##note	sequence extracted from NCBI backbone (NCBIPI:60785)	
REFERENCE	S15362	
#authors	Maeu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.	
#journal	Nature (1991) 349:760-765	
#title	Sequence and expression of a metabotropic glutamate receptor	
#cross-references	MOID:91155047	
#accession	S15362	
##status	preliminary	
##molecule_type	mRNA	
##residues	1-1199 ##label MAS	
##cross-references	EMBL:X57559; NID:g56545; PID:g55647	
KEYWORDS	G protein-coupled receptor; transmembrane protein	
SUMMARY	#length 1199 #molecular_weight 133235 #checksum 5211	
Query Match	13.08; Score 821; DE 2; Length 1199;	
Best Local Similarity	26.99; P-Id. No. 2, 88e-130;	
Matches	213; Conservative 209; Mismatches 314; Indels 56; Gaps 47;	
Db	80 EAMHTLDRINADPVLTNTTGSERDSQWHSVALTEGIEFRSLTSDRDXGLUR	139
QY	76 QAMFTVEELINSSALPNTLTGELYDYDCESA-NVY-AT--LR-VL-ALDGPRI-IE-	127
Db	140 CLPDSGQTLPPGRKRPPIAGVIGSSSSVAIOYONLQLDFDIOAVSATSIDLSDTLYK	199
QY	128 -ICK-D-LR-NHSSKYVA-PIGPDNDHVAITTAALGLPLMLPVLSVSAVSLSAKRKP	182
Db	200 YFLRWPSDTLQARAKMLDIYKRYNMTYVSAVHTEGNIGSGMDAFKELAAQGLCAHSD	259
QY	183 SFLRTVPSDRHOEAVMOLLOSFGWVWISLIGSGYDGLGVALLETLAVPRGICAFKD	242
Db	260 KI-YSN-AGKSRSDRLRLKRLERLPRARVVCCECEMTYRGILSANRRRGVGEFSLIS	317
QY	243 ITPSARVGPGRMOSKMOHL-AO-ARTVVVVFNRHLARVFRSVYLANLTGKYV-VAS	299
Db	318 DGMADRDVEVLEGVEAVANGI-TIKLOSEVVSFDYFLK-LRLDTNRNPFPE-FMOH	374
QY	300 EDMAISTYIITSVIGIGIGITVLGVANQAGVQGLKFFEESSYRAVYAAASA-CPGSGMS	358
Db	375 RFQ-CRLPGLLENPFKRYCTGNESLEENYDQSKXGVFINATYAMAHGLQNMHRA-CP	433



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QY 359 TNOLCR-ECHFTTTRNMPTL--GAFSMSAAY---RV-Y--EAYVAVAHGLHOLL-G-CT 406
Db 434 GHVGLCDLAMPKPIDGRKLDLDFLIKSEFVGSGEWEDEKGDAPGRYDLMNLOYTEANR-Y 492
QY 407 SEI--C-SRGPVYPMOLQOIKYVFL-LHENTVAFDNDGDLGTYYDIAMDNGPEWTF 462
Db 493 DYVHVGVHGVGLNIDYKIQ-MNKSQWVR-SVCSEPLKGQIKYIRGEVSCCMICTAC 550
QY 463 ELIGSASISPVHLDINKRIQWGNKNNQVPVSVCTDCLAGHRRVYV-GSHRCCEVCPC 521
Db 551 KENEVERO-DEF-TCRACDLGMPNMLGCEPIPRYLEMSIESIILASCLGILVTL 608
QY 522 EAGTFLNSELHICQPCETEWAPEKSTCEPRTEFLAMHPISLVLAATLTLILLY 581
Db 609 FVTLIFVLRDPVYKSSRELQYIILAGIFGYVCPF-TLIAKPTTSCYLORLVGLS 667
QY 582 GTAGLFAHHEHTPVYRSNGRCLFLMGLSVAG-SCSFYSFGEPTVACILROFLSELG 640
Db 668 SAMCYSAVLTKTNRIARILAGSKKICTRKPRFSAMAQVILASILISVOLTLYVTLIM 727
QY 641 FAIFSLCLTIRSFOLVILFKFESTK-VPTFYRTMAQNHGAGLEIVASVTHLICLTLMVM 699
Db 728 EPPMILYPSLKE-VYLIC-WTSMGVAVPVGYNGLLIMCTY-YAKTRVNPANFMEA 784
QY 700 WTPRTREYQRPDLVILECTEENSQVFLAETHNILLIS-TFVCSYLKGLPENYNEA 758
Db 785 KYIAFTMTTTCILMAF--VP-ITYGSNWKITTCFAVSLSTVVALGCMFPKMTIILAK 841
QY 759 KCVIFSLINLNFVSWIAFTMASIYOGS-YLPANVNLAGLTILSGSFGLPKCVIILCR 817
Db 842 PERNVRSAPFTS 853
QY 818 PELNTEHFOAS 829

RESULT 14
ENTRY 149142 #type complete
TITLE metabotropic glutamate receptor 8 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Sep-1998
ACCESSIONS 149142
REFERENCE 149142
#authors Duvolsin, R.M.; Zhang, C.; Ramonell, K.
#journal J. Neurosci. (1995) 15:3075-3083
#title A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.
#cross-references MUID:95239344
#accession 149142
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-908 #label RES
#cross-references EMBL:U017252; NID:g854728; PID:g854729
GENETICS
#gene mGluR8
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS #journal neurotransmitter receptor
SUMMARY #length 908 #molecular_weight 101413 #checksum 2996

Query Match 12.7%; Score 806; DB 2; Length 908;
Best Local Similarity 25.2%; Pred. No. 2,78e-127;
Matches 212; Conservative 241; Mismatches 322; Indels 66; Gaps 52;

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QY 136 SSKVAFAGPNDTDAVTAALGPFILMPLYSEASSVILSAKRKPFSLRTVPSDRHQV 195
Db 204 QAMVDIYALCMNVSTLASGNGVGEAFQISREIGVCVIAQSOIKIPREPRGE-- 261
QY 196 EVWQVLQDSFGWVWISLGSIGDYGQLGVQALDELAPRG-TCVAFKDIYPPFSARVSDPR 254
Db 262 FEKIKRLETPNARAVIMFANEDDIGILEAAKLNQSGHFLIGSDSMG-SK-IAPVY 319
QY 255 MQSMQHLAQARTI-VYVVFENRHLARFPFRSVLANLTGR-VVVAEDMALISYIISVT 312
Db 320 QOEELAES-AVTLIPKR-ASIDGDFRFRSTLANNRNVAFAFSEGNCGCKSGSKR 377
QY 313 GIGGIGVLGVAAVOORVPGLEKEEESY-VAAVTAAPSACPEGSCWSTNOICRE-CH-TF 369
Db 378 NSHIKCTGELRIRADSSEYDEGVQFVIDAVYMAVALNHMHRELPGYIGLPPRWYTI 437
QY 370 TTR-NMPT-LGAFSMSAAY---RV-Y--EAYVAVAHGLHOLL-G-CTSEL--CSR-GPV 415
Db 438 DGKELGIRAVNNGSAGTPVTENGDAPGRYDFOYQINNKSTYKIGWNT-NQLH 496
QY 416 YPMQLQOIKYVNFLEHENT-VAFDDNDGDLGYDIIAMDNGPEWTFEILIGSASISPVH 474
Db 497 LKVED--MQANREHTHPASCSLPCKPGERKKYKGVPCCMHCGREGVNY-QVDELS- 552
QY 475 LDINKTKIQWGNKNNQVPVSVCTDCLAGHRRVYVGSCHCCFECVPCBAGTFILMSDLHI 534
Db 553 CELCPDLDRPNINRNGCORPIIKLEWSPVAVVPVLAIGLITATFVITFVRYNDTP 612
QY 535 COPGTEPMAREKSTCTCPRTVEFLANHEPISLVLIANTLILLLVGTAGLFAHHEHTP 594
Db 613 TVRSGRELSTVLTGIFLCYSITFL-MIAPDTIISFRIRIFGLMCFESYALLTKTN 671
QY 595 VYRSAGRLCLFLM-LGSLVAGSCSFYSFGEPTVPACILRQPLSLGPAIFLSCLTIRSF 653
Db 672 RIHRIFEGKKSQVTA-PKFT-SPASQVITFSLISVOLLGTFVAFVVDPPITIIDYGEQR 729
QY 654 QLVILFKSTVPTFRTMAQNHGAGLEIVS-STVHLLICLTMLVMTPTPTREY--QR 710
Db 730 TLDPENARGVLC-K-DISPLSICLSGSIILMVCYVAIKTRGVPEPFNEAKPIGFTMY 788
QY 711 -F-P-HL-VILECTEENSQVFLAETHNILLISISTFVCSYLKGLPENYNEAKCVTISL 766
Db 789 TTCIITMAFIPDFGTAQSAEKMTIQTTLTVSNS-LSASVSLGMLYMPKVIITIFPEQ 847
QY 767 LNFVSWIAFTMA-SIYOGS---YLPANVNLAGLTILSGFS-G-YFLPKCVIILCRPEL 820
Db 848 N 848
QY 821 N 821

RESULT 15
ENTRY JH0562 #type complete
TITLE metabotropic glutamate receptor 3 precursor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
ACCESSIONS JH0562
REFERENCE JH0561
#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glutamate receptors.
#cross-references MUID:92110002
#accession JH0562
#molecule_type mRNA
#residues 1-879 #label TAN
#experimental_source brain
COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS #journal G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
FEATURE

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MParch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:09:42 2000; Maspar time 14.57 Seconds

Tabular output not generated. 766.385 Million cell updates/sec

Title: >US-09-361-652-1  
Description: (1-840) from US09361652.pep  
Perfect Score: 6338  
Sequence: 1 MLFWAAHLLSLQLVYCAWF.....NTEHFQASIDYTRCGTT 840

Scoring table: PAM 150  
Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:5\_COMB 4:PCR9\_COMB 5:backfiles1

Statistics: Mean 36.328; Variance 178.464; scale 0.204

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1311	20.7	1085	1	US-08-484-Sequence 5, Applicatio	3.70e-99
2	1311	20.7	1085	1	US-08-485-Sequence 5, Applicatio	3.70e-99
3	1311	20.7	1085	2	US-08-480-Sequence 5, Applicatio	3.70e-99
4	1311	20.7	1085	2	US-08-943-Sequence 5, Applicatio	3.70e-99
5	1311	20.7	1085	3	US-08-353-Sequence 5, Applicatio	3.70e-99
6	1290	20.4	1078	2	US-08-943-Sequence 7, Applicatio	2.40e-97
7	1290	20.4	1078	3	US-08-353-Sequence 7, Applicatio	2.40e-97
8	1290	20.4	1078	1	US-08-485-Sequence 7, Applicatio	2.40e-97
9	1290	20.4	1078	1	US-08-484-Sequence 7, Applicatio	2.40e-97
10	1290	20.4	1078	2	US-08-480-Sequence 7, Applicatio	2.40e-97
11	1285	20.3	1079	2	US-08-480-Sequence 8, Applicatio	6.48e-97
12	1285	20.3	1079	2	US-08-480-Sequence 8, Applicatio	6.48e-97
13	1285	20.3	1079	3	US-08-353-Sequence 8, Applicatio	6.48e-97
14	1285	20.3	1079	2	US-08-943-Sequence 8, Applicatio	6.48e-97
15	1285	20.3	1079	1	US-08-485-Sequence 8, Applicatio	6.48e-97
16	1198	18.9	1088	1	US-08-484-Sequence 6, Applicatio	2.04e-89
17	1198	18.9	1088	2	US-08-353-Sequence 6, Applicatio	2.04e-89
18	1198	18.9	1088	2	US-08-480-Sequence 6, Applicatio	2.04e-89
19	1198	18.9	1088	2	US-08-943-Sequence 6, Applicatio	2.04e-89
20	1198	18.9	1088	1	US-08-485-Sequence 6, Applicatio	2.04e-89
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23	862	13.6	1180	1	US-08-486-Sequence 8, Applicatio	1.27e-60

24	862	13.6	1180	3	US-08-367-Sequence 8, Applicatio	1.27e-60
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26	862	13.6	1212	3	US-08-367-Sequence 10, Applicati	1.27e-60
27	855	13.5	877	3	US-08-367-Sequence 12, Applicati	5.01e-60
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34	825	13.0	1056	2	US-08-687-Sequence 7, Applicatio	1.79e-57
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37	821	13.0	1199	1	US-08-455-Sequence 2, Applicatio	3.93e-57
38	821	13.0	1199	1	US-08-041-Sequence 2, Applicatio	3.93e-57
39	821	13.0	1199	4	PCT-US91-0 Sequence 2, Applicatio	3.93e-57
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41	815	12.9	906	3	US-08-367-Sequence 2, Applicatio	1.27e-56
42	804	12.7	879	1	US-08-072-Sequence 6, Applicatio	1.09e-55
43	804	12.7	879	3	US-08-367-Sequence 6, Applicatio	1.09e-55
44	804	12.7	879	1	US-08-486-Sequence 6, Applicatio	1.09e-55
45	806	12.7	1056	2	US-08-687-Sequence 8, Applicatio	7.40e-56

## ALIGNMENTS

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DT				
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DE	Sequence 5, Application US/08484565			
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CC	Sequence 5, Application US/08484565			
CC	Patent No. 5763569			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Edward M. Brown			
CC	APPLICANT: Steven C. Hebert			
CC	APPLICANT: James E. Garrett, Jr.			
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE			
CC	TITLE OF INVENTION: MOLECULES			
CC	NUMBER OF SEQUENCES: 20			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSES: Lyon & Lyon			
CC	STREET: First Interstate World Center			
CC	STREET: Suite 4700			
CC	STREET: 633 West Fifth Street			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90071			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: FASTSEQ			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/484,565			
CC	FILING DATE: 7 June, 1995			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	PRIOR APPLICATION DATA: including application			
CC	PRIOR APPLICATION DATA: described below: 9			
CC	APPLICATION NUMBER: 08/353,784			
CC	FILING DATE: 9 December, 1994			
CC	APPLICATION NUMBER: PCI/US/94/12117			
CC	FILING DATE: 21 October, 1994			
CC	APPLICATION NUMBER: U.S. 08/292,827			
CC	FILING DATE: 23 August, 1994			
CC	APPLICATION NUMBER: U.S. 08/141,248			
CC	FILING DATE: 22 October, 1993			



CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044  
CC FILING DATE: 11 February, 1992  
CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Hebert, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/006  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ ID NO: 5:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1085 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1085 AA; 121170 MM; 6189757 CN;  
Query Match 20.7%; Score 1311; DB 1; Length 1085;  
Best Local Similarity 31.9%; Pred. No. 3,70e-99;  
Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;  
Db 31 GDIILGLFPIHNG-VAVKODLKSREPSEECIRNFRGRMTQAMTFAIEBINSSPALL 89  
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Db 150 ISTAVANLGLFYIPQVSVASSRLSNKQKSFRTIPNDEHOATAMADIIEPRMN 209  
Qy 150 HAVTTAALLGPFLMPVLYSVASSVYLSAKRKFPSLRTVPSDRHQVEVMVQLQSFQWV 209  
Db 210 VGTIADDDYGRGIEKFEAEERDIDCFSELI--SQYSDEKIQVVEVIONSTAKY 267  
Qy 210 ISLIGSGYDGLQVQALELAVPRGCAFKDIVPSAVGDPKMQSMQHQIAQARTTV 269  
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XX  
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Sequence 5, Application US/08485588  
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CC Sequence 5, Application US/08485588  
CC Patent No. 5688938  
CC GENERAL INFORMATION:  
CC APPLICANT: Edward M. Brown  
CC APPLICANT: Steven C. Hebert  
CC APPLICANT: Forrest H. Fuller  
CC APPLICANT: James E. Garrett, Jr.  
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: First Interstate World Center  
CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTSEQ  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/485,588  
CC FILING DATE: 7 June, 1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION DATA: including application  
CC PRIOR APPLICATION DATA: described below: 9  
CC APPLICATION NUMBER: 08/353,784  
CC FILING DATE: 9 December, 1994  
CC APPLICATION NUMBER: PCT/US/94/12117  
CC FILING DATE: 21 October, 1994  
CC APPLICATION NUMBER: U.S. 08/292,827  
CC FILING DATE: 23 August, 1994  
CC APPLICATION NUMBER: U.S. 08/141,248  
CC FILING DATE: 22 October, 1993  
CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044











CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 1085 AA; 121170 MW; 6189757 CN;

Query Match 20.7%; Score 1311; DB 2; Length 1085;  
Best Local Similarity 31.9%; Pred. No. 3,70e-99;  
Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;

Db 31 GDIIIGGLFPIHFG-VAVKODLKRPESEVECIIRNFRFRRLQAMIFAIEINSSPAL 89  
OY 35 GDFLAGLFLSLDGLQVHRPLVSCDPPS--ENGHGYHLFQAMRTVEINNSSALL 92  
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Db 210 VGIADDDYGRPGIEKFRFEAEERDIDFSELI--SQYDSEKIQVVEVIQNSTAKV 267  
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OY 463 EIIG--SA-SLSPVHLINKTKIQWGNQVPSVCTTCLAGHRRVY--GSHHCCEC 518  
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OY 696 WLVMTPRPTREYQRFPHLVILECTEVN--SVGFLLAFTNHLISITFVCSYLKELEPE 753  
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OY 813 VILGRPELNTE 824

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ID US-08-353-784-5 STANDARD; PRT; 1085 AA.  
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AC xxxxxx

DE Sequence 5, Application US/08353784

XX Sequence 5, Application US/08353784

CC Patent No. 6011068

CC GENERAL INFORMATION:

CC APPLICANT: Edward F. Nemeth, Edward M.

CC APPLICANT: Brown, Steven C. Hebert,

CC APPLICANT: Bradford C. Van Wageningen, Manuel

CC APPLICANT: F. Balandrin, Forrest H. Fuller,

CC APPLICANT: Eric G. Delmar, and Scott T. Moe

CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

CC MOLECULES

CC NUMBER OF SEQUENCES: 20

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Lyon & Lyon

CC STREET: First Interstate World Center

CC STREET: Suite 4700

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90071

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: FASTSEQ

CC CURRENT APPLICATION DATA:

CC FILING DATE: 9 December, 1994

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION DATA: including application

CC PRIOR APPLICATION DATA: described below: 8

CC APPLICATION NUMBER: PCI/US/94/12117

CC FILING DATE: 21 October, 1994

CC APPLICATION NUMBER: U.S. 08/292,827

CC FILING DATE: 23 August, 1994

CC APPLICATION NUMBER: U.S. 08/141,248

CC FILING DATE: 22 October, 1993

CC APPLICATION NUMBER: U.S. 07/934,151

CC FILING DATE: 21 August, 1992

CC APPLICATION NUMBER: U.S. 07/834,044

CC FILING DATE: 11 February, 1992

CC APPLICATION NUMBER: U.S. 07/749,451

CC FILING DATE: 23 August, 1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Hebert, Sheldon O.

CC REGISTRATION NUMBER: 38,179

CC REFERENCE/DOCKET NUMBER: 209/069

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (213) 489-1600

CC TELEFAX: (213) 955-0440

CC TELEX: 67-3510

CC INFORMATION FOR SDO ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 1085 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 1085 AA; 121170 MW; 6189757 CN;

Query Match 20.7%; Score 1311; DB 3; Length 1085;  
Best Local Similarity 31.9%; Pred. No. 3,70e-99;  
Matches 272; Conservative 232; Mismatches 275; Indels 73; Gaps 50;







Dh	149	VSTAANATLGFYIPQVYASSSSLSKNOKEFELRIPDENQOATAMADIIEYFEMN	208
Qy	150	HAVTIATALLGFLIMPLVSYEASSVYLAKKRPBFLTVSDRQOVYVMQLOSTFQW	209
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Dh	267	IVPSSSGDLEPLI-KELVRNITIGKIMLASMAASSLIAMPQYEFHWGCTIGFALKAG	325
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Qy	579	LLVGTAGLFAWHFHTPVYRSAGRLCFLMIGSLVAG-SCSFYSFGEPTVPACLLKQPL	636
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Dh	800	NFNNAKFTTESMLIFFIWISFIPAYASTY-GKVSAYEVIAIILIASFGLLACFEFKIY	858
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Dh	859	IILFKSRNTE 870	
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ID	US-08-353-784-7	STANDARD:	PRT: 1078 AA.
XX	xxxxxx		
CC	Sequence 7, Application US/08353784		
CC	Patent No. 6011068		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Edward F. Nemeth, Edward M.		
CC	APPLICANT: Brown, Steven C. Hebert,		
CC	APPLICANT: Bradford C. Van Wageningen, Manuel		
CC	APPLICANT: F. Balandin, Forrest H. Fuller,		
CC	APPLICANT: Eric G. Delmar, and Scott T. Moe		
CC	TITLE OF INVENTION: CALCULI RECEPTOR-ACTIVE		
CC	TITLE OF INVENTION: MOLECULES		

```
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 533 West Fifth Street
CC City: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/353,784
CC FILING DATE: 9 December, 1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 8
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 209/069
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ. ID NO.: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1078 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
Dd QUERY MATCH 20.4%; Score 1290; DB 3; Length 1078;
Beat Local Similarity 32.0%; Pred. No. 2,40e-97;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;
Dd 30 GDIIILGIFPHFG-VAAKDODLKSRESEVCIKRYNRRGRMQLAMFALEFINSSPALL 88
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Q	y	270	VVIVSN-RHLARVFRSVYLANLIGKRWASEDMA-----IS-T-YTISVYG-IQ-GL--G	318
D	b	326	QIPGFRFLKVRHBRKSVHNGFAKEFMEETFPNCHLOGANGPRLPVDTFLRGHEESGDRFS	385
Q	y	319	TVLG----VA-VQORO--VP-GL-KEF-EESY---VR-AVTAA-P--S---ACEP-GSM--	356
D	b	386	NSSTAFRLCTGDNISSEVERPYIDYTHLRISYNYVLAVYSIAHALODITCLPGRGLFT	445
Q	y	357	-CSTN-Q-LRECHETFTTRNPTLTGAFSMAAYVAAYVAVAAGHLQUL--L-GC--T	406
D	b	446	NGSCADIKRYAMVOLKHLRIINTFNMMGEQVTFDECGDVGANSIIMHLSPEGSIYF	505
Q	y	407	SEICS-RKPYVPQMLLOQIYKVNLLH-ENYVADNDMDLIGYDITIAMQNPGE-WT-F	462
D	b	506	KEGVYNYVAKKGERLFINEEKIIMSQFSREVPFNSCRDCLAQTRKGIIEGPTCCFEC	565
Q	y	463	EIIG--SA-SLSPVHLIDINKTKIOMHGKNNQPVSVCTTDLAGHHRYVY-GSHHCCFEC	518
D	b	566	VECPDGEVSDETDASACKCPDDQMSNNHSCIAKELEPISWTEPBGIALTLFAVLGIF	625
Q	y	519	VPCEAGTFLNMSSELHICOPCGTEEMAPRESTCPRVEFLAMEPISLVLIANTLLL	578
D	b	626	LTAFLVGLYFI-KFRNTPIVKATNRELSTLLFLSLCCFSSSLF-FIGEPDWTCLRLOPA	683
Q	y	579	LLVAGLGFAMHFH-TPVYRSAGGRCLCFMLGSLVAG-SCSFYFGEPEPVPACLLRPL	636
D	b	684	FGISFVLCISCIILVKNRVLLVFE--AKIPTSFHRKMWGLNQLFVLCTFMQIVCVI	741
Q	y	637	FSLQAFILSCQITKRSFLVLIFFESTVPT-FYRTWAONHGAGLEFYVSVTTLICLT	695
D	b	742	WLTYAPSSYNOELIEDLIFITGHEGSLMAGFLIGYTC-LLAALCFPF-AFESRKLPE	799
Q	y	696	WLVNMTPEPRTREYOFPLVLLECTEVN--SVGLLAFTHNILLISTFPCSTYKGLPE	753
D	b	800	NFNEAKFTTFESMLIFFYIMISFIPAYASTY-GKFSVAVEVYIAILMAFGLLACIFEFKIY	858
Q	y	754	NYNEAKCTFELLNLFVSWIAFFIM-ASLYGSLPRAVNYLAGLTTISGGFSGFLPKCY	812
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CC		Sequence 7, Application US/08485588		
CC		Patent No. 5688938		
CC		GENERAL INFORMATION:		
CC		APPLICANT: Edward M. Brown		
CC		APPLICANT: Steven C. Hebert		
CC		APPLICANT: Forrest H. Fuller		
CC		APPLICANT: James E. Garrett, Jr.		
CC		TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
CC		TITLE OF INVENTION: MOLECULES		
CC		NUMBER OF SEQUENCES: 20		
CC		CORRESPONDENCE ADDRESSES:		
CC		ADDRESSEE: Lyon & Lyon		
CC		STREET: First Interstate World Center		
CC		STREET: Suite 4700		
CC		STREET: 633 West Fifth Street		
CC		CITY: Los Angeles		
CC		STATE: California		
CC		COUNTRY: USA		

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CC      ZIP: 90071
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: FASTSEQ
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/485,588
CC      FILING DATE: 7 June, 1995
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      PRIOR APPLICATION DATA: including application
CC      PRIOR APPLICATION DATA: described below: 9
CC      APPLICATION NUMBER: 08/353,784
CC      FILING DATE: 9 December, 1994
CC      APPLICATION NUMBER: PCT/US/94/12117
CC      FILING DATE: 21 October, 1994
CC      APPLICATION NUMBER: U.S. 08/292,827
CC      FILING DATE: 23 August, 1994
CC      APPLICATION NUMBER: U.S. 08/141,248
CC      FILING DATE: 22 October, 1993
CC      APPLICATION NUMBER: U.S. 08/009,389
CC      FILING DATE: 23 February, 1993
CC      APPLICATION NUMBER: U.S. 08/017,127
CC      FILING DATE: 12 February, 1993
CC      APPLICATION NUMBER: U.S. 07/934,161
CC      FILING DATE: 21 August, 1992
CC      APPLICATION NUMBER: U.S. 07/834,044
CC      FILING DATE: 11 February, 1992
CC      APPLICATION NUMBER: U.S. 07/749,451
CC      FILING DATE: 23 August, 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Heber, Sheldon O.
CC      REGISTRATION NUMBER: 38,179
CC      REFERENCE/DOCKET NUMBER: 213/005
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (213) 489-1600
CC      TELEFAX: (213) 955-0440
CC      TELEX: 67-3510
CC      INFORMATION FOR SEQ ID NO: 7:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 1078 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
Query Match 20.4%; Score 1290; DB 1; Length 1078;
Best Local Similarity 32.0%; Pred. No.2,40e-97;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49
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CC Sequence 7, Application US/08484565  
CC Patent No. 5763569  
CC GENERAL INFORMATION:  
CC APPLICANT: Edward M. Brown  
CC APPLICANT: Steven C. Hedert  
CC APPLICANT: James E. Garrett, Jr.  
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
CC TITLE OF INVENTION: MOLECULES  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: First Interstate World Center  
CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTSEQ  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/484,565

CC FILING DATE: 7 June, 1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION DATA: including application  
CC PRIOR APPLICATION DATA: described below: 9  
CC APPLICATION NUMBER: 08/353,784  
CC FILING DATE: 9 December, 1994  
CC APPLICATION NUMBER: PCT/US/94/12117  
CC FILING DATE: 21 October, 1994  
CC APPLICATION NUMBER: U.S. 08/292,827  
CC FILING DATE: 23 August, 1994  
CC APPLICATION NUMBER: U.S. 08/141,248  
CC FILING DATE: 22 October, 1993  
CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044  
CC FILING DATE: 11 February, 1992  
CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Heber, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/006  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ. ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1078 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;  
SQ

Query Match 20.4%; Score 1290; DB 1; Length 1078;  
Best Local Similarity 32.0%; Pred. No. 2,40e-97;  
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

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QY 357 -CSTN-O-LCRECHTFTTRNPTLGASMSAAYRYEAVVAHGHQL--L-GC--T 406  
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 DT  
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 CC Patent No. 5858684  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Edward F. Nemeth  
 CC APPLICANT: Edward M. Brown  
 CC APPLICANT: Steven C. Hebert  
 CC APPLICANT: Forrest H. Fuller  
 CC APPLICANT: James E. Garrett, Jr.  
 CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
 CC TITLE OF INVENTION: MOLECULES  
 CC NUMBER OF SEQUENCES: 20  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Lyon & Lyon  
 CC STREET: First Interstate World Center  
 CC STREET: Suite 4700  
 CC STREET: 633 West Fifth Street  
 CC CITY: Los Angeles  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 90071  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: FASTSEQ  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/480,751  
 CC FILING DATE: 7 June, 1995  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC PRIOR APPLICATION DATA: including application  
 CC PRIOR APPLICATION DATA: described below: 9  
 CC APPLICATION NUMBER: 08/353,784

CC FILING DATE: 9 December, 1994  
 CC APPLICATION NUMBER: PCT/US/94/12117  
 CC FILING DATE: 21 October, 1994  
 CC APPLICATION NUMBER: U.S. 08/292,827  
 CC FILING DATE: 23 August, 1994  
 CC APPLICATION NUMBER: U.S. 08/141,248  
 CC FILING DATE: 22 October, 1993  
 CC APPLICATION NUMBER: U.S. 08/009,389  
 CC FILING DATE: 23 February, 1993  
 CC APPLICATION NUMBER: U.S. 08/017,127  
 CC FILING DATE: 12 February, 1993  
 CC APPLICATION NUMBER: U.S. 07/934,161  
 CC FILING DATE: 21 August, 1992  
 CC APPLICATION NUMBER: U.S. 07/834,044  
 CC FILING DATE: 11 February, 1992  
 CC APPLICATION NUMBER: U.S. 07/749,451  
 CC FILING DATE: 23 August, 1991  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Hebert, Sheldon O.  
 CC REGISTRATION NUMBER: 38,179  
 CC REFERENCE/DOCKET NUMBER: 213/004  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (213) 489-1600  
 CC TELEFAX: (213) 955-0440  
 CC TELEX: 67-3510  
 CC INFORMATION FOR SEQ ID NO: 7:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 1078 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQ ID NO: 7  
 CC SEQUENCE: 1078 AA; 120573 MW; 6153012 CN;  
 SO  
 Query Match 20.4%; Score 1290; DB 2; Length 1078;  
 Best Local Similarity 32.0%; Pired. No. 2,40e-97;  
 Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;  
 DB 30 GDIIIGLGPRIHNG-VAAQDQKSRPESVEICIRNFQFRLQAMFAIERINSPLL 88  
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 OY 210 ISLISGYDGYGOLVQALBELVAPRGICVAFKDIYFSAKVDGDRMOSMOMHLAQARTV 269  
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ID US-08-353-784-8 STANDARD; PRT; 1079 AA.
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DE Sequence 8, Application US/08353784
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CC Sequence 8, Application US/08353784
CC Patent No. 6011058
CC GENERAL INFORMATION:
CC APPLICANT: Edward F. Nemeth, Edward M.
CC APPLICANT: Brown, Steven C. Hebert,
CC APPLICANT: Bradford C. Van Wageningen, Manuel
CC APPLICANT: F. Balandrin, Forrest H. Fuller,
CC APPLICANT: Eric G. Delmar, and Scott T. Moe
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/353,784
CC FILING DATE: 9 December, 1994
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 8
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CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141,248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009,389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017,127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934,151
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834,044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE//DOCKET NUMBER: 209/069
CC TELECOMMUNICATION INFORMATION:

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	Query Match	20.3%	Score 1285;	DB 3;	length 1079;
CC	TELEPHONE: (213) 489-1600				
CC	TELEFAX: (213) 955-0440				
CC	TELEX: 67-3510				
CC	INFORMATION FOR SEQ ID NO: 8				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 1079 amino acids				
CC	type: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	SEQUENCE 1079 AA; 120867 MW; 6054255 CN;				
Db	Best Local Similarity 31.5%; Pred. No. 6,488-97;				
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Db	149 VSTAAANLGLFIYPOVSYASSSSLLSNKQKSFLETINDEHQRAAMDIEYFNMW 208				
QY	150 HAVTTAALLGFLMPLIVSYEASVYLAKRKFSELPRTVPSDRQVEVKNQLOLQSTGW 209				
Db	209 VGTIADDDYDRPGIEKFEFEAEERDIDIPSELI--SOYSDEEIQOQVEVIONSTAKV 266				
QY	210 ISLIGSYDYDQGLQVQALEELAVRGICVAFKDIVPFSARVGDPRMOMQHLQARTY 269				
Db	267 IVTFSSGDELEPLI-KEIVRRNITGRIMLASEAWASSSLIAMEYFHVVGITGFGLKAG 325				
QY	270 VVFSFN-RHLARVFEFRSVVLANTLKGWVASEDMA---IS-T-YRSTVG-IO-GI--G 318				
Db	326 QIPGREFLOVHRKSYSHNGFAKEFMEDEFNCHLQSGAGPLPVDTPFVASHDEGGRL 385				
QY	319 TVLG---VA-VQQRQ--VP-GL-XEF-EESY---VR-AVTA-P-S-A-CPE--GSM-- 356				
Db	386 NSTAFRLPCLGDNENINSEVTPYDYDEHLRSYVYLAVSIAMALODIYTCPLGRFLT 445				
QY	357 -CSTN-Q-LCECHGFTTRKNPTIGATSMASAVIVYNAVVAHGLHQL---L-GC---T 406				
Db	446 NGSCADIKKVEAMOVLKLRLNFTNNMGQVTFDECCD;LVGNSYLSINHWLSPEDSIVF 505				
QY	407 SEIDS-RGPVYPQWLLQOIYKVNFLH-EMTVARDNGDTLGYDYDIAMQWNPB-WT-F 462				
Db	506 KEVGYNNYAKKGRRLITNEKILMSGFSREVPFSNCSRDCQATRKGITIEGPTCCFEC 565				
QY	463 EIIG--SA-SLSPYHLINKKXLCWGRKNNOVPVSVCTCLGHHRVVV--GSHCCFEC 518				
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QY	519 VPCEAGFTLNWSELHIDOPCGTEEMAKESTCTCPRTVEFLAMHEPISLVIANTLLLL 578				
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QY	637 FSLGFAILSCLTIRSPOLVILFEFSTKVPF-FRTWAQNRHGAGLEVIYVSYVHLICLT 695				
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QY	696 WLVMKTPPTPEYQRPPLVILDETEVN--SVGLLFTFINLLISTFSCSTIGELPE 753				
Db	800 NENAKFTFESMLFFIYMWISFIYAVASTY-GKFSVAEVIALLAASFGILACIFPNKYV 858				
QY	754 NYNNAKCTVTELLNLFYSWIAFLFM-ASIVQGSILPRAVNVLAGITLISGFSQYFLPKCY 812				
Db	859 IILFSPRNTIEVRSSTAHA 880				







DT Sequence 8, Application US/08485588  
XX  
CC Sequence 8, Application US/08485588  
CC Patent No. 5686938  
CC GENERAL INFORMATION:  
CC APPLICANT: Edward M. Brown  
CC APPLICANT: Steven C. Hebert  
CC APPLICANT: Forrest H. Fuller  
CC APPLICANT: James E. Garrett, Jr.  
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
CC TITLE OF INVENTION: MOLECULES  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: First Interstate World Center  
CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTSEO  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/485,588  
CC FILING DATE: 7 June, 1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION DATA: including application  
CC PRIOR APPLICATION DATA: described below: 9  
CC APPLICATION NUMBER: 08/353,784  
CC FILING DATE: 9 December, 1994  
CC APPLICATION NUMBER: PCT/US/94/12117  
CC FILING DATE: 21 October, 1994  
CC APPLICATION NUMBER: U.S. 08/292,827  
CC FILING DATE: 23 August, 1994  
CC APPLICATION NUMBER: U.S. 08/141,248  
CC FILING DATE: 22 October, 1993  
CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044  
CC FILING DATE: 11 February, 1992  
CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Hebert, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/005  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEO ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1079 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;  
SO

Query Match 20.3%; Score 1285; DB 1; Length 1079;  
Best Local Similarity 31.5%; Pred. No. 6,48e-97;  
Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

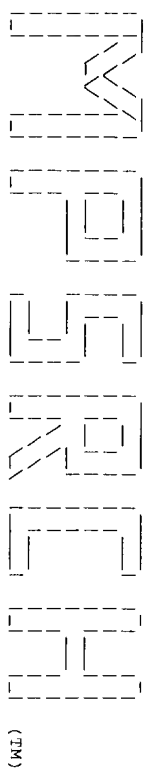
Db 30 GDIIILGIFPIHFG-VAAKDODLKSRPESEVCIIRYNGFERMLOAMIFAIEIINSSPSLL 88  
QY 35 GDFLLACLFLSHGDCLOVRRHRPLVTSQDRPDS--FNCHGYHLQAMFTVEEINSSALL 92  
Db 89 PNMTLGRIFDTCNTVSKALEATISVAONKIDSLNIDFCNCSSEHPIPTIAVATGSG 148  
QY 93 PNITLGEYELDVCSSEANVY-ATLRVALOGPRIHEIOK--DLRNHSSKVAFAIGPDNTD 149  
Db 149 VSTAVANLLGIFYIPQVSYASSSSRLSNKNOYKSFRTIINDENQOARAMDIEEFPMW 208  
QY 150 HAVTTAALGFFLMPPLVSYEASSVYLSAKKRPSELTVPSDRQVEVMQVLQSGFWM 209  
Db 209 VGTIAADDDYGRGIEKFESEAEERDICIPISEI--SQYSDEEIQOQVEVIONSTAKY 266  
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Db 267 IIVFSSGPDLEPLI-KEIVRNITGRILWLASEMASSSLIAMPBYHVGGTIGFGIKAG 325  
QY 270 VVVFPSN-RHLARVFFRSVLANLIGKVVASEDMA---IS-T-YITSYG-IG-GI--G 318  
Db 326 QIPGFRFELQVHRKSVNHGFAKEFEETFNCHLOGAGPLPVDTFVSHERGRL 385  
QY 319 TVLG---VA-VQORQ-Vp-GL-KEF-EESY---VR-AVTAA-P-S-A-CPE--GSW-- 356  
Db 386 NSSIAFRPLCGDENINSVETPYMDYELRISYVYLAWSIAHALODITYCLPGRLFT 445  
QY 357 -CSTN-Q-LRECHTFTTRMKPTLGATSMANARVYAVVAHGLHQL---L-GC---T 406  
Db 446 NGSCADIKVYEAQVNLKHLNLTNNKSGQVTFDECGDIVGNSITNHLSPEDGSIVF 505  
QY 407 SEICS-RGPVYPMQLOQIKVNFLLH-ENTVAFDNGDITLGYYDIAMDMNGPE-WT-F 462  
Db 506 KGVYVYVAKKGRRLINEKEILIMSGFSREVPFNSRCCQGRKGIIEGPTCFEC 565  
QY 463 EIIG--SA-ELSPVHLIDINKTIQWBGKNQVPSVCTDCLAGHRRVV-GSHHCCFEC 518  
Db 566 VECPDGESETPDASACDKCPDFFWSNENHTSCIAKEIEFLWATEPGIALTLFAVLGIF 625  
QY 519 VPCAGAGFLNMSLHICQPGTEEMAKESTICPRIVERLANHEPISTVLIAANTLLL 578  
Db 579 LTVAGTAGLFAMHFR-FPVVASAGRGLOFLMGSLVAG-SCSFYSFGEPTVPACILRQPL 636  
QY 637 FSLGFAFLFSLCLTRISFQVLIIFKFSIKVPT-FYRTMAQNHGAGLFIYVSTVHLICLT 695  
Db 742 WLYTAPSSYRNHLEDEILFITCHEGSLMALGSLIGYC-LLAICGFF-AFKSRKLP 799  
QY 696 WLVKMTFRPFRYQRPFHVLIECTEVN--SVGFLAFTNILLISTFVCSLIGKELPE 753  
Db 800 NFNDAKPIESMLIFLIWISFIIPAVASY-GRFVSAVEVYIALAASFGLLACIFENKVV 858  
QY 754 NYNDAKCVTFSSLNLEFWSIAFTM-ASIVQGYLPAVNVLAGITLISGSGFGLPKCY 812  
Db 859 IILFKPSRNTIEVRSSTAAH 880  
QY 813 VILCRPELNTEHFOASIDQYT 834

Search completed: Fri Mar 17 13:10:13 2000  
Job time : 31 secs.









(TM)

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Msarch\_bp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:00:08 2000; Maspar time 39.94 Seconds

Tabular output not generated. 498.146 Million cell updates/sec

Title: >US-09-361-652-1

Description: (1-840) from US09361652.pep

Sequence: 1 MLFMAHLLSLQLVYCAAF.....NNTFFQASIDYTRCGCT 840

Scoring table: PAM 150

Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-geneseq36

1:geneseqp

Statistics: Mean 38.602; Variance 175.356; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1311	20.7	1085	1	Bovine parathyroid cal	1.79e-106
2	1311	20.7	1085	1	Bovine parathyroid cal	1.79e-106
3	1311	20.7	1085	1	Bovine parathyroid cal	1.79e-106
4	1290	20.4	1078	1	Human parathyroid calc	1.61e-104
5	1290	20.4	1078	1	Human parathyroid calc	1.61e-104
6	1290	20.4	1078	1	Human parathyroid calc	1.61e-104
7	1290	20.4	1078	1	Human parathyroid calc	1.61e-104
8	1285	20.3	1078	1	Rat kidney extracellular	4.71e-104
9	1285	20.3	1078	1	Rat kidney extracellular	4.71e-104
10	1285	20.3	1078	1	Rat kidney extracellular	4.71e-104
11	1285	20.3	1078	1	Rat kidney extracellular	4.71e-104
12	1230	19.4	1026	1	Dogfish shark kidney c	6.16e-99
13	1199	18.9	1088	1	Human parathyroid cell	5.80e-96
14	1198	18.9	1088	1	Human parathyroid cell	5.80e-96
15	1198	18.9	1088	1	Human parathyroid cell	5.80e-96
16	1198	18.9	1088	1	Human parathyroid cell	5.80e-96
17	1045	16.5	1219	1	Amino acid sequence of	8.87e-82
18	1030	16.3	1058	1	Amino acid sequence of	2.16e-80
19	972	15.3	779	1	Rat pheromone receptor	4.92e-75
20	861	13.6	1180	1	Human mglur5a	8.15e-65
21	862	13.6	1212	1	Human mglur5b	6.10e-65
22	855	13.5	877	1	Human mglur5c	2.90e-64
23	844	13.3	850	1	Mouse pheromone recept	2.96e-63

24	838	13.2	872	1	R95052	Human metabotropic glu	1.05e-52
25	837	13.2	912	1	R82658	Human mglur4	1.30e-62
26	834	13.2	912	1	R72092	Human mglur4	2.45e-62
27	821	13.0	906	1	R25081	GLU-G-R subtype 1b.	3.81e-61
28	825	13.0	1036	1	W25764	Amino acid sequence of	1.64e-61
29	821	13.0	1199	1	R25080	GLU-G-R subtype 1a.	3.81e-61
30	819	12.9	872	1	R89580	Metabotropic glutamate	5.82e-61
31	815	12.9	906	1	R64250	Human mglur1b	1.35e-60
32	812	12.8	1194	1	R42199	Hmglur1	2.55e-60
33	808	12.7	866	1	W94920	Rat pheromone receptor	5.92e-60
34	808	12.7	877	1	R82657	Human mglur3	5.92e-60
35	804	12.7	879	1	R64252	Human mglur3	1.38e-59
36	805	12.7	1056	1	W25765	Amino acid sequence of	1.12e-59
37	800	12.6	908	1	K41568	Human metabotropic glu	3.20e-59
38	799	12.6	908	1	K41568	Human metabotropic glu	3.95e-59
39	795	12.5	803	1	W94903	Mouse pheromone recept	9.18e-59
40	779	12.3	877	1	W01099	Metabotropic glutamate	2.67e-57
41	760	12.0	867	1	R72093	Human mglur7 clone cmr	1.46e-55
42	758	12.0	915	1	R72097	Human mglur7a	2.22e-55
43	760	12.0	922	1	R72098	Human mglur7b	1.46e-55
44	755	11.9	667	1	W94919	Rat pheromone receptor	4.17e-55
45	755	11.9	915	1	R80479	Rat metabotropic gluta	4.17e-55

## ALIGNMENTS

RESULT 1  
ID W89563; standard; Protein: 1085 AA.

AC W89563;

DT 19-MAR-1999 (first entry)

DE Bovine parathyroid calcium receptor BopCar 1.

KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

KW neonatal distress; neurodegenerative disease; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; dementia; muscle tension;

KW depression; anxiety.

OS Bos sp.

PN US5858684-A.

PD 12-JAN-1999.

PF 07-JUN-1995; 480751.

PR 07-JUN-1995; US-480751.

PR 23-AUG-1991; US-764551.

PR 11-FEB-1992; US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-012117.

PR 08-DEC-1994; US-353784.

PA (BGM ) BRIGHAM & WOMENS HOSPITAL.

PA (NPSP-) NPS PHARM INC.

PI Balandrin MF, Brown EM, Del Mar EG, Garret JE,

PI Hebert SC, Nemeth EF, Van Wageningen BC;

DR WPI: 99-119871/10.

DR N-PSDB: V82483.

PT Screening for calcium receptor active compounds - by recombinant

PT expression of nucleic acid encoding calcium receptor and determining

PT the effect of compounds on calcium receptor activity

PT Claim 1: Fig 47: 175pp: English.

CC A method has been developed of screening for a compound able to affect

CC one or more activities of a calcium receptor (CR) comprises: (A)

CC contacting a recombinant cell with a test compound, where the

CC recombinant cell comprises a recombinant nucleic acid expressing the CR,

CC provided that the cell does not have functional CR expression from

CC endogenous nucleic acid; (B) determining the ability of the test

CC compound to affect one or more activities of the calcium receptor; and

CC (C) comparing the ability with the ability of the test compound to

CC affect the one or more CR activities in a cell not comprising the

CC recombinant nucleic acid. The present sequence represents bovine

CC parathyroid CR, designated a BopCar 1. The nucleic acid sequence of

CC BopCar 1 can be used as part of the recombinant nucleic acid in the







Db	387	NSPAPRFLCTGGEINSSVEHPYMDYTHLRISYNYVLAVYSIAALODITYCPGRDLFT	446
Oy	358	-S-TN-Q-LQECHTFTTRNPTIGAFSMAAYVEVAVIAVAGHLQGLCTSE-I--	409
Db	447	NGSCADIKYVAMOVILKHLRLNLTSSMNGEAVTEDECGLDAGNSINIMHLSPEDSIVF	506
Oy	410	--CS-RKPYVPMQLLOIYKYNLH-ENYVADNDGDILGYDILIAMDNNGE-WT-F	462
Db	507	KEGVYVYVAAKGERLFINDEKILMSGFSREVPFNSRDCLAGTRKGIIEGPTCFEC	566
Oy	463	EIIIG-SA-SLSPYHLIDINKTKIGMCHKNNQNPVSVCTTCLAGHHRVAV-GSHHCCFEC	518
Db	567	VECPDGEUSDITDASADCKCPDDFWSNENHTSCIAKLEIFLSTWTEPFGIALFLFAVLGI	626
Oy	519	VPCEAGTFLNNSLHITCOPCGTEEMAPRESTCPRIVEFLAMEHPSILVLIANLTLL	578
Db	627	LTAFLVGLFI-KFENFTPVKATNRELTYLLFLSLLCFSSSLF-FIGEPDWTCLRLOPA	684
Oy	579	LVVGTAGLGFAMHFR-TPVVRAGAGRLCFMLGSLVAG-SCSFYSFBEFPVPACLRQPL	636
Db	685	FGISFVLCISCIILVKNRVLVFE--AKIPTSFHKMWMGLNLOFLVLTCTMQOIVCAI	742
Oy	637	FSLGFALFSLCLTRSPQVLVIFKFSIKVPT-FYRTWAQNMGADLFYIVASTVHLICLT	695
Db	743	WLNTPAPSSYNHLEDEIITTHESGSLAALGLIGTC-LLAALTEFF-AKRSKLPE	800
Oy	696	WLVWMTPTPTREYRPFHVLLECTEVN--SVGFLAFTHHILISTFPCSYLQKLEPE	753
Db	801	NEFEAKFTFEMLEFFIYMWISFIPAVASTY-GKIVSAVEVIAILMAFGLACIFENKRY	859
Oy	754	NYNEAKCTCFELLNFPVSWIAFFTM-ASTYQSLTPAVNVLAGLITLSSGSGFIPLKCY	812
Db	860	IILKPSKNTIE 971	
Oy	813	VILCRPELNTE 824	
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ID	W38272	standard: Protein; 1085 AA.	
AC	W38272;		
DT	08-MAY-1998	(first entry)	
PR	23-AUG-1991	US-749451.	
PR	11-FEB-1992	US-834044.	
PR	21-AUG-1992	US-934151.	
PR	12-FEB-1993	US-011727.	
PR	23-FEB-1993	US-009389.	
PR	22-OCT-1993	US-141248.	
PR	19-AUG-1994	US-292827.	
PR	21-OCT-1994	WO-012117.	
PR	08-DEC-1994	US-353784.	
PA	(BGHM.)	BRIGHAM & WOMENS HOSPITAL.	
PA	(NPSP-)	NPS PHARM INC.	
PI	Brown EM, Fuller FH, Garrett JE, Hebert SC;		
DR	WPI; 98-008040/01.		
DR	N-PSDB: 195857.		
PT	DNA encoding calcium receptor polypeptide(s) - useful for		
PT	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis		
PS	Claim 4; Columns 107-116; 174pp; English.		
CC	The present sequence is bovine parathyroid cell calcium		
CC	receptor 1 (BoPar 1).		
CC	The specification includes details of molecules that can modulate		
CC	one or more inorganic ion receptor activities, and antibodies and		
CC	antibody fragments targeted to inorganic ion receptor proteins. The		
CC	proteins, nucleic acids and antibodies may be used to treat		
CC	disorders by modulating one or more inorganic ion receptor		

CC activities, preferably disorders of calcium homeostasis, e.g.  
CC hyperparathyroidism and osteoporosis.  
SQ Sequence 1085 AA;

Query Match	20.7%;	Score 1311;	DB 1;	Length 1085;
Best Local Similarity	31.9%;	Pred. No. 1.79e-106;		
Matches	272;	Conservative	232;	Mismatches 275;
			Indels	73;
			Gaps	50;

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D	b	90	PNNLTGRIFDPTCTVSKALTEALISFYAOKNKIDSLN-DEFCNGSEHPISTIAVGAATGSG	149
O	y	93	PNITLGEYLDVCGESANVY-ATLRVALDQPRHIE-CK--DLRNHSSKVAFIIGPDNT	149
D	b	150	ISTAVANLGLFYIPQVSYASSFLSKNKKOFKSFLETTFINDEHQATAMADITEFRMNM	209
O	y	150	HAVTAAALGLFELMPLVSYEASSVYLSAKRPFSEFLRTVSDRHOQVEVMVOLLQSEGMW	209
D	b	210	VGTLAADVDRPRDIEKFRFAEERDQICDESELI--SQSDEKIQQVVEVIONSNAXY	267
O	y	210	ISLIGSIDYDQLCVQALEELAVRGICVAKDIPVPSANVDPRMSKHQALQATTV	269
D	b	268	IVFSSSGDEPLI-KEIVRNNIGRIWLSEAWASSSLIAMPYEFHWGGTIGFGKAG	326
O	y	270	VVPSF--RHLLARVEFRSVLANLTKGWASSEDMA---IS-TYIISVIG-IQ-GI--G	318
D	b	327	QIPGRFELQVHPRRKSVHNGFAKEMEETFPNCHLOGAKGPLEVDITFLRGHEGGARLS	386
O	y	319	TVLQ---VA-VQORQ--VP-GL-KEF-EESY---VR-AVTA-P--S---ACEEG--SM-C	357
D	b	387	NSPTAFRLCGEENISSVEIPVNDYTHLRISYVYLYAVYSIAHLODITICIPGRSLFT	446
O	y	358	-S-TN-Q-LCECHTETTRNPTLIGATSKSAAYVYEAIVAAHGLQHLQCTSE--I--	409
D	b	447	NGSCADIKRYAMCVLXHLRELNTSNKGEQVTFDECDGLAGNYSIINMELSPEDGSIVF	506
O	y	410	--CS-RQPYVPQQLQGIYKVNFLH-EMTVAFDDNGDITLGYDITIAMDNQPE-WT-F	462
D	b	507	KEYGYINYAKKGERLFINDEKILMSGFSRVPFSSNCSRDLACITRKGITIEGPTCCFEC	566
O	y	463	EIIQ--SA-SLSPVHLDINKRKIQMHKRNNOVPVSVCTDCLAGHARVVY--GSHCCFEC	518
D	b	567	VECPGGEVSDETDASADCKDDPWSNENHSCIAKEIEFLSWTEPRGIALTLFAYGVIF	626
O	y	519	VPCEAGITLNLSEHLICOPCTEEMAKR3TCTCPRYVFLAMHEPISLVLIANITLL	578
D	b	627	LTAFLVGFYI-KFRNTPIYKATNRELSYLLFLSLCCFSSLF-FIPEPDWTCRLROPA	684
O	y	579	LLVAGAGLFAHHF--TPVRSAGRGLOCFMLGSLVAG--SCSFYSFEPEPIVPACLLNPL	636
D	b	665	FGISVLCISGILVKTNRVLVFE--AKIPISFRKKMGJNLQFLVLTCTMVOYICAI	742
O	y	637	FSLGFAILSCILIRISQOLVYIEFFSTRKPT-FPRTAQNHHGAGLFYIVASTVHLLCLT	695
D	b	743	MLNAPRPSYNNHLEDEIIFITHEGSMALQGLIOTC-LLAALCFE-ARKSRKLE	800
O	y	696	WLVMNTPPTREYRPPHVLVLEETEVN--SVGLLMEFTHNILLISTFVCSYUGKLEP	733
D	b	801	NFNENAKPIFESMLIEFTIWMISIFIPAVASY-GKFSVAVEYIALIASFGLLACIFPKVY	859
O	y	754	NYNEAKCVTFEILLNPFWSIAFFM-ASIVOGSLPRAVNVLAGITTLGSGFSGVFLKCY	812
D	b	860	IILKPSRNTE 871	
O	y	813	VILCRPELNTE 824	











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DB 209 VGTIAADDDYGRPGIEKFEFEEAEEDICIDSELI--SQSDEEELIÖHVEVIONSTAKV 266
QY 210 ISLIGSGDYGQGLQALAEELAVPRGICVAFKDIYFSAFARVGDPRMOSMÖHQAARTV 269
DB 267 IYVSSSGDLEPLI-KEIVRNITGKIWLASEMASSLLAMPYFHYVGGTIGFALKAG 325
QY 270 VVFSN-RHLARVFFRSVLANLKGKVVASEDMA---IS-T-YITSVYG-IG-GI--G 318
DB 326 QIPGREFELKHPKRVHNGFAKFEETFNCHLQEGAKPVPVDITFLNGHESGDRFS 385
QY 319 TVLG----VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356
DB 386 NSSTAFRPLCTGDNISSEVTPYIDYTHLRISYNYLAVYSIAHALODIYTCPLGRGLFT 445
QY 357 -CSN-Q-LCRECHTFTRMPTLGAFMSAAYVEAVVAAGHLQ--L-GC---T 406
DB 446 NGSCADIKKYEAMQVLAHLRLNTNMGEOYTFDECGDLVGNSTIINHLSPEDGSIVF 505
QY 407 SEICS-RGPVYPMQLQOIKRVNFLH-ENTVAEDDNGDTLGYYDIAMDNQPE-WT-F 462
DB 506 KEVGYVNVYAKKGERLFINKEILMSGFREVPSNCSROCIARNGIIGEPDCCFEC 565
QY 463 EIIG--SA-SLSPVHLINTKIKIOMHGKNNQVPVSCITDCLASHHRYV-GSHHCCFEC 518
DB 566 VECPDGEYSDETDASACNKPDDFWSNENHTSCIAKEIEFLSTWTEPRGIALTLFAVLGIF 625
QY 519 VPCEAGTFLLMSELIHOCPTGEEMAPKESYTCPRVTEFLAMEHPISLVLIANTILL 578
DB 626 LTAFLVGLFI-KERNTPIVATNRELSTLLFSLCCFSSSLF-FIGEPDWTCKRQPA 683
QY 579 LVGTAGLAFAMHFR-TPVVSAGGRCLCFMLGSLVAG-SCSFYSFGEPTVPACLLRQPL 636
DB 684 FGISFVLCISCIIVKTNRLVLFEE-AKIPTSFHRKMWGMLQFLVLCFQMOIYICVI 741
QY 637 FSLGALFSLCITRISFOLVIFEFSTIKVP-FYRTAQNÖHAGLPIYVSTVILLICLT 695
DB 742 WLVTAPSSYRNQÖLEDEIIFITCHESSLMALGFLIGYTC-LLAALGFF-AFKSRKLP 799
QY 696 WLVMYTRPREYORFPHLVILLECTEVN--SVGFLLAFTHNILLISFVCSYLGKELPE 753
DB 800 NFNARKEITSMLEFIVWISFIAKASTY-GKRVSAEVAITLAAASGLLACIFENKIY 858
QY 754 NYNARKEITSMLEFIVWISFIAKASTY-GKRVSAEVAITLAAASGLLACIFENKIY 812
DB 859 ILLEKPSRNTIE 870
QY 813 VILCRPELNTE 824

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PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-U12117.
PR 08-DEC-1994; US-353784.
PA (BGM ) BRIGHAM & WOMEN'S HOSPITAL.
PA (NPS-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
DR WPI; 98-008040/01.
DR N-PSDB; T95859.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PS therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 20; Columns 125-134; 174pp; English.
CC The present sequence is human parathyroid cell calcium
CC receptor 4.0 (Hupcar 4.0).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 1078 AA;

Query Match 20.4%; Score 1290; DB 1; Length 1078;
Best Local Similarity 32.0%; Pred. No. 1.Gie-104;
Matches 273; Conservative 230; Mismatches 276; Indels 73; Gaps 49;

DB 30 GDILGLGFPIHNG-VAADKQDKSRPSEVCIRYNGRFRMLOAMFAIEINSPALL 88
QY 35 GDFLAGLESFHGDGCLQVRRRPPLYTSCDRPD--FNGHGLHQAHFVEELINSSALL 92
DB 89 PNILGIRIDTONTYKALEATLSFVAONKIDSLNDEFNCSEHPISTIYAVGATGSC 148
QY 93 PNILGELDVCSSEANVY-ATLRVALQGRHIEIÖK--DLRNHSSKVVAFIGPNDT 149
DB 149 VSTRVANLLGLFIPOVSYASSRLLSNKNOFKSEFLRTIPNDEHQATAMADIIYFRMNM 208
QY 150 HAYTATLALPFLMPLVSYASSRLLSNKNOFKSEFLRTIPNDEHQATAMADIIYFRMNM 209
DB 209 VGTIAADDDYGRPGIEKFEFEEAEEDICIDSELI--SQSDEEELIÖHVEVIONSTAKV 266
QY 210 ISLIGSGDYGQGLQALAEELAVPRGICVAFKDIYFSAFARVGDPRMOSMÖHQAARTV 269
DB 267 IYVSSSGDLEPLI-KEIVRNITGKIWLASEMASSLLAMPYFHYVGGTIGFALKAG 325
QY 270 VVFSN-RHLARVFFRSVLANLKGKVVASEDMA---IS-T-YITSVYG-IG-GI--G 318
DB 326 QIPGREFELKHPKRVHNGFAKFEETFNCHLQEGAKPVPVDITFLNGHESGDRFS 385
QY 319 TVLG----VA-VQORQ-VP-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356
DB 386 NSSTAFRPLCTGDNISSEVTPYIDYTHLRISYNYLAVYSIAHALODIYTCPLGRGLFT 445
QY 357 -CSN-Q-LCRECHTFTRMPTLGAFMSAAYVEAVVAAGHLQ--L-GC---T 406
DB 446 NGSCADIKKYEAMQVLAHLRLNTNMGEOYTFDECGDLVGNSTIINHLSPEDGSIVF 505
QY 407 SEICS-RGPVYPMQLQOIKRVNFLH-ENTVAEDDNGDTLGYYDIAMDNQPE-WT-F 462
DB 506 KEVGYVNVYAKKGERLFINKEILMSGFREVPSNCSROCIARNGIIGEPDCCFEC 565
QY 463 EIIG--SA-SLSPVHLINTKIKIOMHGKNNQVPVSCITDCLASHHRYV-GSHHCCFEC 518
DB 566 VECPDGEYSDETDASACNKPDDFWSNENHTSCIAKEIEFLSTWTEPRGIALTLFAVLGIF 625
QY 519 VPCEAGTFLLMSELIHOCPTGEEMAPKESYTCPRVTEFLAMEHPISLVLIANTILL 578
DB 626 LTAFLVGLFI-KERNTPIVATNRELSTLLFSLCCFSSSLF-FIGEPDWTCKRQPA 683
QY 579 LVGTAGLAFAMHFR-TPVVSAGGRCLCFMLGSLVAG-SCSFYSFGEPTVPACLLRQPL 636
DB 684 FGISFVLCISCIIVKTNRLVLFEE-AKIPTSFHRKMWGMLQFLVLCFQMOIYICVI 741

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QY 637 FSLGFAIFLSCLTIRSPQVLIIEFKSTKVPD-FYRTWAQNAGLIFYVSSVTHLLICLT 695  
 DB 742 WLTAPSSRYNDELDEIIFITCHEGSLMAGLIGYTC-LLAALCFPF-AFKSRKLPE 799  
 QY 696 WLWMTPRPRFQRPFHVLIECTEVN--SVGFLLAFTHNLLISTFVCSYIGKELPE 753  
 DB 800 NFEAKETIFSMIIFFIWISFIPAVASTY-GKFSVAVEVIALIASFGGLACIFFEKIY 858  
 QY 754 NYNEAKCVTSSLINFSWIAFFTM-ASIQSGSLPRAVNLAGLITLISGSGSGYFLKCY 812  
 DB 859 IILFKPSRNTIE 870  
 QY 813 VILCRPELNTNTE 824

RESULT 8  
 ID W94928 standard: Protein: 1079 AA.  
 AC W94928;  
 DT 04-MAY-1999 (first entry)  
 DE Rat kidney extracellular calcium/polyvalent cation-sensing receptor.  
 KW Pheromone receptor; signal transduction; fertility; behaviour;  
 KM reproduction; rodent; insect; rat.  
 OS Rattus sp.  
 PN W09900422-A1.  
 PD 07-JAN-1999.  
 PE 30-JUN-1998; U13680.  
 PR 30-JUN-1997; US-051284.  
 PA (HARD) HARVARD COLLEGE.  
 PI Buck L, Dulac C, Herrada G, Matsunami H;  
 DR WPI: 99-095684/08.  
 PT New isolated pheromone receptor polypeptides - used to develop  
 PT products for controlling fertility and behaviour in vertebrates and  
 PT invertebrates  
 PS Disclosure: Page 169-170; 308pp. English.  
 CC The invention relates to polynucleotide sequences encoding mammalian  
 CC pheromone receptor polypeptides. The polypeptides are expressed in  
 CC murine and rat vomeronasal organ. The products can be used for modifying  
 CC pheromone activity, e.g. for decreasing pheromone receptor mediated  
 CC signal transduction. They can be used for controlling fertility and  
 CC behaviour in vertebrates and invertebrates. Compositions comprising the  
 CC polypeptides are particularly useful in e.g. controlling fertility in  
 CC livestock and controlling reproduction in rodents or insects by  
 CC interrupting the normal behaviours of rodents or insects that result in  
 CC reproduction. The present sequence represents a rat kidney extracellular  
 CC calcium/polyvalent cation-sensing receptor.  
 CC Sequence 1079 AA.

Query Match 20.3%; Score 1285; DB 1; Length 1079;  
 Best Local Similarity 31.6%; Pred. No. 4,71e-104;  
 Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

DB 30 GDIIILGLFPIHFG-VAAKQODLKSRESVECTRYNFRGRWLQAMFAIEINSSSLL 88  
 QY 35 GDFLLGLFSLHGDCLQVRRHPLVTSCDRPDS--FNGHGHLFOAMRFTVEEINNSSL 92  
 DB 89 PNMTLGRIPDTCNTYSKALEATISFYAOKKIDSLNDEFCONSEHTPTIAVGATGSG 148  
 QY 93 PNTTLGEIYDVSESANV-ATLRVIALOGPRRIEIQK--DLRNHSSKVAFAFGPNID 149  
 DB 149 VSTAVANLGLFYIPOVSYASSRLLSNKQYKSFLLTIPNDEHQATAMADIIEFRMNW 208  
 QY 150 HAVTIALLAGPFLMPLVSYEASSVLSAKRKPFSLRTVPSDRQVEVMQVOLLQSGFMW 209  
 DB 209 VGTIADDDYGRGIEFREAEERDICIPISELI--SQVSDEEIQOVVEIVONSIAKY 266  
 QY 210 ISLIGSTGDDGQGVQVQALELAVPRGICVAFKDIVPSARVGPROMQXMOHLAQARTTV 269  
 DB 267 IVVSSSGDLEPLI-KEIVRRNITGRIMLSEAMASSLITAMPYEFHWGTTIGFGKAG 325  
 QY 270 VVVFNSN-RHLARFRRSVLANLTGKVMVASEDMA----IS-T-YTISVYG-IO-GI--G 318  
 DB 326 QIDGFEFLQKVRKRSVHNGFAKFEWEETFNCHLOGAGAKGPLVDITFVRSHEGGRRL 385

QY 319 TVLQ----VA-VQQRQ-VP-GL-KEF-EESY---VR-AVTAA-P--S-A-CPE--GSW-- 356  
 DB 386 NSSTAFRPLCTGDNISVETPRMDENHLRISVNIYAVYSIAHALODITCLPGRSLFT 445  
 QY 357 -CSTN-Q-LRCHETFTTRNPTLGAFSMSAAARYEAAYAAVAGHQQL--T-GC--T 406  
 DB 446 NSCAD-KRKEAMQVJLHLNLTFTNMNGQVTFDECDGLVGNVSTIIMHLSPEDGSIVF 505  
 QY 407 SEICS-NGPYRPMQLQCIKYVFLH-ZYTVAFDDNGDILGYDITAMWNGPE-WT-F 462  
 DB 506 KEVGYNVYAKKERLFIINEKILMSGFSREVPFSCSPDQGRKGIIEGPTCFEC 555  
 QY 463 EIIG--SA-SLSPYHLDINKTKIOWHGKNNQVPSVCTDCLAGHHRVVY-GSHHCCFEC 518  
 DB 566 VECPDGEYSEPTASACDKPDPDFMSNENFTSCIAKEIEZPLATEPFGILTFPAVLGIF 625  
 QY 519 VPCEAGTFLLNMSLHICQPGCTEAMFRESITCFPIVEFLAHEPISYLIAMANTLLL 578  
 DB 626 LFAFVLGVFI-KFRNPYVATNRELSTLLFLSLCTSSSLF-FIGSPQDWTGRJQPA 683  
 QY 579 LVGTAGLAFMWHH-TPVNASAGRLCFLMGLSVAG-SCSFYSFGEPYVPAQLRPL 636  
 DB 684 FGISEVLCISCLIVKTNRLVLEE-AKIPTSFRKRWGLNLOFLVLCIFYQILICIT 741  
 QY 637 FSLGFAIFLSCLTIRSPQVLIIEFKSTKVPD-FYRTWAQNAGLIFYVSSVTHLLICLT 695  
 DB 742 WLTAPSSRYNDELDEIIFITCHEGSLMAGLIGYTC-LLAALCFPF-AFKSRKLPE 799  
 QY 696 WLWMTPRPRFQRPFHVLIECTEVN--SVGFLLAFTHNLLISTFVCSYIGKELPE 753  
 DB 800 NFEAKETIFSMIIFFIWISFIPAVASTY-GKFSVAVEVIALIASFGGLACIFFEKIY 858  
 QY 754 NYNEAKCVTSSLINFSWIAFFTM-ASIQSGSLPRAVNLAGLITLISGSGSGYFLKCY 812  
 DB 859 IILFKPSRNTIEVRSSTAHA 880  
 QY 813 VILCRPELNTNTEFQASIDQYT 834

RESULT 9  
 ID W54847 standard: Protein: 1079 AA.  
 AC W54847;  
 DT 01-SEP-1998 (first entry)  
 DE Rat kidney calcium receptor 3A protein 4kb fragment.  
 KW Calcium ion concentration; parathyroid hormone; homeostasis; kidney;  
 KM calcium receptor; detection.  
 OS Rattus sp.  
 PN US5763569-A.  
 PD 09-JUN-1998.  
 PE 07-JUN-1995; 484565.  
 PR 07-JUN-1995; US-484565.  
 PR 23-AUG-1991; US-749451.  
 PR 11-FEB-1992; US-834044.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009339.  
 PR 22-OCT-1993; US-161248.  
 PR 19-AUG-1994; US-282827.  
 PR 21-OCT-1994; WO-012117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPSF-) NPS PHARM INC.  
 PI Brown EM, Garfield JE, Hebert SC;  
 DR WPI: 98-347412/30.  
 DR N-PSDB: V26965.  
 PT Calcium receptor poly:peptide(s) - useful for drug screening or  
 PT antibody production  
 PS Claim 8: Fig 50: 174pp. English.  
 CC The tissue from which the rat kidney calcium receptor and receptors from  
 CC bovine parathyroid and rat kidney are derived, respond to changes, and  
 CC control changes, in calcium ion concentration, e.g. parathyroid hormone  
 CC regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney  
 CC function alters through changes in Ca2+ levels in juxtaglomerular and



CC proximal tubule cells in the kidney. The purified receptors (produced  
CC recombinantly) can be used to screen for compounds that modulate calcium  
CC receptor activity, especially those that can be used to treat diseases  
CC associated with the receptors in these tissues. They can also be used  
CC to raise antibodies for use in detection assays.

Sequence 1079 AA;

Query Match 20.3%; Score 1285; DB 1; Length 1079;

Best Local Similarity 31.6%; Pred. No. 4.71e-104;

Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

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Db      30 GDIIILGGLPIHNG-VAAKDQDKSRPESVEICIRYFRGRFMLOAMIFAIEINSSPSLL 88
      35 GDFLLAGLFSLHGDCLQVRRRPLVTSQDRPDS--FNGHGHLFQAMRFEVEEINNSSALL 92
Db      89 PNMILGRIFDTCNTVSKALEATLSFYAQNKIDSLNIDEPONCEHPIPTIAYVAGATGSG 148
      93 PNTILGRIELDYDCESEANVY-ATLRVIALOGPRHIEIÖK--DLRNHSSKVVAFTIGPDNTD 149
Db      149 VSTAVANMLGLFIPOVSYASSSRLLSNKQYKSFRLTIPNDEHQATAMADIIEFRMNW 208
      150 HAYTTALLGLPFLMPLVSYEASSSVLSAKRRKPSFLRTVPDRHQVEVMVOLLÖSGFWW 209
Db      209 VGTIADDDYGRGIEKFRFEAEERDIDCFSELI--SQSDEEIOQVEVIONSTAKV 266
      210 ISLIGSYGDYGOGLVQALAEILAVPRGICVAFKDIYPSARVGDPRQSMQHLQARTTV 269
Db      267 IYVSSSGPDLEPLI-KEIVRRNITGRIMILASEAMASSLLAMPFYHVGGTIGFGKAG 325
      270 VVAFSN-RHLARVFRSVLVANLTKGVAVASEDMA---IS-T-YITSVVG-ID-GI- 318
Db      326 QIDGFRFLQVHPRKSVHNGFAKEFEWETFNCHLOGAKGPLVPDFFVSHBEGNRLL 385
      319 TVLG---VA-VQÖRQ-VP-GL-KEF-EESY--VR-AVTRÄ-P--S-A-CPE--GSM-- 356
Db      386 NSTAEPPLCTGDNINSVETPIYDYLHLRISTVYLAIVSIAMADODITCLPRLFT 445
      357 -CSIN-O-LCRECHTFTRNPTLGAFSMAAYRYEAVYAVAHGLHQL--L-GC--T 406
Db      446 NSGADIKRYAMOVYLKHLRLNFTNMGEQVTEDEGDIYGNSTIINHLSPDSIVF 505
      407 SEIICS-RGPYPMOLLQÖIKVNFLL-ENVAPDDGDITIGYDILIAMDNNGPE-WT-F 462
Db      506 KEVGYVNVYAKGERLFINEEKILMSGFSRVPFNSCRDQÖATRGKIIIEGPTCCFEC 565
      463 EIIG--SA-SLSPVHLIDNKTIKMGHKNQVYPSVCTTÖCLAGHHVYV-GSHCCFEC 518
Db      566 VECPDGEYSETDASADCKPDDFWSNENHTSCIAKIEFLAMTEPGIALTLFAVLGIF 625
      519 VPCEAGTFLLMSELHICQPCGTEEMAREKSTCPRTVEFLAMEPISLVLIANTLILL 578
Db      626 LTAFLVGLVFI-KFRNPYVATNRELSYLLFSLLCCFSSSLF-FIEGPDWÖTRLRÖPA 683
      579 LVGTAGLFLFMHHR-ITVVSASGRCLCFMLGSLVAG-SCSFYFSEBPYPOLLÖPL 636
Db      684 FGISEVLCISCIIVKTNRLVLPVE--AKIPTSFRRKMGWGLNÖFLVFLCTFMOILCII 741
      637 FSLGFAFLSCLTIRSQÖLVIIFFKSTKVPF-FYRTWÄQNNGALFLVYSVVALLCIT 695
Db      742 WLTAPSSSTRNHELEIITFITCHESGLMALGSLIGTC-LLAICFFP-AFKSRKLP 799
      696 WLWMTPRPRYÖRPHLVILECTEVN--SVGFLAFTHNLISITFVCSYLGKELPE 753
Db      800 NNEPAKFTSMIIEFTVWISFIPAVASTY-GKFSVAVEVAILAIFGLACIEFNKY 856
      754 NYEAKCVTISLLENFSWIAFFPM-ASTYÖGYLPAVNVLAGLTLSSGGFSYFLPKCY 812
Db      859 IILFKPSRNTIEEYRSSTAHA 880
      813 VILCRPELNTTEHFOASIDYT 834

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RESULT 10

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ID      W89566 standard; Protein; 1079 AA.
AC      W89566;
DT      19-MAR-1999 (first entry)
DE      Rat parathyroid calcium receptor prakcar 3A.
KW      Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
KW      calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
KW      spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
KW      neonatal distress; neurodegenerative disease; Alzheimer's disease;
KW      Huntington's disease; Parkinson's disease; dementia; muscle tension;
KW      depression; anxiety.
OS      Rattus sp.
PN      US585684-A.
PD      12-JAN-1999.
PF      07-JUN-1995; 480751.
PE      07-JUN-1995; US-480751.
PR      23-AUG-1991; US-749451.
PR      11-FEB-1992; US-834044.
PR      21-AUG-1992; US-934161.
PR      12-FEB-1993; US-017127.
PR      23-FEB-1993; US-009389.
PR      22-OCT-1993; US-141248.
PR      19-AUG-1994; US-282827.
PR      21-OCT-1994; WO-012117.
PR      08-DEC-1994; US-353784.
PA      (BGMH ) BRIGHAM & WOMENS HOSPITAL.
PA      (NPSD-) NPS PHARM INC.
PI      Balandrin MF, Brown EM, Del Mar EG, Garrett JE,
PI      Hebert SC, Nemeth EF, Van Wagenen BC;
DR      WPT; 99-119871/10.
DR      N-PSDB; V82486.
PT      Screening for calcium receptor-active compounds - by recombinant
PT      expression of nucleic acid encoding calcium receptor and determining
PT      the effect of compounds on calcium receptor activity
PS      claim 1: Fig 50; 176pp; English.
CC      A method has been developed of screening for a compound able to affect
CC      one or more activities of a calcium receptor (CR) comprises: (A)
CC      contacting a recombinant cell with a test compound, where the
CC      recombinant cell comprises a recombinant nucleic acid expressing the CR,
CC      provided that the cell does not have functional CR expression from
CC      endogenous nucleic acid; (B) determining the ability of the test
CC      compound to affect one or more activities of the calcium receptor; and
CC      (C) comparing the ability with the ability of the test compound to
CC      affect the one or more CR activities in a cell not comprising the
CC      recombinant nucleic acid. The present sequence represents rat
CC      parathyroid CR, designated a prakcar 3A. The nucleic acid sequence of
CC      prakcar 3A can be used as part of the recombinant nucleic acid in the
CC      method described above. The compounds identified can be used to treat
CC      diseases or disorders characterised by abnormal calcium homeostasis, e.g.
CC      hyperparathyroidism, osteoporosis and other bone and mineral-related
CC      disorders. They can also be used for the treatment of diseases and
CC      disorders associated with disrupted Ca2+ responses, e.g. seizures,
CC      stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC      cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC      diseases such as Alzheimer's disease, Huntington's disease and
CC      Parkinson's disease, dementia, muscle tension, depression, and anxiety.
SQ      Sequence 1079 AA;

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Query Match 20.3%; Score 1285; DB 1; Length 1079;

Best Local Similarity 31.6%; Pred. No. 4.71e-104;

Matches 272; Conservative 232; Mismatches 285; Indels 73; Gaps 50;

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Db      30 GDIIILGGLPIHNG-VAAKDQDKSRPESVEICIRYFRGRFMLOAMIFAIEINSSPSLL 88
      35 GDFLLAGLFSLHGDCLQVRRRPLVTSQDRPDS--FNGHGHLFQAMRFEVEEINNSSALL 92
Db      89 PNMILGRIFDTCNTVSKALEATLSFYAQNKIDSLNIDEPONCEHPIPTIAYVAGATGSG 148
      93 PNTILGRIELDYDCESEANVY-ATLRVIALOGPRHIEIÖK--DLRNHSSKVVAFTIGPDNTD 149
Db      149 VSTAVANMLGLFIPOVSYASSSRLLSNKQYKSFRLTIPNDEHQATAMADIIEFRMNW 208
      150 HAYTTALLGLPFLMPLVSYEASSSVLSAKRRKPSFLRTVPDRHQVEVMVOLLÖSGFWW 209

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D	b	209	VGIAADDDYRPGREKTERAEAEKDIDISELI--SQSDEEIQOYVEVYQNSIAKY	269
O	y	210	ISLISQYDIDYDQLGQAEELEAVRGLCTVPAKRDVPPSARVGRPMOSNQHQIAQATTY	269
D	b	267	IVFSSSGDLEPLI-KEIVRNRITGRIMLAESMASSSLIAMPDEFFVVGITIGFGKAC	325
O	y	270	VVPSR-RHLRAVFRFSRYVLANLIGKQVVASEDMA-----IS-T-YTISYIG-IQ-GI--G	318
D	b	336	QIPGREFLEQVHBRKSYVHNGFAKEFWEETFNCHLQEGAGKGPDPVDITFVSHSEGGNRL	385
O	y	319	TVLG---VA-VQQRQ--VP-GL-KEF-EESY---VR-AVIAA-P--S-A-CPE--GSW--	356
D	b	366	NSSTAERPLCTGDENINSVEPYNDYELRISIVYIAYVSIANAADIDITCIPGRGLT	445
O	y	357	-CSTN-Q-ICEKCHTFTIRNPTLTGAESMSAAKYRYVEAYVAVAHGLHQL--L-GC--T	406
D	b	446	NGSCADIKYVAMOVLLKRLRLNTNNMGDQVTEDECGDLGVNSIINHLSPEDSIYF	505
O	y	407	SEIGS-RGPVYPMQLDQIYKVNFLH-ENVVAFDQDGTLLGYDITIAMQNGPE-WT-F	462
D	b	506	KEVGYYNYAKKGRLEFINEREKILMSGFSRPFNSNRDQAGTRKGIIEGPTCCFEC	565
O	y	463	ELIG--SA-SLSPVHLDNKRKIQMHGKNNOVPYSCVTTDCLAGHANYV-GSHRCFEC	518
D	b	566	VECPDGEYSGETDASACDKCPDDEFWNSNENHTSCIAKEIEFLAMTEPGIALTLFLVAGIF	625
O	y	519	VPCEAGTFLNMSLEHICOPCTIEEMAKRESITCPFRVEEFLAMHEPISVLIAANLTL	578
D	b	626	LTAFLVGLFI-KFENTPIYKATNNEISYLLFLSLCCFSSLP-FIGEPDWMCRLRQ	683
O	y	579	LIVGAGLFAWHFH-TPVVRSGAGRLCFELMGISLVAG-SCSFYSFEGEPVPAQLRQ	636
D	b	684	FGISVLCISCIILKTRNLVLVE--AKIPSFHRKMGGLNGLQELFLCTFQILICIT	741
O	y	637	FSLGFAITLSCLTRISQOLVIEFNSKVPF-FRTAQNQHGAGLFPYIVSYTHLICTL	695
D	b	742	WLXTAPSSYNNHLEDELIIFITCHEGSLMALGSLIGYC-LLAALCFP-AFKSRKLE	799
O	y	696	WLVMVTPRPTREYQRPFLVLILECTEVN--SVGFLAFTNNILSLISTFVCSYLGKEL	753
D	b	800	NENNAKFTTESMLFFIYIWSIFITAVSYT-GKVSAYEVETIALIASFGILACIFPNKY	858
O	y	754	NYNEAKCTFSLNLFVSWIIFFTM-ASIQGSYLPAVNVLAGITLTSGGFSGCYFLPKCY	812
D	b	859	IILFKSRNTIEEVSRFAHA	880
O	y	813	VILCRPELNTNEHFOASTIDYIT	834
RESULT 11				
ID	M38275 standard: protein: 1079 AA.			
AC	M38275.			
DT	08-MAY-1998 (first entry)			
DE	Rat kidney cell calcium receptor 3A (RakCar 3A).			
KW	Rat kidney cell calcium receptor 3a; RakCar 3A;			
KW	calcium homeostasis; hyperparathyroidism; osteoporosis.			
OS	Rattus sp.			
PN	U5688938-A.			
PD	18-NOV-1997.			
PF	07-JUN-1995; 485588.			
PR	07-JUN-1995; US-485588.			
PR	23-AUG-1991; US-749451.			
PR	11-FEB-1992; US-834044.			
PR	21-AUG-1992; US-934161.			
PR	12-FEB-1993; US-017127.			
PR	23-FEB-1993; US-009389.			
PR	22-OCT-1993; US-141248.			
PR	19-AUG-1994; US-292827.			
PR	21-OCT-1994; WO-012117.			
PR	08-DEC-1994; US-353784.			
RA	(BGHM ) BRIGHAM & WOMENS HOSPITAL.			
RA	(NPSP-) NPS PHARM INC.			
SI	Brown EM, Fuller FH, Garrett JE, Hebert SC			

DR	WPI: 98-008040/01.	20.3%:	Score 1.95:	D3 1:	Length 1079:
DR	N-PSDB: 195860.				
PI	DNA encoding calcium receptor polypeptide(s) - useful for				
PI	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis				
PS	Claim 20: Columns 133-142: 114pp: English.				
CC	The present sequence is rat kidney cell calcium				
CC	receptor 3A (Rakkar 3A).				
CC	The specification includes details of molecules that can modulate				
CC	one or more inorganic ion receptor activities, and antibodies and				
CC	antibody fragments targeted to inorganic ion receptor proteins. The				
CC	proteins, nucleic acids and antibodies may be used to treat				
CC	disorders by modulating one or more inorganic ion receptor				
CC	activities, preferably disorders of calcium homeostasis, e.g.				
CC	hyperparathyroidism and osteoporosis.				
CC	Sequence 1079 AA:				
Query Match	20.3%:	Score 1.95:	D3 1:	Length 1079:	
Best Local Similarity	31.6%:	Pred. No. 4.7e-104:			
Matches	277:	Conservative 232:	Mismatches 285:	Indels 73:	Gaps 50:
D3	30 GDIIIGGLFPHFG-VAAKDDDKSRPESVCIRYFNGFWLQAMFAEINSSPLL 88	:     :	:     :	:     :	:     :
QY	35 GDFLLAGLFSLHGDCLOVRRPRLVTSQDRPDS--FNGHGLFAMARTVEINSSALL 92	:     :	:     :	:     :	:     :
D3	89 PNMILGRIFPTDCTNVSKALEATISFYAONKIDSLNDFEFCSEHPTSTAVVATGSG 148	:     :	:     :	:     :	:     :
QY	93 PNTILGYELLYOVCSANVY-ATLRVLALQGRHIELOK--DLRNHSSKYVAFIQRPTND 149	:     :	:     :	:     :	:     :
D3	149 VSTAVANLLGLFYIPQVSYASSSRLSKKNQYKSFRTIPNDEHQATAMADIIYFRKNW 208	:     :	:     :	:     :	:     :
QY	150 HAVTAAALLGLFELMPLVSEYSAVYLSAKRKFPEFLRTPVSDRHQVEVMQDLOSFQWV 209	:     :	:     :	:     :	:     :
D3	209 VGTIADDDYVRPGIEKREAEERDIDKSELI--SQYSEDEEIQVNVYIONSTAKY 266	:     :	:     :	:     :	:     :
QY	210 ISLISYDYOVLQOALELAVRPGICVAKDIPVSARVGRDPMQSMQHLQARTV 269	:     :	:     :	:     :	:     :
D3	267 IVFSSGGDEPLI-KEIVRRNITGRILVSEMASSLLIMPEYFHVVGSTIGFKAG 325	:     :	:     :	:     :	:     :
QY	270 VVVEN-RHLARVFRSVYLANLIGKVVAVSADMA---IS-T-YIYSYG-IG-GI-T 318	:     :	:     :	:     :	:     :
D3	326 QIPGRREFLQVHPKRSYVHNGFAKEFWEETFNCHLQEGAKGPLVDVTVRSHEEGNRL 385	:     :	:     :	:     :	:     :
QY	319 TVLG---VA-VQORQ-VP-GL-KEF--EESY---VR-AVTPA-P-S-A-CPE--GSM-- 356	:     :	:     :	:     :	:     :
D3	386 NSTAFRRLCTGDEKINSEVTPFYADYHLRTSYVYLAYSIALADODIYTLCPGRGLFT 445	:     :	:     :	:     :	:     :
QY	357 -CSTN-Q-LCEECHTFTTRNPTLTGAFSMAAUYVAYVAAGLHQL--L-GC--T 406	:     :	:     :	:     :	:     :
D3	446 NGSCADIKRYVAMQVCLKRLHNTNNNGEQTVEDECGDLVAGNSIINMHLSPDGSIVF 505	:     :	:     :	:     :	:     :
QY	407 SEICS-RQPPVPMQLOQIYKVNLLH-ENVAADNDNGDITIGYDITIAMDNQPE-WT-F 462	:     :	:     :	:     :	:     :
D3	506 KEVGYNYVAKKGERLFINEBKILMSGFSRPVPSNCSRDQACTRKGIIIEGPTCCFEC 565	:     :	:     :	:     :	:     :
QY	463 EIIG--SA-SLSPVHLIDINKTKIQWGHKNQOVPVSVCTDCLAGHRRVY-GSHHCFCFC 518	:     :	:     :	:     :	:     :
D3	566 VECPRGEISGETDASADCKPDDPWSNENHNSCLAKELFELAMTERPGIALTEPAVLGIF 625	:     :	:     :	:     :	:     :
QY	519 VPCEAGITLNNSEHLIQCPCIEWAPRSESTICPRVEFLAMEHPSLVIADANTLLL 578	:     :	:     :	:     :	:     :
D3	626 LTAFLVGLFYI-KERNTPIVAKTARELSYLLFSLCCFSSSLF-FIGEPQWQTRLROPA 683	:     :	:     :	:     :	:     :
QY	579 LLVGTAGLFAMNHFH-TPYVRASGRCLCELMGSLVAG-SCSFYFSEBPYVPAOLLQPL 636	:     :	:     :	:     :	:     :
D3	684 FGISFVLICSLIVKTNRLVLF--AKIPTSFHRKMWGLNLOFLVLEFCTMQLICII 741	:     :	:     :	:     :	:     :
QY	637 FSLGAFPLISCLTIRSPQVLIIFKSTIKVPT-FYRTANQNHGALFVIVSTVHLICLT 695	:     :	:     :	:     :	:     :
D3	742 WLTPAPPSYNHLEDEIITFTHESGLMALGSLIGTC-LLAALIGFF--AFRSKLPE 799	:     :	:     :	:     :	:     :
QY	696 WLVMVTPPTREYORFPLHVLLECTEVN--SVGLLAFTHHILISTFVCSYSGKELPE 753	:     :	:     :	:     :	:     :
D3	800 NENAEKTFITFMLFFFIYWISIFIPAVASTY-GKFSVAVEVATIAASFGLACIFENKVV 858	:     :	:     :	:     :	:     :



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OY 754 NINENKCVFFSLNLFVSWIAFFTM-ASIIQSGSYLPVAVNLAGLITLSSGGSGFYFLPKCY 812
DB 859 IILFKRSRTIEVRSSTAAHA 880
OY 813 VILCRPELNTEHFQASIODYT 834

RESULT 12
ID W32059 standard; Protein: 1026 AA.
AC W32059.
DE 27-MAR-1998 (first entry)
KW Dogfish shark kidney calcium receptor related protein (SKCAR-RP);
KW Calcium receptor related protein; Car-RP; dogfish shark; SKCAR-RP;
KW polycation-sensing receptor; aquaculture; fish farming;
KW salinity tolerance.
OS Squalus acanthias.
FH Key
FH Region Location/Qualifiers
FT 351..395
FT /note="region in extracellular domain that is
FT highly divergent from mammalian PVCR"
FT
FT Region 870
FT /note="region in C-terminal domain that is
FT highly divergent from mammalian PVCR"
FT
FT MO9735977-A1.
PD 02-OCT-1997.
PD 27-MAR-1997; U05031.
PR 27-MAR-1996; US-622738.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI Brown E, Harris HW, Hebert S;
DR N-PSDB; T89290.
PT New isolated Aquatic polyvalent cation-sensing receptor - used to
PT develop products for increasing or decreasing the salinity tolerance
PT of fish for use in aquaculture
PS Claim 9; Fig 5A-B; 57pp; English.
CC This protein comprises dogfish shark kidney calcium receptor
CC related protein (SKCAR-RP), an aquatic polyvalent cation-sensing
CC receptor (PVCR). Its amino acid sequence was deduced from a kidney
CC cDNA clone (see T89290). It shows 74% homology to rat kidney
CC PVCR and bovine parathyroid PVCR and possesses general features
CC that are homologous to PVCR proteins, including a large
CC extracellular domain, 7 transmembrane domains and a cytoplasmic
CC C-terminal domain. Also claimed are: an isolated PVCR present in
CC the plasma membranes of aquatic species, especially on the apical
CC membrane of epithelial cells of elasmobranch fish particularly
CC from cells found in the collecting duct or late distal tubule in
CC the kidney, intestine, gill, rectal gland, gonad or brain; an
CC antibody that specifically binds to a PVCR; and a method of
CC screening for aquatic PVCR agonists and antagonists. Modulation of
CC the expression of the aquatic PVCR activates or inhibits aquatic
CC PVCR mediated ion transport and endocrine changes that permit fish
CC to adapt to fresh or salt water. The method facilitates the
CC aquaculture of marine fish and can provide for the development of
CC marine fish that are easily adaptable to fresh water aquaculture.
SQ Sequence 1026 AA;

Query Match 19.4%; Score 1230; DB 1; Length 1026;
Best Local Similarity 30.8%; Pred. No. 6,166-99;
Matches 261; Conservative 236; Mismatches 277; Indels 74; Gaps 46;
DB 34 GDIIIGGLFPIHFG-VAAKDODLSKPEATKCIYRNFGRFLQAMIFAIEEINNSMPL 92
OY 35 GDFLAGLGLSLGDCLOVHRPLVTSQDRPS--FNGHYHFLQAMRFVEIEINNSALL 92
DB 93 PUITLGIYRDTQNTVSKALEATLSFVAONKIDSLNDFECSDSHIPSTIIVAGATGSG 152
OY 93 PUITLGIYRDTQNTVSKALEATLSFVAONKIDSLNDFECSDSHIPSTIIVAGATGSG 152
DB 153 ISTAVANILGLTYIPQVSAASSRLSNKNEKAFRTIPNDEQQTAAAEIIEHQMWW 212
OY 150 HAVTTALGLPLMLPLVSTYEAASSVLSAKRKPPSFRLTYPSDRHOVEYVOLLQSGWW 209

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DB 213 VGTIAADDYGRPGIDKREERAVNRDIDCFSEMI--SOYTOROLEFIADVIIONSSAKV 270
OY 210 ISLIGSYGDIYQGLQVQALAEELAVPRGICVAFKDIIVPSABRGDPRMOMQHLAQRITV 269
DB 271 IYVPSNGDLEPLI-QEIVRNITDRITLASEANASSLAKPEYFHVYGGTIFALRAG 329
OY 270 YVVFESN-RHLARVFEFRSVLANLTGKVVASEDA---IST-YITSV-T-G-10-G 316
DB 330 RLPGNKFLKEVHPAGPMTGLSSRSSGRRLQLLHREDLTOLKNSKVSHPGAQDQSK 389
OY 317 -I-G--TVL-GV-AVQQRV-----PG--LKEF---EE-STVR-A-VTA-APSAPEBSW 356
DB 390 AGNSRRALRHPCTGEENITSETPYIDYTHLRISYNYAVYSAHALADIHSCPKPTG 449
OY 357 CSTNQ---LCREC---HFTIRNMPDTGAFMSAARYEAVYAVAHGLHQLCCT--SE 408
DB 450 IFANGSCADIKKVENAQVNLHLHKTPTSNGEQYDDPDQDGLNGNTIIMQLSADES 509
OY 409 I----CS-RGPVYPMOLLOIYKVNFLH-ENTVAFEDNGDITGYDILAMDNGP-EW 460
DB 510 VLFHEGVNMYNAPKSDRLNINEKKILMSGFSKVPFSCSRDCVPGTRKGIIGEPTCC 569
OY 461 T-FEITGS-ASLS-PV-HLDINKTIOMHGKNNOVPVSVCTTDCLAGHRRVY-GSHHC 515
DB 570 FECAACAGEFSDENDASACTKCPNDFWSNENHTSCIAKEIEYLSWTEPFQIALTIRAVL 629
OY 516 FECVPCGAGTFLNMSSELHICQPCGHEWAPKSESTCFPRVEFLAHMBPISLVLIANTL 575
DB 630 GILITSEVLGFI-KFRNTPYKATNRELSTLLFSLICCCSSSLIFIGERDMTCRLRQ 688
OY 576 LLLLVGTAGLFAWHFH-TPVVRSAGRLCFMLGSLVAGSCSPFSGEPTVPACLLRQ 634
DB 689 PAFGISFLVCSCLIVKTRNLVFE--AKIPTSLHRKWLINLOFLVFCILVOIYTC 746
OY 635 PLFSIGFAIFLSCLTIRSFOLVITFKFSTKVPY-FYRMAONHGAGLFVITYSVYHLIC 693
DB 747 IIVLYTADPSSYRNHELEDEVIPTFCDEGSLMAGFLIGYTC-LIAAICFFP-AFKSRKL 804
OY 694 LTMVWMPRPRTYRQRPHPHVLIECTEVN--SVGFLAFHNIILISTEVCSTYKEL 751
DB 805 PENFNEAFITFMSLIFITWISFIRAVSTY-GKFAVAVIATLASSPDLCCIYRNK 863
OY 752 PENYEACVFFSLNLFVSWIAFFTM-ASIIQSGSYLPVAVNLAGLITLSSGGSGFYFLPK 810
DB 864 CYIIFKP 871
OY 811 CIVILCRP 818

RESULT 13
ID W38273 standard; Protein: 1088 AA.
AC W38273.
DE 08-MAY-1998 (first entry)
KW Human parathyroid cell calcium receptor 5.2 (Huppar 5.2);
KW Human parathyroid cell calcium receptor 5.2; Huppar 5.2;
KW calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
FH US5688938-A.
FH 18-NOV-1997.
FH 07-JUN-1995; 485588.
FH 23-AUG-1991; US-485588.
FH 11-FEB-1992; US-834044.
FH 21-FEB-1993; US-017127.
FH 12-FEB-1993; US-017127.
FH 23-FEB-1993; US-009389.
FH 19-AUG-1994; US-141248.
FH 12-AUG-1993; US-292827.
FH 21-OCT-1994; WO-012117.
FH 08-DEC-1994; US-353784.
FH (BGHM ) BRIGHAM & WOMENS HOSPITAL.
FH (NPSP-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;

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Db 326 QIPGFEELKVKHPRKSVHNGFAKEFWETFNCHLOEGAKGPLVDFLGHESGDRFS 385  
 Qy 319 TVLG---VA-VQOQO-VP-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356  
 Db 386 NSSAFRPLCTGDNISSEVETPYIDYTHLRISYNYLAVYSIAHALODITYCLPGRGLFT 445  
 Qy 357 -CSTN-Q-LRECHTFTTRNMTPLGAFMSMAARYEYAVAVAGHLQJL---L-GC---T 406  
 Db 446 NGSGADIKKVAQVVKHLRLNFTNNGBOVTFDECGDLVGNSTIIMHLSPEGDSIVF 505  
 Qy 407 SEICS-RGPVYPMOLLOQIYKYNFLH-ENTVAFDDNGDITGLYDIAMDNNGPE-WT-F 462  
 Db 506 KEVGYNYVYAKGGERLFINERKILMSGFSRPLTFVLVLQVPSNCSRDCLAGTRKGI 565  
 Qy 463 EIIG--SA-SLSPYHDLINKIKIOMHG--KN-----N-QVPVSVCTDCLAGHHRVYV 509  
 Db 566 EGEPTCCFECEVCPDGEYSDETDSACNCPDDFWSNENHTSCIAKEIEFLSTWTEPGIA 625  
 Qy 510 -GSHHCCFECEVCPDGEYSDETDSACNCPDDFWSNENHTSCIAKEIEFLSTWTEPGIA 568  
 Db 626 LTFRAVIGIFLTAFLVGLVFI-KFRNTPIVKATNRELSTYLLFSLCCFSSSLF-FIGEPQ 683  
 Qy 569 LIAANTLLLLVGTAGLFAWHFHTPVVRSAGRLCLMLGSLVAG-SCSFYSFGEPT 626  
 Db 684 DWTCLRPAPAGISFVLCISCLVKNRVLVFE-AKIPTSFRKMWGLMLOFLVFLC 741  
 Qy 627 VPALLKQPLFSLGFAIFLSCITRSPLVLIIFKSTKVPF-FRTYMAQNNAGLFIYVS 685  
 Db 742 TFMQIVCVIWLVTAPSSSYNOLEDEIIFITCHESSLMALGLIGYTC-LLAICFEF 800  
 Qy 686 STVALLCLTLMVMTPTREYORFPLVILECTEVN--SVGFLTAFTNHLISSTFV 743  
 Db 801 -AFKSRKLPENENAKFTFTEMLFEIYVWISFPAVASTY-GKFSVANEVAILAASGL 858  
 Qy 744 CSTYKLEPENTENAKFTFTEMLFEIYVWISFPAVASTY-GKFSVANEVAILAASGL 802  
 Db 859 LACIFENKIYILFKPSRNTIE 880  
 Qy 803 FSGYFLPKCYVILCRPELNMTE 824  
 RESULT 15  
 ID W89564 standard; Protein; 1088 AA.  
 AC W89564;  
 DT 19-MAR-1999 (first entry)  
 DE Human parathyroid calcium receptor PHUPCAR 5.2.  
 KW Parathyroid calcium receptor; Inorganic ion receptor; osteoporosis;  
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;  
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;  
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;  
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;  
 KW depression; anxiety.  
 OS Homo sapiens.  
 PN US583684-A.  
 PD 12-JAN-1999.  
 PE 07-JUN-1995; 480751.  
 PR 07-JUN-1995; US-480751.  
 PR 23-AUG-1991; US-748451.  
 PR 11-FEB-1992; US-834044.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; WO-012117.  
 PR 08-DEC-1994; US-353784.  
 PR (BGM ) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPS-) NPS PHARM INC.  
 PI Hebert SC, Nemeth EF, Van Wagenen BC.  
 DR WPI; 99-119871/10.  
 DR N-PSDB; V82484.

PT Screening for calcium receptor-active compounds - by recombinant  
 PT expression of nucleic acid encoding calcium receptor and determining  
 PT the effect of compounds on calcium receptor activity  
 PS Claim 1, Fig 48; 176pp; English.  
 CC A method has been developed of screening for a compound able to affect  
 CC one or more activities of a calcium receptor (CR) comprising: (A)  
 CC contacting a recombinant cell with a test compound, where the  
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,  
 CC provided that the cell does not have functional CR expression from  
 CC endogenous nucleic acid; (B) determining the ability of the test  
 CC compound to affect one or more activities of the calcium receptor; and  
 CC (C) comparing the ability with the ability of the test compound to  
 CC affect the one or more CR activities in a cell not comprising the  
 CC recombinant nucleic acid. The present sequence represents human  
 CC parathyroid CR, designated a PHUPCAR 5.2. The nucleic acid sequence of  
 CC PHUPCAR 5.2 can be used as part of the recombinant nucleic acid in the  
 CC method described above. The compounds identified can be used to treat  
 CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.  
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
 CC disorders. They can also be used for the treatment of diseases and  
 CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures,  
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
 CC diseases such as Alzheimer's disease, Huntington's disease and  
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
 SQ Sequence 1088 AA.  
 Query Match 18.9%; Score 1198; DB 1; Length 1088;  
 Best Local Similarity 31.88; Pred. No. 5,80e 96;  
 Matches 274; Conservative 231; Mismatches 274; Indels 83; Gaps 52;  
 Db 30 GDILGLGFIHFG-VAKQDQKSRPESVECTRYNRRGRMIOAMIFAEINSPALL 88  
 Qy 35 GDFLALGFLHODCLOVRRHPLVTSQDRPDS--FNCHGHLQAMFTYELINSSALL 92  
 Db 89 PNLTGIRIDTCNTVSKALEATLSEYVQNKIDSLNDEFCONSEHITPSTIYVATGATG 148  
 Qy 93 PNLTGIRIDTCNTVSKALEATLSEYVQNKIDSLNDEFCONSEHITPSTIYVATGATG 149  
 Db 149 VSTAVANLLGLFYIPQVSYVSSRLSNKQFSELTINDEHQATAMDIIEYFPMW 208  
 Qy 150 HAVTTAALGFLMPLVSYVSSRLSNKQFSELTINDEHQATAMDIIEYFPMW 209  
 Db 209 VGTIADDDYGRPGIEKFEAEERDIDCFSELI--SQYSEDEIQHVEVIONSTAKY 266  
 Qy 210 ISLIGSGDYGVQALDELAIPRGICVAFKDIYPSAVSGPRMGMHLAGARTYV 269  
 Db 267 IVFSSGPDLEPL-KEIVRNITGKIWLASEMASSSLIAMPQYFHVGGTIGFALKAG 325  
 Qy 270 VVAFSN-RHLARFEFRSVLANLTGKVVASDEMA---IS-T-YITSVG-IO-GI--G 318  
 Db 326 QIPGFEELKVKHPRKSVHNGFAKEFWETFNCHLOEGAKGPLVDFLGHESGDRFS 385  
 Qy 319 TVLG---VA-VQOQO-VP-GL-KEF-EESY---VR-AVTAA-P-S---ACPE-GSM-- 356  
 Db 386 NSSAFRPLCTGDNISSEVETPYIDYTHLRISYNYLAVYSIAHALODITYCLPGRGLFT 445  
 Qy 357 -CSTN-Q-LRECHTFTTRNMTPLGAFMSMAARYEYAVAVAGHLQJL---L-GC---T 406  
 Db 446 NGSGADIKKVAQVVKHLRLNFTNNGBOVTFDECGDLVGNSTIIMHLSPEGDSIVF 505  
 Qy 407 SEICS-RGPVYPMOLLOQIYKYNFLH-ENTVAFDDNGDITGLYDIAMDNNGPE-WT-F 462  
 Db 506 KEVGYNYVYAKGGERLFINERKILMSGFSRPLTFVLVLQVPSNCSRDCLAGTRKGI 565  
 Qy 463 EIIG--SA-SLSPYHDLINKIKIOMHG--KN-----N-QVPVSVCTDCLAGHHRVYV 509  
 Db 566 EGEPTCCFECEVCPDGEYSDETDSACNCPDDFWSNENHTSCIAKEIEFLSTWTEPGIA 625  
 Qy 510 -GSHHCCFECEVCPDGEYSDETDSACNCPDDFWSNENHTSCIAKEIEFLSTWTEPGIA 568  
 Db 626 LTFRAVIGIFLTAFLVGLVFI-KFRNTPIVKATNRELSTYLLFSLCCFSSSLF-FIGEPQ 683



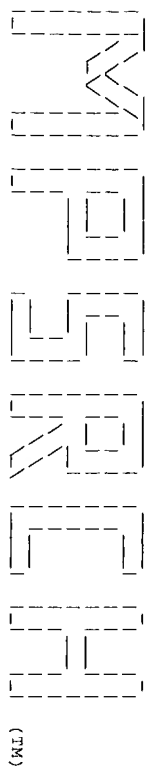
QY 569 LIAANTILLLLLVGTAGLFAMH-FPVRSAGRLCLMIGSLVAG-SCSFVSFFGEP 626  
Db 684 DMTCLROPAFGISFVLCISCIILVKTNRVLVEE-AKIPSEHRKXMGILQFLIVEIC 741  
QY 627 VPACLLRQPLFSLGFAIFLSCLTTRSFQLVITFKSTKVPT-FYRTMAONHAGLEFVIVS 685  
Db 742 TFMQIVICVIMLYTAPPSYRNQLEDEIIFITCHEGSLMALGFLIGYC-LIAAICFF 800  
QY 686 STVHLILCLTLMVMTDRPTREYORFPHVILLECTEVN-SVGFLAFTNHILLISTFV 743  
Db 801 -AFKSRKLPENENEAKITFSMLIFFIWMISFIPAVASTY-GKPVSAVEVIAITLASFGL 838  
QY 744 CSYLGKELPENYNKACVFSLLNLFVSWIAFTFM-ASIVOGSYLPAVNVNLAGLTTLSGG 802  
Db 859 LACIFENKIVYIILEKPSRNTIE 880  
QY 803 FSGYFLPKCYVILCRPELNTE 824

Search completed: Fri Mar 17 13:01:48 2000  
Job time : 100 secs.









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MSPrch\_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:18:18 2000; Maspar time 113.49 Seconds

Tabular output not generated. 514,400 Million cell updates/sec

Title: >US-09-361-652-2  
Description: (1-842) from US09361652.pep  
Perfect Score: 6366  
Sequence: 1 MFWMAHLLLSQLAVAYCW.....NTEHFQASIDYTRCGTT 842

Scoring table: PAM 150  
GAP 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrembl12  
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle  
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
13:sp-vertebrate 14:sp-virus

Statistics: Mean 52.594; Variance 100.413; scale 0.524

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	5839	91.7	840 11	Q920R8	PUTATIVE TASTE RECEPTOR	0.00e+00
2	2026	31.8	843 11	Q920R7	PUTATIVE TASTE RECEPTOR	0.00e+00
3	1421	22.3	868 13	Q73636	PHEROMONE RECEPTOR	9.53e-270
4	1388	21.8	848 13	Q93553	PUTATIVE ODORANT RECEPTOR	1.64e-262
5	1358	21.3	864 13	Q73637	PHEROMONE RECEPTOR	6.14e-256
6	1334	21.0	940 13	Q73635	CALCIUM2+ SENSING RECEPTOR	1.10e-250
7	1279	20.1	880 13	Q73632	PHEROMONE RECEPTOR	1.17e-238
8	1258	19.8	844 13	Q93552	PUTATIVE ODORANT RECEPTOR	4.52e-234
9	1251	19.7	855 13	Q73638	PHEROMONE RECEPTOR	1.52e-232
10	1236	19.4	875 13	Q73640	PHEROMONE RECEPTOR	2.86e-229
11	1160	18.2	912 11	Q70410	PUTATIVE PHEROMONE RECEPTOR	1.03e-212
12	1009	15.8	855 11	Q70409	PUTATIVE PHEROMONE RECEPTOR	5.72e-180
13	974	15.3	779 11	Q93269	PUTATIVE PHEROMONE RECEPTOR	2.06e-172
14	881	13.8	458 13	Q93555	PUTATIVE ODORANT RECEPTOR	2.06e-152
15	832	13.1	850 11	Q93189	PUTATIVE PHEROMONE RECEPTOR	6.33e-142
16	815	12.8	408 13	Q93558	PUTATIVE ODORANT RECEPTOR	2.70e-138
17	798	12.5	803 11	Q93191	PUTATIVE PHEROMONE RECEPTOR	1.14e-134
18	787	12.4	983 11	Q92916	METABOTROPIC GLUTAMATE RECEPTOR	2.50e-132
19	785	12.3	866 11	Q93268	PUTATIVE PHEROMONE RECEPTOR	6.67e-132
20	727	11.4	428 11	Q70413	PUTATIVE PHEROMONE RECEPTOR	1.36e-119

21	727	11.4	667 11	Q93267	PUTATIVE PHEROMONE RECEPTOR	1.36e-119
22	721	11.3	350 13	Q93556	PUTATIVE ODORANT RECEPTOR	2.54e-118
23	717	10.9	908 14	Q95945	METABOTROPIC GLUTAMATE RECEPTOR	1.78e-117
24	697	10.3	548 11	Q93265	PUTATIVE PHEROMONE RECEPTOR	2.98e-113
25	682	10.7	852 11	Q93192	PUTATIVE PHEROMONE RECEPTOR	4.33e-110
26	676	10.6	604 11	Q93195	PUTATIVE PHEROMONE RECEPTOR	7.94e-109
27	669	10.5	604 11	Q93194	PUTATIVE PHEROMONE RECEPTOR	2.36e-107
28	663	10.4	723 11	Q93193	PUTATIVE PHEROMONE RECEPTOR	4.31e-106
29	650	10.2	768 11	Q93266	PUTATIVE PHEROMONE RECEPTOR	2.31e-103
30	628	9.9	1267 5	Q93364	F45H11.4 PROTEIN	9.38e-99
31	625	9.8	339 11	Q70411	PUTATIVE PHEROMONE RECEPTOR	3.98e-98
32	617	9.7	695 11	Q93272	PUTATIVE PHEROMONE RECEPTOR	1.87e-96
33	542	8.5	808 11	Q93190	PUTATIVE PHEROMONE RECEPTOR	6.97e-81
34	528	8.3	251 13	Q73652	PHEROMONE RECEPTOR (FRAGMENT)	5.34e-78
35	523	8.2	251 13	Q73647	PHEROMONE RECEPTOR (FRAGMENT)	5.69e-77
36	519	8.2	251 13	Q73654	PHEROMONE RECEPTOR (FRAGMENT)	3.78e-76
37	509	8.0	251 13	Q73649	PHEROMONE RECEPTOR (FRAGMENT)	4.25e-74
38	508	8.0	251 13	Q73653	PHEROMONE RECEPTOR (FRAGMENT)	6.81e-74
39	507	8.0	311 11	Q93363	CALCIUM SENSING RECEPTOR	1.09e-73
40	500	7.9	250 13	Q73646	PHEROMONE RECEPTOR (FRAGMENT)	2.96e-72
41	505	7.9	251 13	Q73655	PHEROMONE RECEPTOR (FRAGMENT)	2.80e-73
42	505	7.9	251 13	Q73656	PHEROMONE RECEPTOR (FRAGMENT)	2.80e-73
43	502	7.9	301 11	Q93364	CALCIUM SENSING RECEPTOR	1.15e-72
44	491	7.7	250 13	Q73651	PHEROMONE RECEPTOR (FRAGMENT)	2.04e-70
45	487	7.7	250 13	Q73650	PHEROMONE RECEPTOR (FRAGMENT)	1.34e-69

ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	840 AA.
AC	Q920R8			
DT	01-MAY-1999 (TREMUR-rel. 10, Created)			
DT	01-MAY-1999 (TREMUR-rel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMUR-rel. 10, Last annotation update)			
DE	PUTATIVE TASTE RECEPTOR TR1 (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MISTAR;			
RX	MEDLINE: 99159821.			
RA	HOON M.A., ADLER E., LINDEMEIER J., BATTY J.F., RYAN N.J.P., ZUKER C.S.,			
RT	Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity."			
RL	Cell 96:541-551(1999).			
DR	EMBL: AF127389; AAD18069.1; -			
KW	Receptor.			
FT	NON_TER			
SQ	SEQUENCE 840 AA; 93496 MW; B15F564 CRC32;			
Query Match	91.7%; Score 5839; DS 11; Length 840;			
Best Local Similarity	90.0%; Pred. No. 0.00e+00;			
Matches	758; Conservative 55; Mismatches 27; Indels 2; Gaps 2;			
Ds	1 MFWMAHLLLSQLAVAYCWAFSCQRTSSPGSLPDGLLAGLSHGDCLOVRHRLV 58			
Qy	1 MFWMAHLLLSQLAVAYCWAFSCQRTSSPGSLPDGLLAGLSHGDCLOVRHRLV 60			
Ds	59 TSCDRSPSENGRGHVFQANRFVEEINSSALLPNTTGYELYDVCSSEANNTATRYL 118			
Qy	61 TSCDRSPSENGRGHVFQANRFVEEINSSALLPNTTGYELYDVCSSEANNTATRYL 120			
Ds	119 ALOGRPIEFQKDRNRSYVAFFIGPDNDHATVTAALGLPLMPVSYEASSVLSAK 178			
Qy	121 AQOCTGHEMDRDRNRSYVAFFIGPDNDHATVTAALGLPLMPVSYEASSVLSAK 180			
Ds	179 RKPSELRIVPSDRHOEVNVAOLLQSGFWWISLIGYGYGLGYOALEELAVPRGICV 238			
Qy	181 RKPSELRIVPSDRHOEVNVAOLLQSGFWWISLIGYGYGLGYOALEELAVPRGICV 240			



DB	239	AFDIDVPSARQGDGRMSQMOHQAQATVYVVSNSNHLARVFRSVYLANLNGKXWA	298
Oy	241	AFKDDVPVLSAQGDPRMRMRRLARAKTTVYVVSFNSHLLGVFRSVYLANLNGKXWA	300
Db	239	SEDMAISTYITSVTGIQIGTVLGVAVGQROVPGLKEFEESYVAVYAAAPSACEGSMCS	358
Oy	301	SEDMAISTYITVNPQIGIGTVLGVAVIQOOROVPGKKEFEESYVAVYAAAPSACEGSMCS	360
Db	359	TNOLORECHTETTRMPLGAFSPSAARVYEAAYAAVAGHLOLGCSELCSGPPYPM	418
Oy	361	TNOLORECHTETTRMPLGAFSPSAARVYEAAYAAVAGHLOLGCSELCSGPPYPM	420
Db	419	QLLOQIYKVNFLHENTAAFDNDGDTLGYUUIIAMDMNGPEMTEIIGSASLSPVHLIN	478
Oy	421	QLLOQIYKVNFLHKKTYAFDKGDPLGYDIIAMDNGPEMTEIIGSASLSPVHLIN	480
Db	479	KTGIOMHGKNNVOPVSVCTDCLAGHHNVVYVSGHSCFECVPCAGTFLANSEHLICOPC	538
Oy	481	KTGIOMHGKNNVOPVSVCTROCLBEHNLVYVSGHSCFECVPCAGTFLANSEHLICOPC	540
Db	539	GTEENAPKESTTCFPRTYEFLAMHEPISLVYIAANTLILLLLSTAGLFAWHFTPYRS	598
Oy	541	GTEENAPKESTTCFPRTYEFLAMHEPISLVYIAANTLILLLLSTAGLFAWHFTPYRS	600
Db	599	AGGRICFLMLGSLVAGSCSFYSFEGEPVPACLLQPLFSGLFAIPLSCLTIRSFQYII	658
Oy	601	AGGRICFLMLGSLVAGSCSIFYSFEGEPVPACLLQPLFSGLFAIPLSCLTIRSFQYII	660
Db	659	FRFSTKYVTEFRYTMONNAGAGLEFVYVSSTVHLICLTMVMPFRPRPREYORPFLVILE	718
Oy	661	FRFSTKYVTEFRYTMONNAGAGLEFVYVSSTVHLICLTMVMPFRPRPREYORPFLVILE	720
Db	719	CTEVNSVGFLLAFTNHILLLISTEFCVSYLGRKELPENYEAACVTFSLLANFVSNIAEFTM	778
Oy	721	CTEVNSVGFLLAFTNHILLLISTEFCVSYLGRKELPENYEAACVTFSLLANFVSNIAEFTM	780
Db	779	ASTYGGSLPAPNVNVLATLTLGSGSGSYGLPKCVYIICLPELANTEHPOASIOXYTRCG	838
Oy	781	ASTYGGSLPAPNVNVLATLTLGSGSGSYGLPKCVYIICLPELANTEHPOASIOXYTRCG	840
Db	839	TT 840	
Oy	841	TT 842	
RESULT	2		
AC	0920R7	PRELIMINARY;	PRT: 843 AA.
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DE	01-MAY-1999 (TREMBLrel. 10, Last annotation update)		
DE	PURATIVE TASTE RECEPTOR TR2 (FRAGMENT).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-WISTAR;		
RX	MEDLINE; 99159821.		
RA	ZOON C.S.;		
RT	"Putative mammalian taste receptors: a class of taste-specific GPCRs		
RT	with distinct topographic selectivity."		
RL	Cell 96:541-551(1999)		
DR	EMBL; AF127390; AAD18070.1; -		
RM	Receptor.		
FT	NON_TER 843 843		
SO	SEQUENCE 843 AA; 95799 MW; 650A9EE CRC32;		

Query Match	31.8%;	Score 2026;	DB 11;	Length 843;
Best Local Similarity	39.1%;	Pred. No. 0.00e+00;		
Matches 322;	Conservative 182;	Mismatches 296;	Indels 24;	Gaps 21.

D	b	27	NSHFLADYLLGGFTLTHAVKSIHSLSYQVCKNEF-TMKVLGNMQAMFAEEI	85
O	y	30	SPGSELPEDFELLAGJFSJLHACCLOVRHRP-TL-VYSCORSDFSNHGHLCPMFTVEEI	87
D	b	86	NCGSSLPLPGVLLGXYEMDVACYLSNNHIGLGFLLAQDD-DLPLIKDKYSQYPRHVAVIGP	144
O	y	148	DNTDHAVTTLALBPLFMPLVSYBASSYILSGKRRFESFELTIPSDYOVEVYIRLLQSF	207
D	b	205	QMNATVYVSDPDYGRNSHLSLORLTCTSDICAFQGVDFIPSSQVMNSEBRODNI	264
O	y	208	GMWATSLVSGTGDIGQGLQVQALBE-LATPRICYAFKDYVPL-SQAQ--GD-PR-MQM	266
D	b	265	LDKLRTSARVYVVSF-PELSIFYEFHEVLKWNFTGVMWJASMSAIDPVLHNLTELRLHT	322
O	y	261	MLRLARTATVYVVSFNSHLAG-VFRRSVLANLTGKMWISJEDMAISTYITVNPQIGI	319
D	b	324	GTFGLVGTQKRSISGFQSRFRRRKPGVRYVNTNLKTTTC--NDDCACLNTYSFNNIL	383
O	y	320	GTVLGVATAQQQOVQGLKFEESYVQAVGAGARTCPDESGMGTNOLCBCHAFITWMNPEL	379
D	b	382	ILSGERVYYSVYSAVYAAHALHRLGNCNRYCRKOKYPMQOLREIHWYFTLLGNRLF	441
O	y	380	GAFSMAKYNYEAVYAAHABHLOLGLCTSGTCARGPYPMQLOQITKYVFLHKKTTVA	433
D	b	442	FDQOGDMFM-LDITTIQOWODISQNPPOSIASYSPTSKRL-TYINNVSMTYPTNNTVPVSMC	499
O	y	440	FDDKQD-PLGYDDIYIAMONGPEMTFEVIGASLSPLHLDINKTKIOWHGKNNOVPSVC	496
D	b	500	SKSCOPGOMKKSQVGHPCCEFCJLQMPITYNBRSADENCISCGSMWSYKNDITGQOR	555
O	y	499	TRDCLIEGHRILVMSHCCFECMCEACTFIN-TSELHTCOPCETEBNAPRGSSACSRT	557
D	b	560	PTFLEMHVPYIYVAILAALQEFSTALILFT-WRHQTPVWRSAGBPMCFMLDPVLLA	618
O	y	558	VEFLGMHEPISLVLLAANTLTLTLTLIGAGLFAMR-LHTPVRSAGRGLCFMLGSLVAG	616
D	b	619	FGMRYVYVYPPYVSCFQKRAFVYVCSJLCSCTIVSFOYCVCFKARLRPSKSYWMMR	678
O	y	617	SCSLVSFEFGKTPACCLLRQPLSFLGAFILFISCTLRINSFOVLIIFFKSTKPYTHYHWAQ	676
D	b	679	YHGYPVEAFATIAIKVALVYONGMATATNPJGRTDDPDNPIMILSCHPNYENGLLFTMSM	738
O	y	677	NHGACIFIVYSYTHLEFCLTLWLMWMPRRP-REYQRPFLVILDECEYVNSVGLVAFAH	733
D	b	739	DLLSLVLSGFSAYMKELPLTYNNAKFTTSLMTFSSTSSILCTFMSVHGVLTIVMDLL	796
O	y	736	NILLISITFVCSYGLKEPLPENYNAKCWTFSLLLHFVSMIAFFMSSISYQGSYLPAVVL	795
D	b	799	VTVLNFALIGL-GYFGPKCYMILTYPPENYSAVYNSMIGQITMR	841
O	y	796	AG-LATISGGSYFLPKCYVILCPRLENNNEHHQASIQDITR	838

RESULT	3	PRELIMINARY;	PRT;	868	AA.
ID	073636				
AC	073636;				
DT	01-AUG-1998	(TREMblrel. 07, Created)			
DT	01-AUG-1998	(TREMblrel. 07, Last sequence update)			
DT	01-NOV-1999	(TREMblrel. 12, Last annotation update)			
DE	PHEROMONE RECEPTOR.				
GN	CAD2.1.				
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Actinopterygii;				
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphs;				
OC	Tetraodontiformes; Tetraodontoidae; Tetraodontidae; Fugu.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 98226788.				
RA	NATO T., SATTO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,				







DB	Query Match	Best Local Similarity	Matches	Score	Pred	Mismatches	Indels	Gaps
Db	668	21.3%	252	1358	30.7%	226	45	35
Db	671							
Db	748							
Db	731							
Db	808							
Db	791							
Db	329							
Db	396							
Db	378							
Db	456							

QY	429	VNFLLH-KITYAFEDKQDPLGIYDITIMDNNGPEWT-FEYIGASLSYPVH---LDIKTK	483
Db	516	IFWNEFSNRPKPHSVCSSESCPPGTFRMSRRKQAPVCCFDLLCSEKGISNTDSMECTSCPE	575
OY	484	IQWGNKNQVAVSVCTRDCLEGGHRLVWGSHH-CCFECMPCEAGTFLNTELMHCQCGT	542
Db	576	DFWSSPQRDCHVCPKTEFLSTHEPLGICLTAASLIGIVISVVLGITIHRSPTPVAAAN	635
OY	543	EWMAPEGSSACFSTSTVEFLMEHPSPISLVLLAANLTLLELLIGTAGLEPAMRLHTPVASAG	602
Db	636	SELSFLLVSLKLCFLFSL-FLRPRPLMTCOLRHAFAIGISFVLCVSCILYKTVLAVF	694
OY	603	GRCLFLMIGSL-VAGSCSLSTFSGKTPVPACLLRQPLFSIGFALFLSCLTIRSQVLTIF	661
Db	695	RASKPGGGATLKMFAGAVOORGT-VLGLTSIQAAICFAMLLSSBPKPKNTQYHKDKIVFE	753
OY	662	KFSRKVPFPIFYHTW-AQNHGAGIFIVTASVYHFLCLTLMAMPFRPRFREQRPPLVILE	720
Db	754	CVGSGVGFVAVLSTYIGLALISFLAFLARNLPDNEAKLITFSKLFICAAVAVAFPA	813
OY	721	CTEVNSGVFLVAFEAHNLTLSTFVCSYGLKEPLPENYENAKCYFFSLTLHFVSIVIAFTM	780
Db	814	YINSPGKADAVEAFALITSSFGLLVLPFKCYIILFRE	854
OY	781	SSITYGSLTPRANVLAGLTLISGSGSYFLPKCYIILCRE	821
RESULT	6	PRELIMINARY; PRT; 940 AA.	
ID	073635		
AC	073635		
DT	01-AUG-1998 (TREMblrel, 07, Created)		
DT	01-AUG-1998 (TREMblrel, 07, Last sequence update)		
DT	01-NOV-1999 (TREMblrel, 12, Last annotation update)		
DE	CALCIUM-SENSING RECEPTOR.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;		
OC	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RA	NAKANISHI S., BRENNER S.		
RT	"Putative pheromone receptors related to the Ca2+-sensing receptor in Fugu".		
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).		
EMBL	AB008657; BAA26122.1; .		
DR	PFAM; PF00003; 7tm_3; 1.		
DR	PFAM; PF01094; ANF_receptor; 1.		
DR	PRINTS; PR00248; GPCRMR.		
DR	PRINTS; PR00592; CASENSINR.		
SO	SEQUENCE 940 AA; 105814 MW; 034CB09E CRC32;		
Query Match	21.0%; Score 1334; E9 13; Length 940;		
Best Local Similarity	30.7%; Pred. No. 1,10e-250;		
Matches	255; Conservative 238; Mismatches 283; Indels 55; Gaps 35;		
Db	29	MTGIIILGGLEPIHFQ-ISSKDEVLARLPSTKCVRFNFGFRMLQAMVAIEINSSS	87
OY	3	LPGLFLAGLFSLHADCIOVRHRLPVTSCDSDS--FNGHGTHLFQAMRTVEINNSTA	92
Db	88	LLPNTLTGRIFFDCNTVSKALEATLSFVAQNKIDSINLDEFNCQDHPATIAVGAAG	147
OY	93	LLPNTLTGLEYLDVCSSESNVY-ATLAVPQOQGHGLEMR--DLRHSSKVALIOLPDN	149
Db	148	SAVSTAVANLISFLYIPQISYASSSRLLSNKNQYKSFMTIIPDDEHQATAMADYIEYQW	207
OY	150	TDHAVTTAALLSPILMPLVSYEASSVILSGKRPSPFLRTIPSDKYQVEIVIRLLQSGFW	209
Db	208	NWVIAVASDDDYGRPGLEKEFEKEEEDICHLNELISQYFEDCEIR-A-LVDIRIENSTA	265
OY	210	WVILSYSGYGGGLGVOALEEATLPFGICVAFEDVPLLSAOGADPPORMRLARAT	269



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Db 266 KIYVAFAGPIDEPIKIMYARNRITDRLWLSEAMASSSLAKREYLDVAGTIGFPLKA 3205
Oy 270 TVWVFSNRHLAGVFFRSVLANLTGKWIASEMAIITYTN--VPG10G-IGVL- 3233
Db 336 GNIPGFFREELQOVOPKRSNSHNEFVEEMEFNFCLYDESPHLOESENSGSFRLCTSEE 3855
Oy 324 G-VA-IQQ-RQV-P-G-----LKEF-EESYQAVMGAPRTC-PESMSWGTGNDLCECH 3699
Db 386 DITSVEYPLDHTHLRISYNYVAVVYSIAALADJILSCTPEGHLFANNSCADIKKEAWQ 4455
Oy 370 AFTTNMPELAFSMAKYNYEYVAAAHGLHOLLCSIGS-----TCA-RGPVPMQ 4211
Db 446 VLKOLRHLNYSNGEKXHPENDAMENANYIIMHSSAEDGSVAFREYVYHHNARCA 5055
Oy 422 LLOQYYKYNFLHK-KIYAFDQKGPRLCYDIIAMDMWGP-R-W-TFVYISASL-SF-V 4755
Db 506 KLLIDNTMMNNAVSSSEVPFNSCDEDEPGRKGIIDSPCCFECEGSDGEYSDHKA 5655
Oy 476 HLDIKRTIQHGNKNQYVPVSCVCRDCLGHLRLYMS-HHCCECPMCAGIFLNTSEL 5344
Db 566 SICTKPNNSSSGNHTFCFLKEIEFLAWSPEPISALACAVLGULLTAFFVGVYFRN 6255
Oy 535 HTCCPGCTEEMAPRESSACFSRTVEEFGMHBPISLVLANLTLLILLITAGLFAWRLH 5944
Db 626 TPVYASNRRELSYVLLSLICCFSSSL-PIGEQDMTCRLROPABISVLCISCLVK 6644
Oy 595 TPVVASAGRCFLFMLGSLVAG-SCSYISFPGKTPVACLLRPLLESLGIAIFLSCTIR 6533
Db 685 TNRVLAVE-AKIPTSIHRKMKGLNLOFLVFCITPVQVAMCVWLYNMPSSRSHD- 7411
Oy 654 SFQVLVIEKSTKPT-FYHTMAONHNGGIVYSSYVHLFCLCLTWLMMTPRTREYQR 7122
Db 742 IDEIIFITONGSVYALGFLIGYTC-LIAAICFF-AFKSKRLPENFTEAKFTFCCLIF 7999
Oy 713 FPHVLIECIE-VNSVGFVLAFAHNILDLISTFVCSYLGEKLEPENYNAKCVTFSLH 7700
Db 800 FIVMSFIPIAFSTY-GKFSVAVEALALASYSGLMACIFFNKYIILLFAP 849
Oy 771 FVSWIAFPTMS-SLYQSGYLPRAVNVLAGLALSGSGFGYFLPKCYVYILCP 820

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Query Match	20.1%	Score 1279;	DB 13;	Length 880;
Best Local Similarity	29.18;	Pred. No. 1,178-238;		
Matches 243;	Conservative 230;	Mismatches 318;	Indels 45;	Gaps 35

Db	53	GDIIILGGLFSLHDWVVE-PNLPETSTPPTCTCTCFSTRTTSMQMTQVFAVEAVERINMEIL	11
Oy	37	GDFELIAGLFLSHADLCLOVRHRLPRLVITSCDRSD-S-FNGHGLHFDAMRTYVEEINNSTALL	94
Db	112	PNILGVYIYSCSTPHOSLTKAAIDLMGSEKSDQFEGEKLQHEGDCGVNPAVIGDGSTOS	171
Oy	95	PNILGVYLYLYVSESSSNVY-ATLRVPAQOQTGHEWQRDRNNHSSRYVALIGDPTNDHA	155
Db	172	LVVARFLGVHFVPOVSYESSCACISDKTORPAPLRKTPSDLFVOGA-VOLVKYFGXTWG	233
Oy	154	VTTAALISPLMPLVSYEASSVILISGRKRFPSFPRITIPSDKYQVEVIVRLLOSFGKWIS	215
Db	232	VIAGDDAGRGCAIFAEVNRRLACIALYLMIP-KTOS-QAALSSIINSRSGAVVL	285
Oy	214	LVGSGTGDGQGLQVLALELATPRICVAFKQVVLISQAQGPORQRMRLRARRRTTVV	273
Db	290	VEAVEODVARLFDEAVRKLGTIGIOMLASEAMSTAAISTPRYHIILOGSMGFARADI	349
Oy	274	VFSNRHLAGVFRFSVLANLTKGWISSEDAISTYITNPQIOGT-GYLVGAIQORQY	333
Db	350	PGLODFELRLHPSSAEADDDFLLIPMEEVFOCSLDPHGHSSEAKRPGSGTEELRSXNII	405
Oy	333	PGLKEF-E-ESYVOAVMGAPRTCP-EGSW-CGTN-Q-LC--RECHAFTT-WMPDEL-	379
Db	410	SDVOSLRISTYVYKAVYALALAIKAMSCSEKSGSPFSDQACPDLDNTHPMOLHHYICVN	465
Oy	380	GAFS-MSAAYVYEVYAAVAAGHLQQLDGC-F-SG----TCAR-GPAYPMLODOIYVN	439
Db	470	YTNRFDEIKCEDNGDDPAAAMDLDLNMOLTPCGDGDDFTYGVGDFDIAGTKRNHIEEKI	522
Oy	431	FLHL-KKVAVDDBKGDPLGYIDIITAMDN-GPEPTFEVIGS-ASLSY---HLDINKTKI	485
Db	530	VWNGNTNOPLSVSCSICPGPTRKARIRNPYPICCHDCVCVCTAGEISNOTDAIECARLPE	585
Oy	485	QWGHGNNQVPVSVCTBDLCSEHRLVWGSHH-CCECKPCGAGFLNLSLHTQCPGTE	545
Db	550	FKSNADRPACYPKOVETFSFGDTIGIALLVY-SIGSFLICAAVALFFYHRTSPYRAN	648
Oy	544	EMAEGRSACFSRVEYFGWEPRLSLVLANLTLLLLLTISTAGL-PAMRLHPFVVSAG	602
Db	649	SDLSFLILFSTLCLFCLSL-FFISPPSOWSCMLHRTAFGIFVFCISCIIGKTVVMAF	707
Oy	603	GRCLTMIGSLVAOS-CSUNFSEKRPYPACLLKOPLFSLGFAFLSCLTITRSFOIIF	666
Db	708	R-ATLPGSDVKKMGEGPKOKAIIIF-SILVOVVICYVWLAV-APPTRPVYFRESAIIIL	764
Oy	662	KFSIKVPPFFHYTM-QONNGACITIVYESTVHFLCLTKWLMAMPTRPREY-QRPHVLIL	719
Db	765	LCDBGSTAFSLVGLYGVLCACQCFLLAFLARKLPDNFNEARLTAISMILFCAYVAVFP	824
Oy	720	ECTEENSNGVFAVAHNLILSIFPVCYSYLKECPENYENAKCYFSLLLHFVSMIAFT	779
Db	825	AYISSPKGYSLTILFALMSYGLLDCIFAPKCIYIIMNSEKTRKHMSKSRF	880
Oy	780	MSSTIYGQYLPNAVVLAVLATLSGGFSGYFLPKCYVILCPRELNNTHFQASIDQY	835
RESULT 8 PRELIMINARY; PRT; 844 AA.			
ID	093552		
AC	093552		
DT	01-NOV-1998 (TREMBlrel. 08, Created)		
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)		
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)		
DE	PUTATIVE ODORANT RECEPTOR.		
GN	GPR1.		
OS	Carassius auratus (Goldfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
OC	Neuatergii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinoidae; Cyprinidae; Cyprininae; Carassius.		
RC	[1]		
RP	SEQUENCE FROM N.A.		
TC	TISSUE-OLFACTOR1 EPITHELIUM;		
XC	MEDLINE; 98426265.		



RA CAO Y., OH B.C., STRYER L.;  
RT "Cloning and localization of two multigene receptor families in  
RT goldfish olfactory epithelium";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).  
DR EMBL: AF083080; AAC64075.1; -.  
DR PFAM: PF00003; 7tm\_3; 1.  
DR PFAM: PF01094; ANF\_receptor; 1.  
DR PRINTS: PR00248; GPCRMR.  
SQ SEQUENCE 844 AA: 94599 MW: 7A84F7AC CRC32:

Query Match 19.8% Score 1258; DB 13; Length 844;  
Best Local Similarity 28.9%; Pred. No. 4,52e-234;  
Matches 235; Conservative 216; Mismatches 334; Indels 27; Gaps 24;

DB 32 PLFSKDDVYIGGIFAIHREKTELPSEFFTOKPOPLSCSYNLDRFLAQTMIALQEIINK 91  
QY 31 PGSLPEDFLAGLFSLHA-DCLQVRHRLPLVTSODRSDRSGHGHYLFQAMRFTVEINN 89  
DB 92 NEILLPNISIGYIIYDTGSRSLTMTATMGLMNSQDFGPNIT-CN--GHSP-LHAITGES 147  
QY 90 STALLPNITLGYELDYCES-SNVYATLRVPAQOCTGHLEMDRLNHSKVALALIGPD 148  
DB 148 ETATVILSTGTGPKIPVSHSSCECLSNRKNYPSEFFTISDYNQSLASIVYHFG 207  
QY 149 NTHAVTTAALSPFLPLVYEASVILSGKRFPSEFLITPSDKYQEVYVRLQISFG 208  
DB 208 WSWVGAVNSDNDYGNMGAIFLKVDEGICVEY-SYKRYETET-E-KLKVVDITIKGT 264  
QY 209 WWSVILVGSYGVQGLGVQALELAPRGICVAFKDVYPLSAGDPRMRMLRLARAR 268  
DB 265 AKIVAFISVEWGLLEQSIONITGOMIGVEPWITANTYTP-KSLHMEGSLGFAM 323  
QY 269 TTVVVFVSNHLAGVFRSVLANLTGKWIASEDW-AISTYITNVPGIIGIVLGVAI 327  
DB 324 KVINBGEFAAKKPFMDTAPCSK--EGNY-SKVALSCRYEELLALNYEDYTEHR 380  
QY 328 QORQVGLKFE-ESYQAVMGAPRICEBSWCCTNOL-CRECHAFITWMPGLGAFSMS 385  
DB 381 YSSNYKAVYAVASHLSLCKIQEGCEKGLPIQPOVVELLKKINFATKTDGRWFDS 440  
QY 386 AAVNYEAVYAVAHGHLQGLGCTS-GTCARG-PYPMQLQIQIKVFLHK-KTAVFDD 442  
DB 441 TGGVVALYEVNNQOQSDGYOKRSVGYASLEPTYONLHNVENITWAGHLEKPRSAC 500  
QY 443 KGPPLGYDDIAMDWNGPE-WTEFEVIG--SASISPVH-LDINKTIQMRKKNQVPVSYC 498  
DB 501 SESCPGTRAAQGRPCCYDICIPOAGEISNETRINCKPCGWEMWMAEKKCVLKA 560  
QY 499 TRDCLBCHRLV-MGSHCCFECAPCEAGTFLNTSELHTQCPGTEEMAEBSGASCSRT 557  
DB 561 VEFLESTELMGVVLVFEFLGVGLTLVALIFYNKKDTPVWKAANSSELFLSLTLCF 620  
QY 558 VERLGMHEPISVLAMANTLLLLITAGLFAMRLHTPVYRASGRLCLMLGSLVAGS 617  
DB 621 LGLL-IFIGPTWESCLMTAFGITFVLCISVGLKTIYVLAFAK-ATLPGNNIMKMG 678  
QY 618 -CSLYSFFGKPTVACILRPLPSLGFALFLSCLTIRSFVLIIKFKSTVPTFYHTMAQ 676  
DB 679 PAQORSLAFLTLIOVILCYMLTISPPRYKMKYKKEIIECSGISGTFMAYLYI 728  
QY 677 NHGAGFIVYISVHLFLCTLWLAAMTPTPTREOPRPHVILCEIVNSVGLVAFAHN 726  
DB 739 SLTAFICFLIAPLAPLDPKFNKAITFPMILJFCAMVITFPAVYSSPKFTVAEIFA 798  
QY 737 ILLSISFVCSYIGKELPENYNEAKVTFSLLHLFVSMIAFFMSSYIQSSYLPVAVVLA 796  
DB 799 ILSSSGFLGFIAPKCYITLLKPBONTKQHL 830  
QY 797 GLATLSGGSFGYFLPKCYIILCRPELNTEHF 828

RESULT 9 PRELIMINARY; PRT; 856 AA.

AC 073638;  
DT 01-AUG-1998 (TREMblrel. 07, Created)  
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE PHEROMONE RECEPTOR.  
GN CAL2.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 98226788.  
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,  
RA NAKANISHI S., BRENNER S.;  
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in  
RT Fugu";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).  
DR EMBL: AB008860; BAA26125.1; -.  
DR PFAM: PF00003; 7tm\_3; 1.  
DR PFAM: PF01094; ANF\_receptor; 1.  
DR PRINTS: PR00248; GPCRMR.  
KW Pheromone.  
SQ SEQUENCE 856 AA: 94590 MW: 7B8395C7 CRC32:

Query Match 19.7% Score 1251; DB 13; Length 856;  
Best Local Similarity 29.7%; Pred. No. 1.52e-232;  
Matches 246; Conservative 234; Mismatches 302; Indels 17; Gaps 38;

DB 35 PLISQEDITIGGAFILHQC-MKPSLSEETPEDITCRINLRERFQOMIFALEIN 93  
QY 31 PGSLPEDFLAGLFSLHADCLQVRHRLPLV-TSCRS-DSFGHGHYLFQAMRFTVEINN 88  
DB 94 NSSSLPNISIGKYVDTGTLPLSTRAV-MALMNGKTRTP-EGGSSRTS-VHAIGAS 150  
QY 89 NSTALLPNITLGYELDYCESSESNYATLRVPAQOCTGHLEMDRLNHSKVALALIGPD 148  
DB 151 ESSSTIQLQISGIFQIPYISHFATCACLNSRKEYPSPFRITPSDFYQSRALAKYKMG 210  
QY 149 NTHAVTTAALSPFLPLVYEASVILSGKRFPSEFLITPSDKYQEVYVRLQISFG 208  
DB 211 WTVVGAVKSNDYGNGLTFTMAEQEGVCEYSBGS-WTDPS-QLARVYTYKSS 268  
QY 209 TTVVVFVSNHLAGVFRSVLANLTGKWIASEDMAISTYITNVPGIIGIGT-VLGVAI 327  
DB 269 ARVLAFLAQSSEKSALEAVYKONLTGLQWGSSESTTGHIA-LKYSAILTGLSIFPI 327  
QY 269 TTVVVFVSNHLAGVFRSVLANLTGKWIASEDMAISTYITNVPGIIGIGT-VLGVAI 327  
DB 328 RKTITGLOEFLQVNPSONPNLLKEFWETTFGCSFQSDVHGATQCSGVERKLDIQNP 387  
QY 328 QORQVGLKFE-ESY-QAVMGAP-RICEPSW-CG--TN-QLCRECHAFITW-NMPE- 378  
DB 388 FTVDSELRISNNYKAVYAVAHAMSMKCGSGEAVNSCTTKKDFELKQYVEHLSQYN 447  
QY 379 LGAES-MSAAYEVYAVAHGHLQGLCT-SG-----TCARGPYPW-QLLQIYKYN 430  
DB 448 FTLOSGERVYFDYGPDAFYEVLVNNQSRPEGTVVVGANDASOPNOCFTMMNINIT 507  
QY 431 FLHKK-KTAVFDDKGPPLGYITDIAMDWNGPEPT-FEVIGSLSL-PV-HDINKTKIQ 485  
DB 508 WAARLQKRLSYCSOSICGFRQAVIKGRPICFTCVACAGEISNSSASACLOPLEF 567  
QY 486 WHGKNQVAVSVCTRCBLG-HHRLVMSHCCFECMPEAGTFLNTSLHRCQCGTBE 544  
DB 568 WSNEDHSQCPVYIEFLSEETMG-ALLAVALFGAALSLVFCVF-PFRHTPLVAKSN 625  
QY 545 WAEQSSAFCSTRTVERLGMHEPISVLAMANTLLLLITAGL-DFAWL-HTPVYRSAG 602  
DB 626 SELSFLTSLTLCFCSL-TFGRSPRMSCVLRHTAFGITFALCQSCYLAAT--VAVLF 682  
QY 603 GRCLTLMGSLVAGS-CSLYSFFGKPTVACILRPLPSLGFALFLSCLTIRSFQLVITF 661



Db	Accession	Score	Length	Matches	Indels	Gaps
Db	683 AFKAPRCPNTEYCS-VPLQTSVACI--TLOVILCVMLTAPRPHKNTAAKRRII 729	19.4%	1236	DB 13	875	
Qy	662 KFTSKVP--T-FYITMAONHGAGIFVYSSVHLFELCLITLMAWTPRPTDYQRFPLVI 718	30.6%	229	115	55	41
Db	740 LECNLGSPWFWVWVLYIGLVLAVICFLIAPLARKLPDNFNKAFITFRSMJFCAWVTFI 729	22%	315	15	5	
Qy	719 LECLEVNVSGLVLAFAHMLLSTIFSTFOSYGRKLPENYNNAKCVTFSLLHFPWSIAFF 778	22%	315	15	5	
Db	800 PAYVSSPEKFTVAVEIFAILASSGCLFCIFAPKCYILLIKPEKNITKH 848	22%	315	15	5	
Qy	779 TMSIYOGSYLPAPVNLVAGLATLSGSGSGVFLPCYVILCPRELNTTEH 827	22%	315	15	5	
RESULT	10	PRELIMINARY	PRT	875	AA	
ID	073640					
AC	073640					
DT	01-AUG-1998 (TREMBlrel. 07, Created)					
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)					
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)					
DE	PHEROMONE RECEPTOR.					
GN	CA15.1.					
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;					
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphs;					
OC	Tetraodontiformes; Tetraodonotoidei; Tetraodontidae; Fugu.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 98226788.					
RA	NATO T., SATO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,					
RA	NAKANISHI S., BRENNER S.;					
RT	'Putative pheromone receptors related to the Ca2+-sensing receptor in					
RT	Fugu.';					
RL	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).					
DR	EMBL; AB008862; BAA26127.1; .					
DR	PFAM; PF00003; Tm_3; 1.					
DR	PFAM; PF01094; ANF_receptor; 1.					
DR	PRINTS; PR00248; GPCRMR.					
KW	Pheromone.					
SO	SEQUENCE					
Query Match	19.4%	Score 1236	DB 13	Length 875		
Best Local Similarity	30.6%	Pred. No. 2.86e-229				
Matches	221	Conservative 222	Mismatches 315	Indels 55	Gaps 41	
Db	30 ALTCQMSPTQGLFODGHVWVGGLENLHPTPDINNFTQOSHXYACTGLENTPLQYI 89					
Qy	21 AFSC-QR-TSSPQFSLRPGDELLAGLEFLSHADQCVNHR-PLVTSQDRDSFNGHYLF 77					
Db	90 YAMFAVEINHSALLPGVKLGTHIDSCALHFWTTQALALVAGDSACELATPADYS 149					
Qy	78 QAMFTVEEINSTALLPNITLGELEYDVS-ESSNYATLR-VPAQGGCHLEMQDLR 135					
Db	150 AETSEEGASVPLIIGASSNAKIIILGTLSPISTISYATSCPCLSRHRYPTFFRPMAS 209					
Qy	136 NHSSKVVALIS-PONTHAVITAA-LSPFLMPL-VSTEASSVLLSKRRPSPFLRTIPS 192					
Db	210 DIVGACALQALVREFNMTIGAVVANNNDGHAIVKAVVQEOGTQKGYCALVETLORETIV 269					
Qy	193 DKYGEVIVIRLQSGFWWISLVSQYDYGDLQVQALBELATPRGICLVARKDVPLSAQA 252					
Db	270 ADAYRAARTI-QASTAR-VILVFS-WYTDGHLFROLOKINVTDRQFLASEANSTSEVL 325					
Qy	253 GDP-RMORFMRRLRAKRTIVVYFNSHLLA-GVFFRSVVLANTLGKWIASEDMAISTYI 310					
Db	326 LKDDTSTVASGVGVVASOHIGDFRPLRGLMPLSRPDKFLQDFWEDEFQSPSPS 385					
Qy	311 TNPVGIGIGI-VLGVAIQORQVPG---LKEF-----ESTYQAVMGAPRTC-PEGSW 358					
Db	386 SETSGDNLASLPPSCGASLEGVQHPETDISHLEVTYVNVLYAAANALASLSCPTIN 445					
Qy	359 CGTN-QI--C-RECHARTTNW-MPE-LGARS-MEAAVNVYEAVYVAHGLHQLLGC--- 407					
Db	446 SPGSTSICHTSKGKTTLELOHLSKVNFTTPROGKHLIFRGADIP-AMVDLINMO-SCIDG 503					

[illegible]











OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

QY 819 RPE 821

Search completed: Fri Mar 17 13:22:28 2000  
 Job time : 250 secs.

RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL6/J;  
 RX MEDLINE; 97433087.  
 RA MATSUMAMI H., BUCK L.B.;  
 RT "A multigene family encoding a diverse array of putative pheromone  
 receptors in mammals."  
 RL Cell 90:775-784(1997).  
 DR EMBL; AF014111: AAC53401.1; -.  
 DR MGD; MGI:1316688; VZr1.  
 DR PFAM; PF00003; 7tm\_3; 1.  
 DR PFAM; PF01094; ANF\_receptor; 1.  
 SQ SEQUENCE 850 AA; 97415 MW; 3CA08744 CRC32;

Query Match 13.1%; Score 832; DB 11; Length 850;  
 Best Local Similarity 26.8%; Pred. No. 6,33e-142;  
 Matches 210; Conservative 195; Mismatches 323; Indels 55; Gaps 49;

DB 75 YEFLVAFPAIDELRNRPYLPLNTLMFS-F-IGNCODLIRVMDQAVTOINGHNFVNY 132  
 QY 74 YHLEQAMRFTEELINNSTALLPNTITGELYDVCSESNVATLRVPAQOGTHLEMQRD 133  
 DB 133 PCYLDSCAIGLGPSPMT-SKLIA-MHSS--MPLVFFGPPNPMLRDRLPHVQVAPK 188  
 QY 134 LRN-HSSKVVALLIPDMDHAYTTAALLSPMLPLVSEASSVILSGKRKPPSFLRTIPS 192  
 DB 189 DTHSHGMVSLMFRMTWIGLVISDDOGIQLSDLRRESQRHGICLAFNMIPENMOI 248  
 QY 193 DKYQVEYIVRLQSGFWWISLVGSGYDGLQVQALELTPRGICAFKDVVPLSAQA 252  
 DB 249 YMTRAITYDKHIMTSKAVVIYIGENSTLEASFRMEELGA-R-RIVITTSQMDVITNK 306  
 QY 253 GDRPMQRMMLRLARARTVYVVFNSRH--LAGVFFRSVLANLGKWIASEDMAISTYI 310  
 DB 307 KDFT-LNLFHGIITFE-HHREIPKLKEMQTMNTAKYPVDISHTILEWNTFNCISKNS 364  
 QY 311 TNVPGIOGIGVLGVAIQOR-QVPLKEFEESYQA--VMGAPRTCPG-GSM-CGTNOLC 365  
 DB 365 IRMHITFNNTLEWTSIHNTYV-AMSDEGYLNNAVAVANTHEHYIFQVESOKKAKPK 423  
 QY 366 RECH-AFT-T--W-NMPELCAFMSA-AYNVYEAVAVAHGLHQ-LLG-CTSGTCARGP 416  
 DB 424 RYFTACQOVSSIMKTRVFTNVEGLVNMKHKRENOCTEYDIFI-IMNFPQIGLKYKIGSY 482  
 QY 417 VY-PW-QLLQOIYKVN-FLHK-KTVAFDKGDPLGYDDIAMDNGPE-WTFEV-IGS- 469  
 DB 483 LPCFPOROKLHISDD-LEMAKGTSPOVPSVSVACTAGFRKIYQKETADCCFDCVQCP 541  
 QY 470 -ASISPVH-LDINKTKIQW-HG-KNQVPVSVCTRDCLGHHRLV-MGSHHCCECPMCE 524  
 DB 542 ENELSNETDMQCYRCDDKANTIEQTHCSRAVSFLAYEDSLGMAIGMALSFSAITIL 601  
 QY 525 AGFTPLNTSELTCOPCGTEWAPGSSACFSRTVEFLGWHEPISLVL-LAANTLLDLL 582  
 DB 602 ILVT-EVKYK-DPTVANNRILSYILLISLVEFCISIL-FIGPPQVTCIFQOTTEGV 658  
 QY 583 IGTAGLFLAMRHHTPVASAGRLCFIMGLSVAGS-CSLYSFFGRKPYVACLRLQPLPSL 641  
 DB 659 LFTVSVSTVLAKITVYMAFKLTTPGRRM-RG-MMMTGAPRLVIPICTLIQVLGIMLV 716  
 QY 642 GFAIFLSCLFTRSPQVLIIFKSTKVPFTFYHTMAQNHGAGIFVL-VSSVHLFLCLTFLA 700  
 DB 717 TSPFIDRDIOSEHGKIVIL-CNKGSVIAPHVULGIGSLAGSFTLAFIARNPDTFNE 775  
 QY 701 MTRPRPTREYQR-PPHLVILECTEVSNGFLVAFAHNILLISITFVCSYLKELPENYNE 759  
 DB 776 AKFLTFSLV-FCSWITFLPVYHSTGRVWVVEVSIASSAGLLMCIFVPCYVILI 834  
 QY 760 AKCYTFSLHLHFS-WIAFTMSIYQGSYLPANVNLGIALTISGFSGYFLPKCYILC 818  
 DB 835 RPD 837







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FT CHAIN 20 1085 EXTRACELLULAR CALCIUM-SENSING RECEPTOR.
FT DOMAIN 20 613 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 614 636 I (POTENTIAL).
FT DOMAIN 637 650 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 651 671 II (POTENTIAL).
FT DOMAIN 672 682 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 683 701 III (POTENTIAL).
FT DOMAIN 702 725 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 726 746 IV (POTENTIAL).
FT DOMAIN 747 770 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 771 793 V (POTENTIAL).
FT DOMAIN 794 806 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 807 829 VI (POTENTIAL).
FT DOMAIN 830 837 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 838 863 VII (POTENTIAL).
FT DOMAIN 864 1085 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 91 91 POTENTIAL.
FT CARBOHYD 131 131 POTENTIAL.
FT CARBOHYD 262 262 POTENTIAL.
FT CARBOHYD 288 288 POTENTIAL.
FT CARBOHYD 401 401 POTENTIAL.
FT CARBOHYD 447 447 POTENTIAL.
FT CARBOHYD 469 469 POTENTIAL.
FT CARBOHYD 489 489 POTENTIAL.
FT CARBOHYD 542 542 POTENTIAL.
FT CARBOHYD 595 595 POTENTIAL.
SQ SEQUENCE 1085 AA; 121170 MM; 501F66CD CRC32;

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Query Match 20.7%; Score 1316; DB 1; Length 1085;

Best Local Similarity 31.9%; Pred. No. 9,34e-272; Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;

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DB 31 GDIILGGLPIHNG-VAVKQDQKSRPEVECIYRNFGRFWMQAMIFAEINSSPALL 89
QY 37 GDFLAGLGFSLHADCLQVRRHPLVTSQDRSDS--FNGHGHLQFQARFTEELINNSTALL 94
DB 90 PNNLTGRIPTDONTYNSKALEATLSYAONKIDSLNDEFCNSENIPSTIYAVGATGSG 149
QY 95 PNTTIGLEYLYDVCSSESNY-ATLRVPAOOGTGHLEMQR--DLRNHSSKVALIGDPDNT 151
DB 150 ISTAVANLGLFIYPOVSAYSSRLSNKQNFSPRTIPNDEHOATAMADIEYFRMWN 209
QY 152 HATTTALLSPFLMPLVSYSAVVIIISGKRKFSLRTIPSDYQVEYVIRLQSGWVW 211
DB 210 VGTIADDDYGRGRIEIKFREAEERDICIPELSIOYDE-B-KIQOVVEYIQNSTAKV 267
QY 212 ISLVGXYDYGQGVQALELATPRGICVAFKQVPLSAQAGPRQRMRLRLARATTY 271
DB 268 IYVFSSGPDLEPI-KEIYRNRITGRWLAASEMASSSLIAMEYFRHVGGTIGFGLKAG 326
QY 272 VYVFSN-RHLAGVFRRSVYLANLTGKWLIASEDMA---IS-T-YITNPG-IO-GI-G 320
DB 327 QIIGFREFLOKVPKRSVNHNGFAKEFEWERTFNCHLOEGAKGPRVPDTFLGHHEGGARLS 386
QY 321 TYIGV-A-IO--O-RO-VP-GL-KEF-EESY---VO-AVWGA-P-----RTCEEG-SW-C 359
DB 387 NSPTARPLCTGENISVETPYMDYTHLRISYNYLAVYSIAHLODIYTCIPGRGLFT 446
QY 360 -G-TN-O-LCRCHAFITWMPGLGAFMSGAAYVEAYVAHGLHQLLGC-----T 408
DB 447 NSGCAIDIKYEAOMVYLKHLNFTSMGEQVTFDECGDLAGNYSTIIMHLSPEDSIYF 506
QY 409 SGICA-RGPYPMQLOQIYKVNFLHK-KTVAFDKGDPLGYDIIAMDMNGPE-WT-F 464
DB 507 KEYGYNYVAKKGRLEFINDERKILMSGFSEVPEFNSCRDCLAGTKRGITIEGPTCCFEC 566
QY 465 EYIG--SA-SLSVYHLDINKTKIOMHGKNQVSVCTRCLEGNHR-LWGSHHCCFEC 520
DB 567 VECPEDEYSDTDASACDKCPDDEFSNENHTSCIAKEIEFLSTWEPGLALTFAYLGI 626
QY 521 MPEAGFLNTSLHNCQPCGTEGMAPEGSSACFSRIVELGWHFPISTVLAAANTLLLL 580
DB 627 LTFVYLGVFIFKR-NTPYIKATNRELSYLLFLSLCCFSSSLF-FIGEPDQWTCRLQPA 684

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QY 581 LLIGTAGLPA-WRLHPVYRSAGRGICFLMGLSIYAG-SCSIYSEFGKPTVPACLLRPL 638
DB 685 FGISFPLCISCLIVKRNRLVVE--AKIPTSFHRKMWMLNQFLIVFICTMOIVICAI 742
QY 639 FSLGFIPLSCLTIRSFQVLITFKSTKVP-FYHTMAONHAGIFVIVSSVHLFLCT 697
DB 743 WNTAPSSYRNHLEDELFITCHEGSLMALGFLGYTC-LLAACPEFF-AFKSRKPL 800
QY 698 WLAMPPTREYQRPHLVILECTEVN--SVGLVAFAHNILLISTFVCSYLGKREPE 755
DB 801 NNEAFITFSMLIFITWISFIPAVASTY-KREYSAVEVILIASFGLACIFENKY 859
QY 756 NNEACVFSFSLHNVSIATFTM-SSIYQSGYLPVAVNLGLATLSGSGFYPLKCY 814
DB 860 IILFKPSRTIE 871
QY 815 VILCRPELNNT 826

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## RESULT 2

ID CASR HUMAN STANDARD; PRT: 1078 AA.

AC P41180: Q13912; Q16379; Q16108; Q16109; Q16110;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID

DE CELL CALCIUM-SENSING RECEPTOR).

GN CASR OR PCAR1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

RP [1]

RA SEQUENCE FROM N.A.

RL PEARCE S.H.S., THAKKER R.V.;

RL submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-PARATHYROID;

RX MEDLINE: 95279439.

RA GARETT J.E., CAUQUAN I.V., HAMMERLAND L.G., HUNG B.C., BROWN E.M.,

HEBERT S.C., NEMETH E.F., FULLER F.;

RT "Molecular cloning and functional expression of human parathyroid

calcium receptor cDNAs."

RL J. Biol. Chem. 270:12919-12925(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY.

RX MEDLINE: 95408281.

RA AIDA K., KOISHI S., TAMATA M., ONAYA T.;

RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from

human kidney."

RL Biochem. Biophys. Res. Commun. 214:524-529(1995).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96343808.

RA FREICHEL M., ZINK-LORENZ A., HOLLOSCHI A., HAFNER M., FLOCKERZI V.,

RAUPE F.;

RT "Expression of a calcium-sensing receptor in a human medullary

thyroid carcinoma cell line and its contribution to calcitonin

secretion."

RL Endocrinology 137:3842-3848(1996).

RN [5]

RP VARIANTS FHH GLU-185, LYS-297 AND TRP-795.

RX MEDLINE: 94094324.

RA POLAK M.R., BROWN E.M., CHOU Y.H., HERBERT S.C., MARX S.J.,

STEINMANN B., LEVI T., SEIDMAN C.E., SEIDMAN J.G.;

RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial

hypocalcemic hypercalcemia and neonatal severe

hyperparathyroidism."

RL Cell 75:1297-1303(1993).

RN [6]

RP VARIANT ADH ALA-127.











Query Match 20.1% Score 1282; DB 1; Length 1079;  
 Best Local Similarity 31.2%; Pred. No. 1,446-263;  
 Matches 269; Conservative 240; Mismatches 280; Indels 73; Gaps 50;

FT CARBOHYD 488 488 POTENTIAL.  
 FT CARBOHYD 541 541 POTENTIAL.  
 FT CARBOHYD 594 594 POTENTIAL.  
 SO SEQUENCE 1079 AA; 120867 MW; 341188B9 CRC32;

Db 30 GDILGLGFPPIHFG-VAAKDDDLKSRPESVECIKRNFGFRLQAMTAIEFINSPSL 88  
 37 GDFLLAGLESLHACLOVRRHRLVTSQRSDS--FNGGYHLFQMRPTEINNSTALL 94  
 Db 89 PNMTLGIPIPTCNVSKALPATISEVQNKIDSLNDEFCNCSHPHISTAVAGATSG 148  
 95 PNITLGLYLIVCSSESNVY-ATLRVPQOQGTGHEMR--DLRHSKVALALPDNTD 151  
 Db 149 VSTAVANLGLFYIPQVYASSSRLSNKQKSFRTIPNDEHOATAMADIIEYFRMW 208  
 152 HAVTTALLSPFLMPLVSEYASVYLSGKRKPFSLRTIPDKQOVEYIVRLQSGKWM 211  
 Db 209 VGTIAADDDYRPGIEKREAEERDIDFSELISQTSDEE--IQQVVEYQNSTAKV 266  
 212 ISLVSGYGDYQQLGVQALELATRPGICVARKDVVPLSAQADPRMQRMRLARATTV 271  
 Db 267 IVFSSSGPDLPLI-KEIVRRNITGRIMVLASEAMASSSLIMPEYFHVVGITGFLKAG 325  
 272 VVVSNN-RHLGCVFFRSYVNLNIGKVIASEDMA---IS-T-YITVPG-IQ-GI--G 320  
 Db 326 QIPFREFRLQVHRPKSVYHNGFAKEFMEETFNCHLOEGAKPLPYDFVRSHEEGNRL 385  
 321 TVLGV-A-IQ--Q-RQ--VP--GL--KEF--ESY--VQ--AVMGA-P-----RTPCES -W-- 358  
 Db 386 NSSATFPLCTGDNINSEVTPYMDYELRLISYVLAIVYIAHALQDIYLCPEKGLFT 445  
 359 -CGTN-Q-LCECHAFITWNPDELGAFFMSAANYEVAVAHQHL--L-GC--T 408  
 Db 445 NGSGADIKKYAMOVKLRLRLNFTNNMGEOVTEDECDLGNGYSIIMHLSPEDSIVF 505  
 409 SGTRA-RGPVFPWOLLQOIKYVNLHK-KTVAEDDKDPLGIYDIIAMDNKGP-WT-F 464  
 Db 506 KEVGYVYNAKGRERLFINEKILMSGFREVPSNCSRDCAQTRKGIIEGEPTCFEC 565  
 465 EVIG--SA-SLSPVHLIDINKTKIQHGKNNQVPVSVCTRDLGHRH-LVYSGHCCREC 520  
 Db 566 VECDEGSEGTDAACDKCPDFTWSNENHTSCIAKELEFLAMTEPFGIALTLVAIGIF 625  
 521 MPCAGTFLNLTSELTQPCCTEEMAPGSSACFSRTVEFLGMHEPISLVLAANTLLL 580  
 Db 626 LTAFLVGLVFIKFR-NPIVKAINELSYLLFLSLCCFSSSLF-FIGEPDMOTRLQPA 683  
 581 LLITAGLIFA-WRLHTPVRSAGRLCLMLGSLVAG-SCSLYSEFGFPTVPACLLRPL 638  
 Db 684 FGISFVLQISCIIVKINVLVFE--AKIPTSFHRKMWGLNQLFLVLCFTMOILCII 741  
 639 FSLGFALFSLCLIRSPGLVITFPSTKVPF-FYHTMAQNNGAGFVIVSTVHFLDIT 697  
 Db 742 WLTYAPSSVYNNHLEDEIITTCHEGSLMALGSLIGTC-LLAIGCF--AFNSRKPE 799  
 698 WLAAMTPTPTREYORFPLVILECTEVN--SVGFLVAFANHLLISITFVCSYGLKEP 755  
 Db 800 NFNNAKFTFEMLEFIIWISFIPAVASTY-GKPSAFAEVAIIAASGLACIFENNVY 858  
 756 NYNNAKVTESLLHETVSWIAFTM--SIIYGSTLPAVNAVLAGATLSGSGFPLPCY 814  
 Db 859 ILFKPSRNTIEEVRSSTAHA 880  
 815 VILCRPELNTHEFQASTQDT 836

RESULT 4  
 ID MGR5\_HUMAN STANDARD; PRT: 1212 AA.  
 AC P41594;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.  
 GN GRM5 OR MGLUR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN.  
 RA MEDLINE; 94197696.  
 RX MIKAWAMI R., KATSUKI F., YAMAMOTO T., NAKAMURA K., SUGIYAMA H.;  
 RT "Molecular cloning and the functional expression of two isoforms of  
 human metabotropic glutamate receptor subtype 5.";  
 RL Biochem. Biophys. Res. Commun. 199;1136-1143(1994).  
 RN [2]  
 RP REVISIONS.  
 RA KATSUKI F.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 860-952 FROM N.A.  
 RC TISSUE-BRAIN.  
 RX MEDLINE; 93343913.  
 RA MIKAWAMI R., KATSUKI F., SUGIYAMA H.;  
 RT "A variant of metabotropic glutamate receptor subtype 5: an  
 evolutionally conserved insertion with no termination codon.";  
 RL Biochem. Biophys. Res. Commun. 194;622-627(1993).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS  
 MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
 CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED  
 CHLORIDE CURRENT.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE  
 PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF  
 32 RESIDUES.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGLUR1.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: D28538; BAA05891.1; -;  
 DR EMBL: D28539; BAA05892.1; -;  
 DR EMBL: S64316; AAD1954.1; -;  
 DR GCRDB: GCR\_0761; -;  
 DR GCRDB: GCR\_1002; -;  
 DR GCRDB: GCR\_1003; -;  
 DR GCRDB: GCR\_1317; -;  
 DR MIM: 604102; -;  
 DR PROSITE: PS00979; G\_PROTEIN\_RECP\_F3\_1; 1.  
 DR PROSITE: PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.  
 DR PROSITE: PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.  
 DR PFAM: PF00003; 7tm\_3; 1.  
 DR PFAM: PF01094; ANF\_receptor; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KM Multigene family; Alternative splicing.  
 FT SIGNAL 1 20  
 FT CHAIN 21 1212 METABOTROPIC GLUTAMATE RECEPTOR 5.  
 FT DOMAIN 22 579 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 580 602 I (POTENTIAL).  
 FT DOXAIN 603 616 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 617 637 II (POTENTIAL).  
 FT DOMAIN 638 648 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 649 667 III (POTENTIAL).  
 FT DOMAIN 668 693 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 694 714 IV (POTENTIAL).  
 FT



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FT DOMAIN 715 737 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 738 759 V (POTENTIAL).
FT DOMAIN 760 772 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 773 795 VI (POTENTIAL).
FT DOMAIN 796 801 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 802 827 VII (POTENTIAL).
FT DOMAIN 828 1212 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 210 210 POTENTIAL.
FT CARBOHYD 378 378 POTENTIAL.
FT CARBOHYD 382 382 POTENTIAL.
FT CARBOHYD 445 445 POTENTIAL.
FT CARBOHYD 734 734 POTENTIAL.
FT VARSPIC 877 908 MISSING (IN ISOFORM 5A).
SO SEQUENCE 1212 AA; 132468 MW; 1681574 CRC32;

Query Match 12.9%; Score 819; DB 1; Length 1212;
Best Local Similarity 27.0%; Pred. No. 3,02e-153;
Matches 233; Conservative 229; Mismatches 334; Indels 68; Gaps 58;

Db 5 LILSVLLKEEDVRG-SAQSSERRVVAHMGDIIGALFVSHOP-TV-DKVERKCG-AV 60
QY 8 LILSVLLKEEDVRG-SAQSSERRVVAHMGDIIGALFVSHOP-TV-DKVERKCG-AV 67
Db 61 R-EQYIGDVEAMLTHERINSDDLPLNITLGEIRDSCWHSAYALBOSIEFIDSLIS 119
QY 68 SFNGHGHLFQAMRTVEINNSTALLNITLGEYLDVCSSESS-NVY-AT-LR---VP 120
Db 120 SEEEGLVRCVDCSSSSRSKRPYGVYIGPSSSAIVQVOMLQNFNPQVAYSTSD 179
QY 121 AQQGTGHLH-MORDIRN-HSSK-VALLGPDNTDAVTTAALLSFLMPLVSESSVYL 177
Db 180 SDRLEFKFMFVPSDAQAARAMDIVARYMYTVSAVHTGNGESGEAKFKMSAKG 239
QY 178 SGKRKPFELKTIIPBDKQVEIVYRLLOSFGVWMLSVGSIGDQGLQVQALBELATPRG 237
Db 240 ICLASHYKI-YSN-AGEOSFDKLKLLKLSHPKARVAVCFEGMTVRLGLAMARLG-LA 296
QY 238 ICVAFKDVYPLSAQAGDPRMQRMRLA-R-ARTVVVVFNS-RLLAGVFRSVYLANLT 294
Db 297 GEFLLGSDGNA-DRYDVT-DGYQ-REAVGGLTKL-QSPDYKMFDDYLLKRPETNIRN 352
QY 295 GK-WVIASEDMAISTYITNVPGIDQIGVLAIQQRVPLKREESYQAVYKAPRTG 353
Db 353 PMFQEFMOHFRQ-CRLGEPQENSKYKTKNSLTKLTHHODSGMGVINAISMAVGL 411
QY 354 P-EGSMGCTQOLCR-E-CHAFTWMPBELGAFSMAAY--N-V-Y-EAVYAVAHGL 401
Db 412 HNMOMSLCPGYAGLADAKPIDGRKLLSLMKTYETGVSGDTILFENGDSPGRYEIMNF 471
QY 402 HQI-LG-CT--SGTC-ANGPYVPMQLLIQYKVNFL-LHKRTVAFDDKGDPLGYDIAM 455
Db 472 KEMGRDY-FDIYNGSMUNGELAKDDDEV-WSKSNIR-SYCSPECKGQIKYIRKEV 528
QY 456 DWNPDEWTFEYVIGSASLSVPHLDIKTKIOWHGKNQVPSVCTREDCLEGHRVY-MGSH 514
Db 529 SCCTWCPCKENETVE-DE-YTCRACQLGSMPTDITGCDLIPQYLRMGDPPIAAVVE 586
QY 515 HCGEPCMCPEGTFLNSELHTCQPCGTEWAPBEGSSACFSRYEFLQW-H-EPISLVLL 572
Db 587 ACGLGLATLFV-TVFFIYR-DTPVAKSSRELCTYIILAGICLGYLT-FCLIAKPKOY 643
QY 573 AANLGLLILGLTAGLFAWRLHTPTVRSAGRLCFIMLSLVAGS-CLSYFFGFPYPA 631
Db 644 CYLORIGIGLSPAMSYSLVTKTNRIAILGSKKIKTKKPRFMSACQVIAFILICI 703
QY 632 CLNQPLFSLGFAFLFSLCLIRSFQVLIIFKFSK-VPTFHTWAQONAGAFIVYSTV 690
Db 704 QLGIIIVAFIEPDIIMDYPSIRE-VYLICNTN-LGVNPIVNGNGLIISCFE-YAFK 760
QY 681 HFLCLTLMAMTPTPTREYRFPPLVLECTEVANSVDFLFAFANILLIS-IFVCSYL 749
Db 761 TRNVPANENKAKYIAFTWYTCIIMLAF--VP-IFYGSNYKIITWCFVS-LSATVALGC 816

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QY 750 GKELPENYNEAKCVTFSLHFWSWIAFTMSIYQGSYIPAVNVLAGLATISGGRS-GY 808
Db 817 MEVPKVIITLAKPRNRNRSATFS 840
QY 809 -FLPKCYVILCRPELNTNTEHFQAS 831

RESULT 5
ID MGR5-RAT STANDARD; PRT; 1203 AA.
AC P31424;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGLR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 92317054.
RA ABE T., SUGIHARA H., NAWA H., SHIGEMOTO R., MIZUNO N., NAKANISHI S.;
RT "Molecular characterization of a novel metabotropic glutamate
RT receptor mglur5 coupled to inositol phosphate/Ca2+ signal
RT transduction."
RL J. Biol. Chem. 267:13361-13368(1992).
RN [2]
RP SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-BRAIN.
RX MEDLINE; 93343913.
RA NAKAMAKI R., KATSUKI F., SUGIYAMA H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon."
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE
CC CENTRAL NERVOUS SYSTEM.
CC -1- MISCELLANEOUS: ACTIVATED BY GLUTAMATE > GLUTAMATE > IBOTENATE >
CC TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR1.
CC *****
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CC or send an email to license@isb-sib.ch).
CC *****
DR EMBL; D10891; -; NOT_ANNOTATED_CDS.
DR EMBL; S64315; AAB27666.1; -.
DR PIR; A42916; A42916.
DR GCRDB; GCR.0444; -.
DR GCRDB; GCR.0760; -.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PRAM; PF00003; 7tm.3; 1.
DR PRAM; PF01094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1
FT CHAIN 21 1203 METABOTROPIC GLUTAMATE RECEPTOR 5.

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57 DOMAIN 22 578 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 579 601 I (POTENTIAL).
FT DOMAIN 602 615 CYTOPLASMIC (POTENTIAL).
FT TRAMSEM 616 636 II (POTENTIAL).
FT DOMAIN 637 647 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 648 666 III (POTENTIAL).
FT DOMAIN 667 692 CYTOPLASMIC (POTENTIAL).
FT TRAMSEM 693 713 IV (POTENTIAL).
FT DOMAIN 714 736 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 737 758 V (POTENTIAL).
FT DOMAIN 759 771 CYTOPLASMIC (POTENTIAL).
FT TRAMSEM 772 794 VI (POTENTIAL).
FT DOMAIN 795 800 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 801 826 VII (POTENTIAL).
FT DOMAIN 827 1203 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 88 88 POTENTIAL.
FT CARBOHYD 209 209 POTENTIAL.
FT CARBOHYD 377 377 POTENTIAL.
FT CARBOHYD 381 381 POTENTIAL.
FT CARBOHYD 444 444 POTENTIAL.
FT CARBOHYD 733 733 POTENTIAL.
FT VARSPIC 876 907 MISSING (IN ISOCOREM 5A).
SQ SEQUENCE 1203 AA: 131885 MW: 2955EA33 CRC32:

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Query Match 12.8% Score 814; DB 1; Length 1203;
Best local similarity 27.1% Pred. No. 4,52e-152;
Matches 234; Conservative 222; Mismatches 340; Indels 67; Gaps 60;

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5 LITSLVLLKEDVARG-SAQSERRVVAHMPGDIIGALFSVYHNP-TV-DKHERKCG-AV 60
8 LLTSLQLAAYCAWAFSCQRTSSPGSLPQDFLAGLGHADCLQVRHPLVTSQCRSD 67
61 R-EOYQIOVQEAHLHLERINSDPILNTTLCCELRDSCWHNAVALQEOIEIRSLIS 119
68 SFGHGHIHLFOARRFTVEELNSTALPNTTILELYDCSESSNYVA-TLR-VPAQQ-G 124
120 SEEEGLVACVDSSSFRSKRPVIGVIGPSSVAIOVNTLOLDFNIPOIAYSATSDLS 179
125 TGHLE-MQR--D-LRN-HSK--VVALIGPNTDHAVTALLSPFLMPLVSYASSVILS 178
180 DKLFYFEMRVPSDAQARAWYDIKRYIMWYVSAVHEGNGESGEMAEFKMSAKEGI 239
179 GKRFPSFLRTIPSDKYQVEIVRLQSGFWWISLVGSGYQGLQVQALFELAPRGI 238
240 CIAHSKXI-YSN-AGEOSTDKLLKLRSHPRKRVVACRECGTIVGLMAMRLG-LAG 296
239 CVAFKDVVPLSAQAGDPROMQMLRL-AR-ARTVVVFSN-RHLGVEFRSVLANLTG 295
297 EFLLGSDGMA-DRYDVT-DGYQ-REAVGGITIKL-QSPDKWFDDYIKLRPETNLNP 352
296 K-VWASEDMALSTYITNTPGLOGITGLVALQOQROVPGLKFEFESSYQAVNGAP-RTC 353
353 WFOEFMOHNFQ-CREGEFAOENSKYKTCNSLTLPRTHHVODSKMGFVINAISMAVGLH 411
354 -DEGSCGTNQLCR-E--CHAFTTMNPDELGAFSMSAAV--N-V-Y-EAVVAVHGLH 402
412 NMQMSLCPEYAGICDAMKPIDGKLLDSLKTFTGVSGLMIFDENGSPGKYEINERK 471
403 QL-LG-CT--SGTC-ARGPYPMQLQOIKYVFL-LHKRTAFVADKGDGLGYDRIAMD 456
472 EMGKDY-PDYINWSDNDELKMDDEV-MSKKNIIIR-SVCESEPEKGOIKYIRGEVS 528
457 WNPPEMTFEVIGASLSAPHLDINKTKIQMGKNNOVPSVCTRDLEGHRLV-MGSHH 515
529 CCWCTCPCKENEYVF-DE-YTCAQOLGSPNIDTGLGCDLIPVOYLRMGSDPIAAVFA 586
516 CCEPCAPCAAGTFLNTSELHTCOPCGTEEWAPEGSSACFEIRVEFLGW-H-EPISLVLLA 573
587 CGLGLATLEV-YIIFIIR-DTPVWSSSRELCTYIIAGICGLYLT-PELLAKPKQIYC 643
574 ANTLGLLGLTGLFAMRLHTPVRSAGAGLCFLMGSLVAGS-CSLVSEFKPTVPAC 632
644 YIORIGISLSPAMYSALVTKTNRIRIAGSKKICKTKPREMSACQAVIAFIICIQ 703

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QY 633 LIRQPLFSLGFAFLFSLCLIRSRQLVIRKFSRK-VPTRYHWAQNHAGIPIVASTH 691
DB 704 LGITVALFMEPPDINHDPISIRE-VYLCNTN-LGVVTPLOYNGLLISCTF-YAFRT 760
QY 692 LFLCITLWAMMPRPRTYQRPFPPLVILLECTEYNSVGFVAFAHNILSIS-TFVCSYIG 750
DB 761 RNVAPANEAKYALFMYTTCIIMLAF--VP--IYGSNNKIITMCPYSV-TSATVALGM 816
QY 751 KSLPENYNEKCVFSLJLHEVSWIAFTWSSITQSYPAVAVLAGLATLSGGS-GY- 808
DB 817 FVPKYVIIIAKPERNVSATFS 839
QY 809 ELPKCVIILCRPLNTEHFQAS 831

RESULT 6
ID MGR1_RAT STANDARD; PRT: 1199 AA.
AC P23385;
DT 01-NOV-1991 (rel. 20, last sequence update)
DT 15-DEC-1999 (rel. 39, last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
GN GRM1 OR MGLUR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE: 91156047.
RA MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO R., NAKANISHI S.;
RT "Sequence and expression of a metabotropic glutamate receptor."
RL Nature 349:760-765(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE: 92022526.
RA HOUAMED K.M., KUIJPER J.L., GILBERT T.L., HALDEMAN B.A., O'HARA P.J.,
RA MULVIHILL E.R., ALMERS W., HAGEN F.S.;
RT "Cloning, expression, and gene structure of a G protein-coupled
RT glutamate receptor from rat brain."
RL Science 252:1318-1321(1991).
RN [3]
RP ALTERNATIVE SPLICING (1B).
RC TISSUE=BRAIN;
RX MEDLINE: 92110002.
RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;
RT "A family of metabotropic glutamate receptors."
RL Neuron 8:169-179(1992).
RN [4]
RP ALTERNATIVE SPLICING (1C).
RC TISSUE=BRAIN;
RX MEDLINE: 93066232.
RA PIN J.-P., MABER C., PREZEAU L., BOCKAERT J., HEINEMANN S.F.;
RT "Alternative splicing generates metabotropic glutamate receptors
RT inducing different patterns of calcium release in Xenopus oocytes."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).
CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITO-
CC LATED BY A SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
CC ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
CC THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC - ALTERNATIVE PRODUCTS: THREE ISOFORMS, 1A (SHOWN HERE), 1B AND 1C;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY
CC TRUNCATED FORMS OF 1A.
CC - TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR
CC PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND
CC MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.
CC - MISCELLANEOUS: ACTIVATED BY QUISOULALATE > GLUTAMATE > IBOTENATE >
CC TRANS-1-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY
CC 2-AMINO-3-PHOSPHONOPROPIONATE.

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CC -! FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
CC ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
CC THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -! ALTERNATIVE PRODUCTS: TWO ISOFORMS: ALPHA (SHOWN HERE) AND BETA:
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -! SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST: TO MGLURS.
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CC -----
DR EMBL: U31215; AA87843.1; -
DR EMBL: U31216; AA87844.1; -
DR EMBL: L76627; AAB05337.1; -
DR EMBL: L76631; AAB05338.1; -
DR GCRDB: GCR_1825; -
DR GCRDB: GCR_1826; -
DR GCRDB: GCR_1882; -
DR GCRDB: GCR_1883; -
DR PROSITE: PS00979; G-PROTEIN_RECCEP_F3_1; 1
DR PROSITE: PS00980; G-PROTEIN_RECCEP_F3_2; 1
DR PROSITE: PS00981; G-PROTEIN_RECCEP_F3_3; 1
DR PFAM: PF00003; 7tm_3; 1
DR PFAM: PF01094; AAF-receptor; 1
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 18
FT CHAIN 19 1194
FT DOMAIN 19 592
FT TRANSMEM 593 615
FT TRANSMEM 616 629
FT TRANSMEM 630 650
FT DOMAIN 651 661
FT TRANSMEM 662 680
FT DOMAIN 681 706
FT TRANSMEM 707 727
FT DOMAIN 728 750
FT TRANSMEM 751 772
FT DOMAIN 773 785
FT TRANSMEM 786 808
FT DOMAIN 809 814
FT TRANSMEM 815 840
FT DOMAIN 841 1194
FT DOMAIN 1014 1035
FT DOMAIN 1067 1081
FT DOMAIN 1095 1130
FT DOMAIN 1142 1194
FT CARBOHYD 98 98
FT CARBOHYD 223 223
FT CARBOHYD 397 397
FT CARBOHYD 515 515
FT VASAPLIC 887 906
FT VASAPLIC 907 1194
FT VASAPLIC 887 906
FT CONFLICT 593 593
FT SEQUENCE 1194 AA: 132376 MW: 6ACDFEC3 CRC32:
Query Match 12.6%; Score 800; DB 1; Length 1194;
Best Local Similarity 27.3%; Pred. No. 8; 74e-149;
Matches 229; Conservative 217; Mismatches 326; Indels 66; Gaps 52;

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QY	35	LPGLDLAGLGS	LHADCQVRRRLPVTSQDSDSDSNCSNGYHLFQAMRTVEINNSTALL	94
Db	97	PNILIGSEIRDS	CWHSVALDEOSIEFFIRDSLSIRFDEKGINRCLPGDGLSPGRTKKPI	156
QY	95	PNILIGELYIDVCS	SESS-----NV-Y--ATL-RVPAQ-QGTGH-LEMORDER-NHSSKYV	142
Db	157	AGVIRPSSSSVA	LQVQNLLQFLDIPQINVSATISDLSKTIYKFLRVSPDITQARML	216
QY	143	A-LISPCNTHAVTT	AAALSPFLMPEVEKSSVYLSKRRKPSRLRIPSDRQVEYIV	201
Db	217	DIVKRYNNTVYSAV	TEGNEGSGMDAKELKLAAGELIANSDKI-YEN-AGEKSFRL	274
QY	202	RLLOSFGWMI	SVLSYGDYQOLQVQALBELATPGLGTAVAKDYPLISAQGDPRMOMM	261
Db	275	RKLRELRKARVYVC	CEGMYTGLLSAKRRIGVVEFSJIGSDGMADRDEV-IEGYE	331
QY	262	LRL-AR-ARTVYVFSN	-RHLAGEFSSVLANJTGKWLIASEDMIAISTYITNPJIG	318
Db	332	VEANGGITIKL-Q	SEVVSFDDYF-KLNDLTRNPKPPE-FWQHRFO-CRLPGHLENP	388
QY	319	IGTVGVAIQORV	PGLEKEFESEYQAVMGA-PRTC--DESSWCGITNLCR-ECHAFITW	374
Db	389	NFKRICITGNE	SHLENYQDSKXGFVNIYAMAHLOXMHALCGHVGJCDAMPIDGS	448
QY	375	NMPEL-GAFSNAAY	-N--V-Y-EVAVAHSLGLL-G-CTS--GTC-ARSPVPM	420
Db	449	KLDELIFKSEF	IGVSGEVEWDEKGDAPRYDINMLQYTEANR-YDYVHVGITWBGVLNI	507
QY	421	QLQIQIVYVNF	L-HKKTIVAFDGDKDPJGYDIIAMDNGBEMTEVEIGASLSPVHDI	479
Db	508	DDYKIQ-MKKS	VYA-SYCSPECLNGQIKYVRKEVSCCMICTACKENEYVO-DEF-TCK	563
QY	480	NKTKIQMGKNNQ	VPVASCIRQCLEGHHRY-MGSHCCFECMPCDEAGTFLNTSELHTCQ	538
Db	564	ACDLQMWENAD	LTGCEPIPVRYLEMSNEPIIALAFSGTLVTLFVLLFVIVR-DPVP	622
QY	539	PGCTEMAPEG	SSACFSFTVEFLGHEHISLVLLANLLELLLIGTAGLRA-WRLHTPV	597
Db	623	VKSSRELCYII	LAGIFLYVCP-FTLIARPTTSCYQRLRVLVGLSSACYSALVTXNR	681
QY	598	VMSAGRGIC	FLMGLSLVAG-SCSYSEFGKPTVPACLRQPLSFGAIFLSCLTIRSFQ	656
Db	682	IARILAGSKK	IKCTKPPRMSMAQOVIITASILISVQLTVTLIMEPPMPLISPSIKE	741
QY	657	LVILIKFESIK	-VPTFYTHQAONHGAGIEVIAVSIVHLELCITLWAMMPRPTREYQRP	715
Db	742	-VYLIC-MTSN	-GVAPRIGYGLIMSGCY-YAFETRVANPENEAKYIAETMYTCTIC	798
QY	716	LVILECTEVS	NGFIVAAHNLTLSTSTFPCSYSGKELPEYVNAKCVTSLILHPFSW	774
Db	799	LAF--VP-IFY	GSNKIITTCFAVLSVYVALGCFETPKMYIINKPRNRSATFS	853
QY	775	IAFFIMSSIT	QGS-YLRPAVNVLAGIATLSGFSFGFLPKVYIILCRPLNTEHQAS	831
RESULT	10			
ID	AC	GR2_RAT	STANDARD;	PRT; 872 AA.
AC		P31421:		
DT		01-JUL-1993	(Rel. 26, Created)	
DT		01-JUL-1993	(Rel. 26, Last sequence update)	
DT		15-JUL-1999	(Rel. 38, Last annotation update)	
DE		METABOTROPIC	GLUTAMATE RECEPTOR 2 PRECURSOR.	
DE		GRM2 OR MGLUR2.		
OS		Rattus norvegicus (Rat).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC		Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
RN		(1)		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=BRAIN;		
RX		MEDLINE: 92110002.		
RA		TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;		
RT		A family of metabotropic glutamate receptors.;		
RL		Neuron 8:169-179(1992).		







```

CC or send an email to: license@lsb.slb.ch).
CC -----
CC
CC
CC
DR EMBL: X77748; CAA54796.1; -.
DR GCRDB: GCR_2070; -.
DR MIM: 60115; -.
DR PROSITE: PS00979; G_PROTEIN_RECPE_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECPE_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECPE_F3_3; 1.
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR K W G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal:
KW Multigene family.
FT SIGNAL 1 20
FT CHAIN 21 877
FT DOMAIN 21 574
FT TRANSMEM 575 597
FT DOMAIN 598 611
FT TRANSMEM 612 632
FT DOMAIN 633 643
FT TRANSMEM 644 662
FT DOMAIN 663 686
FT TRANSMEM 687 707
FT DOMAIN 708 732
FT TRANSMEM 733 754
FT DOMAIN 755 767
FT TRANSMEM 768 790
FT DOMAIN 791 800
FT TRANSMEM 801 825
FT DOMAIN 827 877
FT CARBOHYD 207 207
FT CARBOHYD 290 290
FT CARBOHYD 412 412
FT CARBOHYD 437 437
SQ SEQUENCE 877 AA; 98619 MW; B5D0AEAS CRC32;

Query Match 12.0%; Score 764; DB 1; Length 877;
Best Local Similarity 25.9%; Pred. No. 2,36e-140;
Matches 207; Conservativity 203; Mismatches 338; Indels 50; Gaps 44;

Db 55 CGRINE-D-RGRIORFEALMFAIDENKSDYLLPGVKLGHIIDTGRPTALQSLSEFVR 112
Oy 63 CDRSSFFNGHGHLFOANRFYEEFINNSTALLPNTLLGVELDVCS-ESSNYATLR-VP 120
Db 113 ASLTIVDEAEVYCPDGSYAIOENIPLLIAGVGYSSYSIOVAVALLRFQIPQISYAST 172
Oy 121 AAOGT-GHLE-M-Q-R-DLRHSSKVVA-LIGPNTGHAVTALLSLPFLPLVSYEAS 173
Db 173 SAKLSDKSRIRYDFATVPDPFYQAKAMAEILRFNWTYVSVYASGVDGETIGAEFEQEA 232
Oy 174 SVILSGKRKFPSEFLITPSDKYQVEIVIRLLDSFQMWVISTLGSYGDYGOGLQVLALELA 233
Db 233 RLNRNICITAEVGRSNIRKSYDSVIRELLOKPNAR--VYVLFMSDDSRRLTAASRAN 290
Oy 234 TPRGICVAFKDVPLSA-QAGDPKORAKMLRLARARTVVVVFSNRHLAGVFFRSVILAN 292
Db 291 -ASFTWVASDGMGAOESITIKGSEHYAQAITLELASCPYRQDFRQSLNPNYNNRNPWF 349
Oy 293 LTGKWIASDEDMALSTIYNVPGIGIGIV-LGVALIQ-RQVPLGKFEFEESYVQAVMGAP 350
Db 350 RDFVEQKQOCGLQNK-RNHRRYCDKHLAIDSNSYQESKIMFVAVYAMAHALHKMORT 408
Oy 351 RTCPGSGW-CGTNOLCRCHAFFTTNMNP-ELGAFSMSAAYN-VYEAVYVAHGLHQLL-G 406
Db 409 LCPNTTKLCDAMKILDGKKLYKLINFLAPFNPNDADSIYKEDIFGSGMGRYNNFN 468
Oy 407 -CTSGT-C-A-R--Gp-VIPWOLQOIYKVFLELHKT--VA-FDQKGPPLGYDITIA 454
Db 469 FQNVGKSYLKVGHMA-ETLSLDVN-S-IHW-SKNS-VPTSGCSDPAPNEMKMNQOGD 523
Oy 455 WDMNRPWMTFEVIGSASLSPLVHDLINKRIQHGKNNQVPSVYCRDLEBGNHRLVMSH 514
Db 524 VCCWICICEPEPEYV-ADEF-TCKMDGSGQWFTADLTGQCYDLPEDIYEMEDAMATGPVTI 581

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[illegible]







Query Match	11.9%	Score 759;	DB 1;	Length 879;
Best Local Similarity	25.8%	Pred. No. 3,488-139;		
Matches	206;	Conservative	202;	Mismatches 340; Idels 50; Gaps 44.
Db	57	CGRIIE-D-RGIQRLEALFAIDELINKDNVLLPGVKLVHLIDTCSPRDYALFEQSEFVR	114	
Oy	63	CDRSQSFNGHGHVLPQANRFVEELNNSTALLPNITLGLDELVDGS-ESSVAVATLR-VP	120	
Db	115	ASLTVDENAEVYKPCDGSIAQDENITPLIAGVIGGSSYSIQVAVNLRLEFOIPQISAST	174	
Oy	121	AQOGT-GHLE-M-O-R-DLNRHSSKYVA-DIGDNTDHAVTALLSPFLMLVSEAS	173	
Db	175	SAKLSDKSRVDFATVPDPDYQAKAAELIRFNWTVSVTVASEGDTGEGTAEFOEA	224	
Oy	174	SVTLGKRRKFPSELTTPISDKYQVEVIRLLQSGWVWISLVGSGYGGQGVQALRELA	233	
Db	235	RLRNICITAEVGSNSLRKSYDSVIRELLQKNR-NVVLEFRSDSRELLAANRVN	292	
Oy	234	TPRGICVAFKDVNPLSA-QAGDPRKQRMMLLARRATTVVVJESNRHLGYFRFSVLAN	292	
Db	293	ASFVTVAASDVGAGAESIVKSGEHVAYGATTELASHPVRQFDRFQSLNPNYNNRPWF	351	
Oy	293	LTGKVMIASDEMAISTVITNPGIQTIV-LGVAIQ-QVPELKEEESYGVAVNGAP	350	
Db	352	RDFWQKRCQCSIQNK-RNHRQVCKKHLADSSNTEQESKIMFVNVAVYAAHAIHKQRT	410	
Oy	351	RCPGPGSM-CGNOLCRCHAFITWNP-ELGAFSMSAANY-VYEAYVAVAHGHQLL-G	406	
Db	411	LCPNTKLCIDAMKILDGKKLYKYLINFPAPNPNKAGDSIYKEDTFGGOMKRVNEN	470	
Oy	407	-CTSGT-C-A-R--GP-VTPWQLLOQIYVNFLLR-KTVA-FDDKGDPLQYDITIA	454	
Db	471	LOOTGKSYLKVGHMA-ETLSLDVD-S-IHW-SRNS-VPTSDCSDCAENEMKNQPCD	525	
Oy	455	MDMNGPEMTFVEIGSASLSYPHLDINKTKIOMHCKNNQVPVSVCTRCCLSGHRLVNGSH	514	
Db	536	VCCWICIDCEPEYR-VDEF-TQMDCCGQWPTADLSGCYNLPEDYIKMEDMAIGVYTI	563	
Oy	515	HCCFCMCPCEAGTFLNITSELHCTQPCGTEEWAPGSSACFSRTVEFLGMHEPISVLLAA	574	
Db	564	ACLGELCTCIYIVTIRKINNTPLYKASRELCITLLGVSLSYCMTEFFLAKPSVICAL	643	
Oy	575	NTLLELLIGTAGLEPAMLHTPVARSAGRCLEFIMLSLVAAGSCLISFEKGKPPVPACL	634	
Db	644	RLIGLGTFAICYASALLTKTNCIARIQD-GVKNQAOBRPKFI-SPSSOVFICLGLIIOIV	701	
Oy	635	RQPLFSLGFAFLFSLTLRSFOLVITFEFSKVTPTFHMAONNGAGIPIVYST-VHLF	693	
Db	702	MYSWVLIETP-GTFRYTLPEKRETVILKC-NVKDSSMLSLIYDVAVLICTVYAKTR	759	
Oy	694	LCITLMAWTPRPRTREYO-RFPH-LVILECTEVSVCPLVAFANILLISTFVCSYLKG	751	
Db	760	KCPENFNARKIIGFMVYTTCILIMAFILPIVTVSSDRVQTTMCISVSLSGFVLOCLE	819	
Oy	752	ELPEVYNKAVCTPESLLHFWPMSIAFTMSSIYOGSYLPAVNVLAGLATISGGS-GY-F	809	
Oy	820	APKVIHLEFQOKNVYTH	837	
Oy	810	LPKCVIILCRELNNTEH	827	

ID	MG36_HUMAN	STANDARD:	PRT:	877 AA.
AC	015303:			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-DEC-1998 (Rel. 39, Last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.			
GN	GRM6 OR MGLUR6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RA	[1]			
RA	SEQUENCE FROM N.A.			
FX	MEDLINE: 97358610.			
RA	HASHIMOTO T., INAZAWA J., OKAMOTO N., TAGAWA Y., BESSHO Y., HONDA Y.,			
RT	NAKANISHI S.			
RT	"The whole nucleotide sequence and chromosomal localization of the			
RT	gene for human metabotropic glutamate receptor subtype 6."			
RL	Eur. J. Neurosci. 9:11226-1235(1997).			
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR			
CC	IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE			
CC	ACTIVITY.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	STRONGEST, TO MGLUR4.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: U82083; AAB82068.1; -			
DR	GCRCB: GCR_2607; -			
DR	MIY: 604096; -			
DR	PROSITE: PS00979; G_PROTEIN_RECPE_F3_1; 1.			
DR	PROSITE: PS00980; G_PROTEIN_RECPE_F3_2; 1.			
DR	PROSITE: PS00981; G_PROTEIN_RECPE_F3_3; 1.			
DR	PFAM: PF00003; 7tm_3; 1.			
DR	PFAM: PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;			
KW	MultiGene family; Vision.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	877	METABOTROPIC GLUTAMATE RECEPTOR 6.
FT	DOMAIN	25	585	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	586	608	I (POTENTIAL).
FT	DOMAIN	609	622	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	623	643	II (POTENTIAL).
FT	DOMAIN	644	654	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	655	673	III (POTENTIAL).
FT	DOMAIN	674	697	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	698	718	IV (POTENTIAL).
FT	DOMAIN	719	748	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	749	770	V (POTENTIAL).
FT	DOMAIN	771	783	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	784	806	VI (POTENTIAL).
FT	DOMAIN	807	819	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	820	845	VII (POTENTIAL).
FT	DOMAIN	846	877	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	296	296	POTENTIAL.
FT	CARBOHYD	451	451	POTENTIAL.
FT	CARBOHYD	479	479	POTENTIAL.
FT	CARBOHYD	567	567	POTENTIAL.
SO	SEQUENCE	877 AA;	95436 MW;	DSA6C038 CRC32;
Db	Query Match	11.6%;	Score 741;	DP 1; Length 877;
	Best Local Similarity	25.3%;	Pred. No. 5,56e-135;	
Matches	204;	Conservative 233;	Mismatches 287;	Indels 71; Gaps 57;
64	CGVRLKMLTALDRVNDPELLPGVRLGALVLTCSQYIALDQALSFVQALIRGSDG	123		
72	HGYHLFGAKRTVEINNSTALPLNTLGKGLVYVCS-ESSNVATLR-VPDQ-QGTGHL	128		







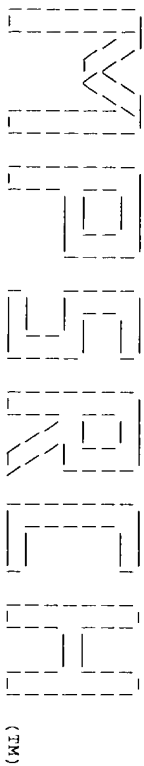
QY 242 FPDVYPLSAQGD-PRMORMLRLARATIVVYFESNRH-LAGVFFRSVYLANLTGK-VW 298  
Db 306 IGSDSMG-SK-IAPVYQOEIAEGAVTILPKRASIDGFDREFSRTLANNRRANVWFAEFS 363  
QY 299 IASEDMAISTYITNVGIGIGTVLGAIAQRO-VPGL-KEFEESTYQAVMGAJR-T-CP 354  
Db 364 EGNFGCKSGSHGRNSHIKKCTGLERIARDSYEOBGKYQVIDAVYSMAVALHNMKEL 423  
QY 355 EGSW-C-GTNOCRECHAFT-T-WN-MPELGATSMSAAYN-YEAVYAVAHGLHOLL-G- 406  
Db 424 CPGYIGLCPRMWTIGKELGIRAVNENGAGTPLYTENENGDAPEGRYDIFQYQINNST 483  
QY 407 CTS--GTGAR-GPVYPMQLQOIYKYNFLHKKT-VAFDCKGDPGLGYDIIAMDWNGPEW 462  
Db 484 EYKIIIGHMT-NQHLKVED--MOMANREHTHPASVCSLPCKPGEKKTYKGVPCCKHGR 540  
QY 463 TFEVIGSASLSPVHLDINKTKIQMHGKNNQVPVSVCTROCLEGHRLVNGSHHCCECMP 522  
Db 541 CEGYNY-QVDEL-SCELCPLDORPINRTGQORIPYIKLEWSPMAVVPVLAIALGIAT 598  
QY 523 CEAGTFPLNTSELHTCOPCGTEEMAREGSSACFSRTVEFLGMHEPISLVLLAANTLILL 582  
Db 599 TEVIYTFVRYNDTPIVRASGRELSYVLTGIFLCISITFLMAAPDTIICSEFRRIFLG 658  
QY 583 IGTAGLFAWRHLHPVYRSAGRLCFELMLGSLVAGSCLYSFEGKPTVPACLLRQPLFSLG 642  
Db 659 MCFVSALLTKNRIHRIEQQKSVTAKFTISPASOLVITFELIS--VOLGVEFWFVY 716  
QY 643 FALFELSLTIRSFQVLIIRKFSK-VPTFYHTWAONHAGIFVYVSSYVHLFLCLTWLAM 701  
Db 717 DPPHTIIDYGEORTLDPENARGYLK-DISDLISLISLGYSIILAMVCTVYAIKTRGVP 775  
QY 702 WTPRPRTREV--QR-F-P-HL-VILECTEVNSGVFLAFANHILSLISTFVCSYLGEKLEP 755  
Db 776 TENEAKPIGFTMYTTCIIMLAFIPFPGTAQSAEKMYIOTTTIVSMS--LSASVSLGMLY 834  
QY 756 NYNEAKCVTFSLHFWISWIAFFTMS-SIYQGS--YLPVAVNLAGLATLSGGFS-G-YF 809  
Db 835 MPKVYIIFHPPEON 848  
QY 810 LPRCYVILCRPELN 823

Search completed: Fri Mar 17 13:17:59 2000  
Job time : 101 secs.









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MSearch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:15:12 2000; Maspar time 35.30 Seconds

Tabular output not generated. 955.673 Million cell updates/sec

Title: >US-09-361-652-2  
Description: (1-842) from US09361652.pep  
Perfect score: 6366  
Sequence: 1 MLFWAHLHLISLQLAIVACW.....NNEHFQASIDYTRRCGTT 842

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r62  
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 52.559; Variance 107.285; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1316	20.7	1085	2 S40476	Ca(2+)-sensing recept	6.36e-231
2	1296	20.4	1078	2 S49341	calcium-sensing recep	7.84e-227
3	1293	20.3	1078	2 A56715	calcium receptor (clo	3.22e-225
4	1282	20.1	1079	2 I59362	calcium/polyvalent ca	5.70e-224
5	1201	18.9	1088	2 B56715	calcium receptor (clo	1.95e-207
6	819	12.9	1180	2 JC2132	metabotropic glutamat	2.87e-130
7	819	12.9	1212	2 JC2131	metabotropic glutamat	2.87e-130
8	814	12.8	1171	2 A42816	metabotropic glutamat	2.86e-129
9	810	12.7	1199	2 A41939	G protein-coupled glu	1.80e-128
10	799	12.5	912	2 JH0563	metabotropic glutamat	2.81e-126
11	798	12.5	912	2 I58149	metabotropic glutamat	4.45e-116
12	797	12.5	1218	2 S71376	glutamate receptor ho	7.04e-126
13	769	12.1	872	2 JH0561	metabotropic glutamat	2.64e-120
14	759	11.9	879	2 JH0562	metabotropic glutamat	2.56e-118
15	740	11.6	908	2 I49142	metabotropic glutamat	1.51e-114
16	730	11.5	915	2 A49874	metabotropic glutamat	1.45e-112
17	727	11.4	871	2 A46742	metabotropic glutamat	5.69e-112
18	241	3.8	958	2 T02741	probable ligand-gated	2.29e-20
19	186	2.9	938	2 T01809	hypothetical protein	2.05e-11
20	175	2.7	934	2 T02742	probable ligand-gated	1.02e-09
21	172	2.7	940	2 T02740	probable ligand-gated	2.90e-09
22	172	2.7	960	2 JEO356	gamma-aminobutyric ac	2.90e-09
23	171	2.7	1005	2 S33525	guanylate cyclase (EC	4.10e-09

24	151	2.4	962	2 C43274	N-methyl-D-aspartate	3.59e-06
25	154	2.4	1203	2 I55456	N-methyl-D-aspartate	1.33e-06
26	155	2.4	1239	2 I49705	glutamate receptor ch	9.54e-07
27	150	2.4	1250	2 945219	N-methyl-D-aspartate	4.98e-07
28	143	2.2	965	2 I51244	N-methyl-D-aspartate	4.82e-05
29	132	2.1	370	2 E70341	conserved hypotheticala	1.52e-03
30	127	2.0	885	2 JN0339	N-methyl-D-aspartate	6.94e-03
31	127	2.0	901	2 JN0337	N-methyl-D-aspartate	6.94e-03
32	127	2.0	922	2 JN0338	N-methyl-D-aspartate	6.94e-03
33	127	2.0	938	2 S19710	N-methyl-D-aspartate	6.94e-03
34	125	2.0	938	2 S21104	N-methyl-D-aspartate	1.26e-02
35	125	2.0	1333	2 S27224	N-methyl-D-aspartate	1.26e-02
36	125	2.0	1323	2 I78557	N-methyl-D-aspartate	1.26e-02
37	125	2.0	1356	2 C45219	N-methyl-D-aspartate	1.26e-02
38	125	2.0	1464	2 S47551	N-methyl-D-aspartate	1.69e-02
39	124	1.9	885	2 A47551	N-methyl-D-aspartate	1.69e-02
40	124	1.9	938	2 A46612	N-methyl-D-aspartate	1.69e-02
41	121	1.9	986	1 OYURGA	speract receptor prec	4.08e-02
42	121	1.9	1125	1 OYURCP	speract receptor prec	4.08e-02
43	121	1.9	1464	2 S29159	glutamate receptor, N	4.08e-02
44	121	1.9	1464	2 A43274	N-methyl-D-aspartate	4.08e-02
45	124	1.9	2731	1 VFIRUH	genome polypeptide 1b	1.69e-02

ALIGNMENTS

RESULT 1  
ENTRY S40476 #type complete  
TITLE Ca(2+)-sensing receptor - bovine  
ORGANISM #formal\_name Bos primigenius taurus #common\_name cattle  
DATE 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999

ACCESSIONS S40476  
REFERENCE S40476  
#authors Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kitor, O.; Sun, A.; Hediger, M.A.; Lytton, J.; Hebert, S.C.

#journal Nature (1993) 366:575-580  
#title Cloning and characterization of an extracellular Ca (2+)-sensing receptor from bovine parathyroid.

#cross-references M01D:94077182  
#accession S40476  
#status preliminary  
#molecule\_type mRNA

SUMMARY ##residues 1-1085 ##label BRO  
#length 1085 #molecular-weight 121170 #checksum 5738

Query Match Score 1316; DB 2; Length 1085;  
Best local similarity 31.9%; Pred. No. 6.36e-231;  
Matches 272; Conservative 234; Mismatches 273; Indels 73; Gaps 51;

DB	31	GDIILGGLPPIHFG-VAVKQDQKSPESVCEIRYRFGFRMLQAMFAIEINSSPALL	89
QY	37	GFLLAGLGLSLHADCLOVRHRLVLTSCDRSDS--FNGHGYHDFQAMRFVEEINNSTALL	94
DB	90	PMMTIGYRIEDCNVYSKSLLEATLSFVAONKIDSLNDFQNCSEHIEPTIIVAGATSGG	149
QY	95	PNITLGEYLEDVCSSESSNY-ATLRVPAQGGTGLEMKR--DURNSSKVVVALIGDNDT	151
DB	150	ISTAVNLGLFYIPQVSVASSSRLLSNKQKSPFRTIPNDEHQTAAADIEFRMWN	209
QY	152	HAVTTAALSLPLMLPVSVLEASSVLSGKRKPPFLRTIPSKYQVEIVRLQSGWWM	211
DB	210	VGTIADDDYSGPGIKFEEAEKSDICIDFSELLISQYSD-E-KIQQVEVYKQNSTAKV	267
QY	212	ISLVGSGYGDGLQVALBELATPRGICVAFKDVPLSLQAQDPPRQMLRLARARITV	271
DB	268	IYFSSGPEPLELI-KEIYRNRITGRIWASAMWSSSIAMPEVHVVGRTGFGKMG	326
QY	272	VVVFSS-RHLAGVFRSVVLANTGKWTASDDWA---IS-T-TITNPG-IO-GI--G	320
DB	327	QIPGFEFFQKYVPRKSVYNGFAKEFWETTFNCHQEGAKGKLPVDTLFGHEEGARLS	386



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QY 321 TVLGV-A-1Q--O-RO-VP-GL-KEF-EESY---VO-AVMGA-P-----RTCPDEG-SW-C 359
Db 387 NSPTAPPLCTGDNISVETPYMDYTHLRISYNYLAVYSIAHLODITCIPGRGLFT 446
QY 360 -G-TN-Q-LCRECHAFITTMPELGAFMSAAYNYEAYVAHGHQOLG-----T 408
Db 447 NGSCADIKKVEAMOVYKHLRHNFETNMGEQVTFDECDLGNYSIINHLSPEDSIVF 506
QY 409 SGCA-RGPVYPMOLLOQIYKVNFLHK-KTVAFDKDGPLGYDIIAMDNGPE-WT-F 464
Db 507 KEVGYNYVAKKGERLFINEKILMSGFSEVFPNSRSCDLAGTRKGIIEGPTCCFEC 566
QY 465 EYIG--SA-SLSFVHLDINTKTIQWHEKNQVPSVCTRDCLGHHN-LVMSGHCCFEC 520
Db 567 VECPEDEYSDTASACNCPDDFMSNENHTSCIAKEIEFLSWTEPFGIALTFVAVGIF 626
QY 521 MPEBAGTFLNTSELHTCQPCGTBEMAPESGACFSRTVEFLGHEPISVLLAANTLILL 580
Db 627 LTAFLVGVIFKFR-NPIVKAATNRELSTYLLFSLCCFSSLP-FIGEPDWTCLRLQPA 684
QY 581 LLITAGLFA-WRLHFPVRSAGGRCLFMLGSLVAG-SCSLYSEFGKPTVPACLLRQPL 638
Db 685 FGSFVLCISCIIVKTNRLVLE--AKIPTSHRKMWGLNQLFLVLCFMQIYCAI 742
QY 639 FSLGFAIFLSCLTIRSFQVIIFKFSKVPF-FYHTWQNHGAGIFIVASTVHLFCLT 697
Db 743 WLNTAPSSRYRNEHLEDEIFITCHEGSLMALGFLIGTC-LTAICGFF-AFKSRKLE 800
QY 698 WLMTMPRPREFRQRPFLHVLTECTEYN--SVGLFVAFANILLISTFSCISLGRLEPE 755
Db 801 NENAEFTFSMLIFLWISFIPAVASTY-GKFSAVEYIAIILAGLACIFENKRY 839
QY 756 NYEACVTFEFLHFEVSWIAFPTM-SIYQSYLPAVNIAGLATSGLGSGFVLPKCY 814
Db 860 IILFKPSRNTIE 871
QY 815 VILCRELNMTE 826

RESULT 2
ENTRY 4
TITLE calcium-sensing receptor - human
ORGANISM Homo sapiens
DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 03-Aug-1995
ACCESSIONS
#accession S49341: A49419; B49419; C49419
#authors Pearce, S.H.S.; Thakker, R.V.
#submission submitted to the EMBL Data Library, August 1994
#accession S49341
#status preliminary
#molecule_type DNA
#residues 1-1078 #label PEA
#cross-references EMBL:X81086
REFERENCE
#authors Poliak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.
#journal Cell (1993) 75:1297-1303
#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism.
#cross-references M01D:94094324
#accession A49419
#status preliminary
#molecule_type DNA
#residues 178-180, 'K', 182-192 #label POL
#experimental_source family N
#note sequence inconsistent with nucleotide translation
#note sequence modified after extraction from NCBI backbone
#note 186-Arg mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism
#note sequence extracted from NCBI backbone (NCBIN:142453)

```

```

#accession B49419
#status preliminary
#molecule_type DNA
#residues 289-303 #label PO2
#experimental_source family E
#note sequence modified after extraction from NCBI backbone
#note 298-Lys mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism
#note sequence extracted from NCBI backbone (NCBIN:142455)
#accession C49419
#status preliminary
#molecule_type DNA
#residues 788-802 #label PO3
#experimental_source family J
#note sequence modified after extraction from NCBI backbone
#note 796-Tyr mutation is associated with familial hypocalcemic hypercalcemia and neonatal severe hyperparathyroidism
#note sequence extracted from NCBI backbone (NCBIN:142457)
SUMMARY
#note #length 1078 #molecular_weight 120672 #checksum 8159

Query Match 20.4%; Score 1296; DB 2; Length 1078;
Best Local Similarity 31.8%; Pred. No. 7, 84e-227;
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

Db 30 GDIILGLFPIHNG-VAADODLKSRESEVCEIRYRFGFRMLQAMIFAEINSSPALI 88
QY 37 GDFLLGLFSLHADCLQVNRPLVTSRSDS--FNGHGYLHFOAKRTVEELNSTALL 94
Db 89 PNLTLGRIFDICNTYSKALEATLSEVAQNKIDSLNDEFCNCSEHPIPTIYVAGATSG 148
QY 95 PNTLTGELYDYCESSESNY-ATLRVPAQGGTGLEMQR--DLRNSKVALIGDNTD 151
Db 149 VSTAVANLLGLPIPOVSTASSRLSNKNOFSRTLPNDHQATADADIIYFRKMW 208
QY 152 HAVTATLSPFLMPLVSEASSYILSGKRKPSFLRTIPSDRYOYEVIRLQSGMW 211
Db 209 VGTIADDDYGRGIEKFEAEERDICIPELISQYDDEE--TOHVEVYQNSTAV 266
QY 212 ISLVSGTGYGQGVADLELATPRGTCYAFKDVPLSLAQADPRQRMRLARAKTIV 271
Db 267 IYVSSGPDLEPL-KEIVRRITGKIWLASBAMSSLIAMPQYFHVVGITGALAKG 325
QY 272 VYVESN-RHLAGYFRSVLANLTGKWIASBDMA---IS-T-YTNVPQ-IQ-GI--G 320
Db 326 QIPGFEPLKAYHPRKSVNGFAKEFWETFNCHQEGKGPLVDVTLRGHESSDRS 385
QY 321 TVLGV---VA-100RO-VP-GL-KEF-EESY---VO-AVMGA-P-----RTCPDE-GSW-- 358
Db 386 NSPTAPPLCTGDNISVETPYIDYTHLRISYNYLAVYSIAHLODITCIPGRGLFT 445
QY 359 -GCTN-Q-LCRECHAFITTMPELGAFMSAAYNYEAYVAHGHQOL---L-GC--T 408
Db 446 NGSCADIKKVEAMOVYKHLRHNFETNMGEQVTFDECDLGNYSIINHLSPEDSIVF 505
QY 409 SGCA-RGPVYPMOLLOQIYKVNFLHK-KTVAFDKDGPLGYDIIAMDNGPE-WT-F 464
Db 506 KEVGYNYVAKKGERLFINEKILMSGFSEVFPNSRSCDLAGTRKGIIEGPTCCFEC 565
QY 465 EYIG--SA-SLSFVHLDINTKTIQWHEKNQVPSVCTRDCLGHHN-LVMSGHCCFEC 520
Db 567 VECPEDEYSDTASACNCPDDFMSNENHTSCIAKEIEFLSWTEPFGIALTFVAVGIF 625
QY 521 MPEBAGTFLNTSELHTCQPCGTBEMAPESGACFSRTVEFLGHEPISVLLAANTLILL 580
Db 626 LTAFLVGVIFKFR-NPIVKAATNRELSTYLLFSLCCFSSLP-FIGEPDWTCLRLQPA 683
QY 581 LLITAGLFA-WRLHFPVRSAGGRCLFMLGSLVAG-SCSLYSEFGKPTVPACLLRQPL 638
Db 684 FGSFVLCISCIIVKTNRLVLE--AKIPTSHRKMWGLNQLFLVLCFMQIYCAI 741
QY 639 FSLGFAIFLSCLTIRSFQVIIFKFSKVPF-FYHTWQNHGAGIFIVASTVHLFCLT 697

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Db	742	WLYAPSPSSYNOCLDEEIIFFITCEGSLMAFLGTC-LIAACPEFF-AFKSKXIDE	799
Oy	658	WLAAMTPPTPTREYORPHHVLIBCTEVN--SVGFLVAFAHNILLSISTVCSYIGKEUDE	755
Db	800	NFNNAKFTTFSMLFFITWISFIPAVASY-GRFVSAVEAIIAASFLLACIFENKIY	858
Oy	756	NYNEAKCVTFSLHLHFWSIAFFIM-SSIYQSGYLPRAVNTAAGLATLSSGFGYFLPKCY	814
Db	859	ILFKPSRNTIE 870	
Oy	815	VILCRPELNNTIE 826	
RESULT	3		
ENTRY	A56715	#type complete	
TITLE	calcium receptor (clone pnpCAR-4.0) - human		
ORGANISM	#formal_name Homo sapiens #common_name man		
DATE	19-Oct-1995	#sequence_revision 19-Oct-1995	#text_change 17-Mar-1999
ACCESSIONS	A56715		
REFERENCE	A56715		
authors	Garrett, J.E.; Capuano, I.V.; Hamerlund, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Follert, F. J. Biol. Chem. (1995) 270:12919-12925		
#journal			
#title	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.		
#cross-references	MolCellBiol 15:5279-5283		
#accession	A56715		
#status	Preliminary		
#molecule_type	mRNA		
#residues	1-1078	#label GAR	
KEYWORDS	#cross-references GB:U0759; NID:p683744; PID:p683745		
SUMMARY	glycoprotein: receptor; transmembrane protein #length 1078 #molecular_weight 120573 #checksum 7868		
Query Match	20.3%; Score 1293; DB 2; Length 1078;		
Best Local Similarity	31.8%; Pred. No. 3,22e-226;		
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;			
Db	30	GDIIIGGLFPIHFG-VAKQODLKSRESEVETIRYFRGFRMTQAMTFEISINSPALL	88
Oy	37	GDPLLAGFSLHADCLDVRHRRPVTSCDRSDS--FNGHGHLFQANRFTVEEINNSTALL	94
Db	89	PNILGRIPDICTVTSKALEATISFAQKIDSLNDEFCONSEHPISTIIVAGTSG	148
Oy	95	PNILGELIHDVCESSNNY-ATLRPAQOGCTHLEKOR--DIRNHSKVVALLIGEDNTD	151
Db	149	VSTAVANLLGFIYIPQVSYASSRSLSNKQKFSPLRTIPNDEHQATAMADIIIEYFRNM	208
Oy	152	HAVTALLSPLMLPVSSEAVSIIISGKRKPSFLRITPSDKYQVEIVRLQSGMWW	211
Db	209	VGTIAADDDVGRPIEKFREAEERDIDCFSLISQISDEEF--IQHYVEYIQNSTAKV	266
Oy	212	ISLVSGYGDGOLGVALLELATPRGICVAKQVPLSAQAGDPROMMLRLARATTV	271
Db	267	IVFSSSPDLEPLI-KRIIVRNITGKIWLASMASSLIAMPQYHVVYGGTIGFALAG	325
Oy	272	VVFESN-RHLAGVFRSVLANLTGKWKISEMA-----IS-T-YITNPQ-IQ-GI--G	320
Db	326	QIPGFEFLKLVHRRKSVHNGFAKFEWEETFNCHLQEGAKGPLPYDTFLRGHEESGDRS	385
Oy	321	TVLQ---VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVWGA-P-----RTCPD-GSW--	358
Db	386	NSSTAFRPLCTGDNISISVETPIIDTHLRISNVYLAIVSTAHADODITYLCPGRGLFT	445
Oy	359	-CGTN-Q-LCRECHAFITMMPELGAFMSAAVNYEAVVAHGHQD--L-QC--T	408
Db	446	NGSCADIKKYEAAMVLEKHLRLHNTNMNGOVFTFGCGDGVGVSYIIMHLSPEGSIYF	505
Oy	409	SGTGA-NGPYVPMQLQIYKVNFLHK-KTVAFDKQDPLGYDIIADNMNGPE-WI-F	464
Db	506	KEGVYINVYAKGERLFINDEKILMSGSEVPFNSCRDCLAGTRKKIIESEPCTCEC	565

[illegible]







[illegible]

Oy	354	P-SEGSMGCTQQLOR-E--CAFTITNMNPELGASMSAAV--N--V-Y--EAVYVAHGL	401
Dd	412	HNMQSLCPAGIACLDADAKPFDIGSKLLLESKMTIFGVSGDTILFDENGSPGYETIMNF	471
Oy	402	HQL-LG-CT--SGTC-ARGPYVMLOOLQIYKVFL-LHKTKVAFDDKGDPGLGYDYDIAM	455
Dd	472	KEMGKDY-FDVIINNGSMONGELMKDDEEV-WRSKSNIIR-SVGESEPOEKQIKYRRGEV	528
Oy	456	DMNGPEWTFEEYGSSLSLVPHHDINKTKIQWHGNKNVPVSVCTRCDLEGGHRLV-XGSH	514
Dd	529	SCCWTCPTCKENNEYVF-DE-VTCAKACQIGSWPIDDLTGCDLIPYQIRMGDPPIAAVF	586
Oy	515	HCFECMCMCEAGTELTNTSELHTQCPCGHEEAPRGSSACSRTVEPLGM-H-EPISLVLL	572
Dd	587	ACLGLATLFV-TYVFITYR-DTPVVWSSSNELCITIYIAGICLGLCT-PCLIAKPQIY	643
Oy	573	AANTLLLLLLLTGTGLPFMRHLTPVRBAGRGLCLFMGISLVAS-CSLVSFFKRPVPA	631
Dd	644	CYLQRIGIGLSPASYSALVKTNRIRIALIAGSKKCICTKKPRFSACAQIVAFILICI	703
Oy	632	CLLRPLESLFAFLPSCLTIISRQVLITFEFSRK-VPTFHMAQNHGAGIPIVYSTV	690
Dd	704	QLGITVALFIKEPPDIMHYPISRE-VYLICNTN-LGVTPPLIGNLLISCIE-YAfk	760
Oy	691	HLFLCLTLAMTWPRPTPREYORFPHELIVILECTEYNVSGLVAFANILLISIS-ITVC	749
Dd	761	TRNVANENNEKIYAFTMYTTCIIWLAF-V-PYFESNYKLIIMCESVS-TSMTVALGC	816
Oy	750	GRELLENENKACYFISLLHFVSIAMIAFTVSYIQGSYLPDAVNVLAGLALSIGFS-GY	808
Dd	817	MFPVKVYIILAKPERNVSASFITS	840
Oy	809	-FLPCRYIILDRPELNNTNEHQAS	831
RESULT	7		
ENTRY	JC2131	#type complete	
TITLE		metabotropic glutamate receptor 5 B - human	
ORGANISM		#formal_name Homo sapiens #common_name man	
DATE		28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996	
ACCSSIONS	JC2131		
REFERENCE	JC2131		
#authors	Minikami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994) 199:1136-1143		
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
	5.		
	#cross-references XrefID:94197696		
	#accession JC2131		
	#molecule_type mRNA		
COMMENT	1-1212 ##label MIN		
KEYWORDS	##residues This protein is coupled to guanine nucleotide binding proteins. glycoprotein; neurotransmitter; receptor; transmembrane protein		
FEATURE			
	580-604	#domain transmembrane #status predicted #label TM1\	
	617-637	#domain transmembrane #status predicted #label TM2\	
	644-664	#domain transmembrane #status predicted #label TM3\	
	694-714	#domain transmembrane #status predicted #label TM4\	
	738-759	#domain transmembrane #status predicted #label TM5\	
	773-794	#domain transmembrane #status predicted #label TM6\	
	803-827	#domain transmembrane #status predicted #label TM7	
SUMMARY	#length 1212 #molecular_weight 132579 #checksum 3155		
Query Match	12.9% Score 819; DB 2; length 1212;		
Best Local Similarity	27.0%; Pred. No. 2,87e+130;		
Matches	233; Conservative 229; Mismatches 334; Indels 68; Gaps 58		
Dd	5	LILSVLLLKEDVRG-SAOSERRRVAAHPGDIIIGALFSVHHOD-TV-DKVERKCG-AV	60
Oy	8	LLLSGLAVACMFSCORTSSPGFSFGPLLAGLFFSLHADLOVHRNPILVSCDRSD	67



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Db      61 R-BOYGIORVEAMLHTLERINSDPTLLPNTLIGCEIRDSCHMSAVALAESIEFIRDSLS 119
      68 SFGHGHYHLEQAMRFTEVEELNINSTALLPNTLIGELDYCVSESS-NY-AT--LR--VP 120
Db      120 SEEBEGLVRCVDSGSSFSRKKPIVIGPGSSVAIQVONLQLENIPQIAYSANSMOL 179
      121 AOGGTGHE-MQDRLRN-HSSK-VVALIGPDNDHATTAALLSPFLMPLYSEASSVIL 177
Db      180 SDTLFEYKRVVPSDAQARAWDIKRYNMTYVSAVHTEGNGESGMEAFKMSAKEG 239
      178 SGRKRPSEFLTPSDYQYEVYIRLQSGFWWISLVSGIDGQUGVQALELAPRG 237
Db      240 ICIAHSYKI-YSN-AGEOSFDKLLKLSHLPKARVAVACEGATVGLMAMRRLG-LA 236
      238 ICVAFKRVVPLSAQAGPRMOMRLA-R-ARTVYVVS-N-RHLAGVFRSIVLANLT 294
Db      297 GEFLLLSGDMA-DRYDT-DGTO-REAVGGITKL-QSPDVKWFDDYUUKLPETNHN 352
      295 GK-VWIASEDMALSTYITNPVIGIGTGVVAIQVQVGLKEFEBSYQVAVGAPRTC 353
Db      353 PMFOEFQNHFO-CRLEGFPOENSKYKTCNSSLTLLTHVQDSKMGFVINAISMAVGL 411
      354 P-BGSMGTNOLCR-E-CHAFTWMPBLGAFSMAA--N--V-Y--EAYVAVAHGL 401
Db      412 HNMOSLCPGAGLIDAMKIDGRKLSLMTNFTGVSQDILFDENDSPGRYEIMNF 471
      402 HQ-LG-CT--SGTC-ARGVYVPMQLQIYKVF-LHKRYAFDCKGRLGYDILAM 455
Db      472 KEMGKDY-FDIYVNGSWDNGELKADDEV-WSKKNITR-SVSEPECKQIKYIRGEV 528
      456 DWNGPWTFFVIGSASISPVHLINKRKIQMHGKNNOVPVSVCTRDCLBHHRLV-MGSH 514
Db      529 SCMTCPCKENEVEF-DE-YTCAQOLGSMPTDDLGCCLIPQYLRMDPREIAVVF 586
      515 HCFECPCEAGFTLNTSELHTCOPCTEKAPBGSSACSRIVEFGW-H-BEISLVLA 572
Db      587 ACGLATLFEV-TVFIYLR-DTPVYKSSRELCYIILAGICGLYCT-FCILAKPKQIY 643
      573 AANTLILLIGTAGLFAWMLHPVVSAGRLCFLMLGSLVAGS-CSLVSFGKPIVPA 631
Db      644 CYIORIGISPAWSYALVTKINRIARILAGSKKICTKPRMSACQDLVAFILICIT 703
      632 CLTRQPFISGFAFLSCLIRSFQVLIIFKFSRK-VPTFYHTWAQNHGAGIFVYSSIV 690
Db      704 QLGIVALEFMEPDMHDPISRE-VYLLCNTN-LGVVTPGYNGLLISCF-YAFK 760
      691 HFLCLTWLMMTPRPTREORPRLVILECTEYNSVGLVAFAHNLISIS-TFVCSYL 749
Db      761 TRNVPAFNEAKYIAFTMYTTCIIMLAF--VP-IYFGSNKIITMCPVS-LSATVALGC 816
      750 GKELPENYNAKCVTFSLHLHFVSWIAFTMSSLYGSIYLPVAVNLGLATLSGSGF-GY 808
Db      817 MFVPKYIILAKPERNVSATTS 840
      809 -FLPKCVIILCRELNTNTEHOAS 831

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RESULT 8  
ENTRY A42916 #type complete  
TITLE metabotropic glutamate receptor mGluR5 - rat  
ORGANISM J. Biol. Chem. (1992) 267:13361-13368  
DATE 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 29-Jan-1999

ACCESSIONS A42916  
REFERENCE A42916  
#authors Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.  
#journal J. Biol. Chem. (1992) 267:13361-13368  
#title Molecular characterization of a novel metabotropic glutamate receptor mGluR5 coupled to inositol phosphate/Ca<sup>2+</sup> signal transduction.  
#cross-references M0ID:92317054

#accession A42916  
#status Preliminary  
#molecule\_type mRNA  
##residues 1-1171 ##label ABE  
##cross-references GB:D10891; NID:g220813; PID:d1002186; PID:g420814  
##experimental\_source brain  
#note sequence extracted from NCBI backbone (NCBI:107749, NCBI:107750)  
KEYWORDS G protein-coupled receptor; transmembrane protein  
SUMMARY #length 1171 #molecular\_weight 128289 #checksum 8594

Query Match 12.8%; Score 814; DB 2; Length 1171;  
Best Local Similarity 27.1%; Pred. No. 2,86e-129;  
Matches 234; Conservative 222; Mismatches 340; Indels 67; Gaps 60;

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Db      5 LILSVLLLEDVNG-SAOSSEKRVVAMHGDIIIGLFEVNHQF-TV-DKVERKKG-AV 60
      8 LILSLQLAAYACWAFSCQRTSSPGFSLGDFPLAGLFSLHADCLOVRRRLVTSQDRSD 67
      61 R-BOYGIORVEAMLHTLERINSDPTLLPNTLIGCEIRDSCHMSAVALAESIEFIRDSLS 119
      68 SFGHGHYHLEQAMRFTEVEELNINSTALLPNTLIGELDYCVSESS-NY-AT--LR--VP 120
Db      120 SEEBEGLVRCVDSGSSFSRKKPIVIGPGSSVAIQVONLQLENIPQIAYSANSMOL 179
      125 TGHLE-MQR--D-LRN-HSSK-VVALIGPDNDHATTAALLSPFLMPLYSEASSVIL 178
Db      180 DKTLFEYKRVVPSDAQARAWDIKRYNMTYVSAVHTEGNGESGMEAFKMSAKEG 239
      179 GKRPSEFLTPSDYQYEVYIRLQSGFWWISLVSGIDGQUGVQALELAPRG 238
Db      240 ICIAHSYKI-YSN-AGEOSFDKLLKLSHLPKARVAVACEGATVGLMAMRRLG-LAG 296
      239 CVAFKRVVPLSAQAGPRMOMRLA-R-ARTVYVVS-N-RHLAGVFRSIVLANLTG 295
Db      297 GEFLLLSGDMA-DRYDT-DGTO-REAVGGITKL-QSPDVKWFDDYUUKLPETNHN 352
      296 K-VWIASEDMALSTYITNPVIGIGTGVVAIQVQVGLKEFEBSYQVAVGAPRTC 353
Db      353 PMFOEFQNHFO-CRLEGFPOENSKYKTCNSSLTLLTHVQDSKMGFVINAISMAVGL 411
      354 P-BGSMGTNOLCR-E-CHAFTWMPBLGAFSMAA--N--V-Y--EAYVAVAHGL 402
Db      412 HNMOSLCPGAGLIDAMKIDGRKLSLMTNFTGVSQDILFDENDSPGRYEIMNF 471
      403 QL-LG-CT--SGTC-ARGVYVPMQLQIYKVF-LHKRYAFDCKGRLGYDILAM 456
Db      472 KEMGKDY-FDIYVNGSWDNGELKADDEV-WSKKNITR-SVSEPECKQIKYIRGEV 528
      457 DWNGPWTFFVIGSASISPVHLINKRKIQMHGKNNOVPVSVCTRDCLBHHRLV-MGSH 515
Db      529 SCMTCPCKENEVEF-DE-YTCAQOLGSMPTDDLGCCLIPQYLRMDPREIAVVF 586
      516 HCFECPCEAGFTLNTSELHTCOPCTEKAPBGSSACSRIVEFGW-H-BEISLVLA 573
Db      587 ACGLATLFEV-TVFIYLR-DTPVYKSSRELCYIILAGICGLYCT-FCILAKPKQIY 643
      574 AANTLILLIGTAGLFAWMLHPVVSAGRLCFLMLGSLVAGS-CSLVSFGKPIVPA 632
Db      644 CYIORIGISPAWSYALVTKINRIARILAGSKKICTKPRMSACQDLVAFILICIT 703
      633 CLTRQPFISGFAFLSCLIRSFQVLIIFKFSRK-VPTFYHTWAQNHGAGIFVYSSIV 691
Db      704 QLGIVALEFMEPDMHDPISRE-VYLLCNTN-LGVVTPGYNGLLISCF-YAFK 760
      692 LFLCLTWLMMTPRPTREORPRLVILECTEYNSVGLVAFAHNLISIS-TFVCSYL 750
Db      761 TRNVPAFNEAKYIAFTMYTTCIIMLAF--VP-IYFGSNKIITMCPVS-LSATVALGC 816
      751 KPELPENYNAKCVTFSLHLHFVSWIAFTMSSLYGSIYLPVAVNLGLATLSGSGF-GY 808
Db      817 MFVPKYIILAKPERNVSATTS 839
      809 -FLPKCVIILCRELNTNTEHOAS 831

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QY 809 FLPRCYVILCRPELNTNEHFOAS 831

RESULT 9

ENTRY A41939 #type complete

TITLE G protein-coupled glutamate receptor - rat

ORANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Mar-1998

ACCESSIONS A41939: S15362

REFERENCE A41939

#authors Houamed, K.M.; Kuiper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, E.R.; Almers, W.; Hagen, F.S.

#journal Science (1991) 252:1318-1321

#title Cloning, expression, and gene structure of a G protein-coupled glutamate receptor from rat brain.

#cross-references M0ID:92022526

#accession A41939

#status preliminary; not compared with conceptual translation

#molecule\_type nucleic acid

##residues 1-1199 ##label HOU

##cross-references GB:M61099; NID:9397806; PID:9204460

##experimental\_source cerebellum

#note sequence extracted from NCBI backbone (NCBID:60785)

REFERENCE S15362

#authors Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.

#journal Nature (1991) 349:760-765

#title Sequence and expression of a metabotropic glutamate receptor.

#cross-references M0ID:91156047

#accession S15362

##status preliminary

##molecule\_type mRNA

##residues 1-1199 ##label MAS

##cross-references EMBL:X57569; NID:956646; PID:956647

KEYWORDS G protein-coupled receptor; transmembrane protein

SUMMARY #length 1199 #molecular\_weight 133335 #checksum 5211

Query Match 12.7%; Score 810; DB 2; Length 1199;

Best Local Similarity 27.6%; Pred. No. 1,806;126;

Matches 231; Conservative 216; Mismatches 325; Indels 66; Gaps 52;

Db 41 MDDVITGALFSVHOPPAEVK-P-ERKC--GEIREQYGIORPEAMFHTLTKINADPVL 96

QY 35 LPBDFLLAGFLSHADCLQYRHRPLVTSCHRSDFNCHGLQAMFTELEINNTALL 94

Db 97 PNITGSEIRDCSWHSSVALEQSIETIRDSLSIRDEKDLNRCPLDGOQLPPGRIKPT 156

QY 95 PNITGSEIRDCSWHSSVALEQSIETIRDSLSIRDEKDLNRCPLDGOQLPPGRIKPT 142

Db 157 AGVIGGSSVAIQVONLQDLPIDPAISATISIDSKTLVYFLAVPSDTLQARAML 216

QY 143 A-DIGDNDHAATTAALLSPFLMPVSYEASSVILSGKRKPFSLTIPSDYQVEIV 201

Db 217 DIYKRYNMIVSAVHTEGNGSGMDAFKELAOEGICIAHSPKI-YSN-AGEKSPRL 274

QY 202 RLIOGSGWVSLVSGISGDTGQLGVQALBELAIPRGICVAFKDVVPSAAGDPRMORRM 261

Db 275 RKLRELRPKARVVVCEGNTVRGLSAMRRLGVGEFSLIGSDQWADRDEV--IEGEY- 331

QY 262 LRL-AR-ARTVVVFSN-RHLAGVFFRSVLANLTGKVIASDMDAISTYITNVPIQG 318

Db 332 VEANGGITTL-OSPEVRSDDYFLKRLDTNTRNPFPE-FMQHRQ-CRLGHLLENP 388

QY 319 IGVLVGAIQOROVPGIKEEESYQAVMGA-PRTC--PGSGMGTNQLCR-ECHAEITW 374

Db 389 NFKVCTGNSLEENYQDSKMGFVIAIYAMAHGIONMHALCPGVGCLDAMKPRDGR 448

QY 375 NMEEL--GASMSAAY-N-V-Y--EAVYAVAHGLHOLL-G-CTS--GTC-ARGPYTPW 420

Db 449 KLIDFLIKSSFVSGEEVWDEKGDAPGRYDINMLOYTEANR-YDYVHVHGVHGEVLNI 507

QY 421 QLLQGIYKAVFL-LHKKTVAFDKGDPLGYVDIIMDMWNPENMTFVIGSASLSPLHDI 479

Db 508 DDYKIQ-MNKGWVR-SYCEPCLKGOIKVIRKGEVSCCNICTACKENEFVO-DEF-TOR 563

QY 480 NKTIKIMHGRKNNOVPYSVCTRCCLBGRHLY-MGSHCCCFECMPCBAGVFTLWTSALTCQ 538

Db 564 ACDIGMWPNAELTGCPEIPRYLEMSDIBSIATAIFSC-GILVTFVLIFVLYR-DIPV 622

QY 539 PCGTETMAPEGGSACHSRVFEFLGWHEPISVLIAMANTLLLLLLIGTALFA-WRLHTVP 597

Db 623 VSSSRELCYIILAGIFLGYCP-FLIAKPTTSCYLDRLLVGSSAMCYSAIYTKINR 681

QY 598 VRSAGRLCTFLMIGSLVAG-SCSLYSFFCKPTVPACLLPQPLFSIGFAIFLSCILIRSPQ 656

Db 682 IARILAGSKKICTRRPRMSAMQVITIASILISQTLIVTLLIMPEMPLTSPSIRE 741

QY 657 LVITFEFSTR-VPTFYHTMAQNHGACIYIVSSIVHFLCLTLMAMWTPRTREIQRPH 715

Db 742 -VYLIC-NTSNLGVAVPVNGLLIMCTY-YAFKRNVPANFNEAKYIAFTYTCTIIM 798

QY 716 LVILCTEVNSGFLVAFANILLSTS-IFVCSYLKELPEYNEAKCVTFILLHFTSM 774

Db 799 LAF--VP-IYFGSNYKIITCFVSLSVYALGCFKPKXYIITIAKPEKNVSAFTTS 853

QY 775 IAFFTMSIYOGS-YLPAYNVLAGIATLISGFGFVLPKCYVILCRPELNTNEHFOAS 831

RESULT 10

ENTRY JH0563 #type complete

TITLE metabotropic glutamate receptor 4 precursor - rat

ORANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 13-Sep-1998

ACCESSIONS JH0563

REFERENCE JH0561

#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.

#journal Neuron (1992) 8:169-179

#title A family of metabotropic glutamate receptors.

#cross-references M0ID:92110002

#accession JH0563

##molecule\_type mRNA

##residues 1-912 ##label TAN

#experimental\_source brain

COMMENT This protein is coupled to a G protein and evokes a variety of functions by mediating intracellular signal transduction.

CLASSIFICATION #superfamily metabotropic glutamate receptor 4

KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

FEATURE 1-32

33-912

588-610 #domain transmembrane #status predicted #label TR1

628-645 #domain transmembrane #status predicted #label TR1

657-675 #domain transmembrane #status predicted #label TR1

700-720 #domain transmembrane #status predicted #label TR1

751-772 #domain transmembrane #status predicted #label TR1

786-807 #domain transmembrane #status predicted #label TR1

822-847 #domain transmembrane #status predicted #label TR1

98,301,454,484, #binding\_site carbonydrate (Asn) (covalent) #status predicted

621,689,695,859, #binding\_site phosphate (Ser) (covalent) #status predicted

870

SUMMARY #length 912 #molecular\_weight 101818 #checksum 808

Query Match 12.6%; Score 799; DB 2; Length 912;

Best Local Similarity 25.9%; Pred. No. 2,816;126;

Matches 206; Conservative 222; Mismatches 307; Indels 59; Gaps 50;

Db 75 GHRLEAMFALDRINNDLLPNITLGARILDTGSRDTHALEQSLTFVQALIEKGTIEV 134

QY 73 GYHLFQAMRTVEIINNSALLPNITLGELVDVCS-ESSNVYATLR-VPA--Q-QGTG- 126



GENETICS	#cros-references GB:M0518; NID:g205400; PID:g205401
CLASSIFICATION	GLUR4
KEYWORDS	neurotransmitter receptor
SUMMARY	length 912 #molecular-weight 101846 #checksum 818
Query Match	12.5%; Score 798; DB 2; Length 912;
Best Local Similarity	25.9%; Pred. No. 4,45e-126;
Matches	206; Conservative 222; Mismatches 307; Indels 59; Gaps 50;
Db	75 G1HRLKAMLEALDRINNDPDLIPNITLGARILDCSDTHALDQSLTFYBALIEKDGTEV 134
Qy	73 GYHFLQARFVEEININSTALPITITGLYELDYVCS-ESSNVAATLR-VA--Q-QGTG- 126
Db	135 RCGSGGPIITKPRRVGVIGACSSSSIMVANILRLFKIPQISYASTADLSDNSYDF 194
Qy	127 H-LEMQRDLNRHSSKVAVALGPDPTDHAVTTALLSPFLMPLVSEKSSVILSGKKRFP 185
Db	195 FSRVPSDPTYOQAQMDIVRALKNNVYSTLASEGSVEGVEAFIQKSRNGVCIA-QS 253
Qy	186 FLRTIPSPKQVEVIVLALDSFGVWVSLVGSYDQDGLQVQLLELATPRG-ICVAFKD 244
Db	254 VKIPREPKTGFDKTIKRLLETSAAG--IITPANEIDIRRVLEAARAOQTGHFFMG 311
Qy	245 V-VPLSAQAQ-PMQRMMLRLAARTTVAVFESNRLAGVFRFSVVALNDTGV-MA 301
Db	312 DSMGSKAPVRLLEVAE-GAV-FILPKRSVRSFDRFSSRTLDNRRNIMFEFEDN 369
Qy	302 EDW-AISYIITNVGIGIGIVGLVALIQQRVPL-KEFESYQAVMGAPRCP--EGS 357
Db	370 FHCKLSRHALKKSHIKCTNRESIGODSAVEDGKVQYVIDAVYAMGHALHANRDLCP 429
Qy	358 W-CG-TNQ-LORECHA--FTTW-NMPELGAFSMSAAVN-YEAAYVAHGHQLD-G-CT 408
Db	430 GRVGLCPMDVDGDTOLLKTYIRNVFSGIAGNPVTENMGDAPRXYDIYQOLKNGSA-E 488
Qy	409 S--GTGAR-GVYVYWMQLQIYKYNFL-LHKTYAFEDKDDPLGYDIIAND-WNGEWT 463
Db	489 YKVIQSWT-DHLHLRIER-MQWPGSQQLPRISCLPQPGERRKTVKMGACCHNCEPC 545
Qy	464 FEVIGSASLSPVHLINKTKIQWGHKNQVAVSCTKDCLEGHRLVWGSHHCCFECMPC 523
Db	546 -TG-YQYQVNDYTKCTQPYDMRPENNTSQPRTIVYLEMDSPPAVLPLPLAVVGIATL 603
Qy	524 EAGFTLNTSELTQPCQTEEMAEQSSAGCSRTVEFLGWER-ISTVL-IAANTLILL 581
Db	604 FVVVY--FVRINDPPIYKASGRELSYLLAGIFLCYATTEFLMAIEDPLGTSLEIRIFGL 661
Qy	582 LIGNAGLEFAMWLHPVVRASAGRCFLMLGSLVAGSCSLVSFEKPIVPACLLNQPLFSL 641
Db	662 GMSISYALALTKNRIYRIPEQGRKRSAPRFISPAQALITFLILSLQ-LGICV-WFV 719
Qy	642 GFALFLSCLTIRSOVLIIFFKSTK-VPTFHTWAQNHGAGIFVYSYVHLFCLTWLA 700
Db	720 VDPSSVYDPODQTLDPREFARGVKC-DISDLILCLIGSMILMTVCYFAATKRGVP 778
Qy	701 MMTPEPTREYO-R-F-PHLY-ILLECTEVNSVGFVAFANITLISLTPYCSLIGKELP 754
Db	779 ETLENAKDIGFTMTTTCVILAFIPIFFGISQASDKLYIQTTLTFVSVLSASVSLGMLY 838
Qy	755 ENYNEAKVCTFSLILHFVSWIAFPTMS-SIVQGSY-L-PAVNVLADGLATLSGGRFS-G-YF 809
Db	839 MKPYIILFHEDN 852
Qy	810 LPKCYVILCPRELN 823
RESULT	12
ENTRY	S71376 #type complete
TITLE	glutamate receptor homolog - cherry salmon
ORGANISM	glutamate receptor homolog masou #common_name cherry salmon
DATE	11-Mar-1998 #sequence revision 17-Apr-1998 #text change



01-May-1998  
#accessions S71376  
#reference KudoKawa, K.; Miyashita, T.; Nagasawa, H.; Kudo, Y.  
#journal FEBS Lett. (1996) 392:71-76  
#title Cloning and characterization of a bifunctional metabotropic  
receptor activated by both extracellular calcium and  
glutamate.  
#cross-references MUID:96354880  
#accession S71376  
#status not compared with conceptual translation  
#molecule-type mRNA  
#residues 1-1218 #label KUB  
#glycoprotein: phosphoprotein  
KEYWORDS  
FEATURE  
603-625 #domain transmembrane #status predicted #label TM1\  
640-660 #domain transmembrane #status predicted #label TM2\  
672-690 #domain transmembrane #status predicted #label TM3\  
717-737 #domain transmembrane #status predicted #label TM4\  
761-782 #domain transmembrane #status predicted #label TM5\  
796-817 #domain transmembrane #status predicted #label TM6\  
826-850 #domain transmembrane #status predicted #label TM7\  
104,223,403,525,  
757 #binding-site carbohydrate (Asn) (covalent) #status  
predicted\  
636,699,961 #binding-site phosphate (Ser) (covalent) (by protein  
kinase C) #status predicted\  
705 #binding-site phosphate (Thr) (covalent) (by protein  
kinase C) #status predicted\  
892 #binding-site phosphate (Ser) (covalent) (by  
CAMP-dependent kinase) #status predicted  
SUMMARY #length 1218 #molecular-weight 136838 #checksum 1674  
Query Match 12.5%; Score 797; DB 2; Length 1218;  
Best Local Similarity 27.8%; Pred. No. 7,04e-126;  
Matches 201; Conservative 195; Mismatches 271; Indels 55; Gaps 44;  
Db 166 IAGVIGPGSSVAIQVQLQFNIPQIAYSAISIDSKITFKYFLRVVPSDILQARAI 225  
141 VVALIGPNDTDAVTTAALLSPFLMPLVSEASSVLSKRRFPSTLRITPSDKOYEVI 200  
Db 226 LDIVKRYNNTYVSAVHTEGNYESGMAEKELASOGLCIAHSDKI-VSN-AGEKHFDRL 283  
QY 201 VLLQSGFWWVILSVGSDYDQGLQVQLLELATPRGICVARKDYVPLSAQAGDPRMQM 260  
Db 284 LRLKLERLPKAVVYVCFCCGATVRCGLMAMRLG-VAGFLLIGSGMADRDVEVEGYEO 342  
QY 261 MLRT-AR-ARTVYVVFNS-RRLAGVFFRSVYLANLTGK-VWIASEDMAISTYITVPGI 316  
Db 343 EAVGGI-TVKLSEEVTSFDYFLKRLNTNTRNPF-PE-FMQHRFO-CRIPGHPLEHM 398  
QY 317 OGIGIVLGVAITGROVPGIKE-FEESYVQAVMGARPTCEGSGKGNOLCREC-HAFTTW 374  
Db 399 NYRKNCSGESLEDNVYDQSKMGFVINAAYMAOGLDHMSHLCPGHVGLCKAMPIDGS 458  
QY 375 NPPEL-GAF-SMSAAY-N-V-Y-EAVYVAVHGHQLLG-CYS-CGTC-ARGPVPM 420  
Db 459 QLLEFLMRLSFVGSVEDYWFDENGDTPGRYELMNLQYEPG-AFPIYVNGSWHEQSLI 517  
QY 421 QLLOQIYKYNFL-LHKRIYAFDDKGPDLGYDIIAMDWMGPETFEVISAASISLPHDI 479  
Db 518 DDYMQO-IVRSOMV-LTSVSEPCSKGEIVIRKGEVSCWICITACADNDIYO-DEF-TCT 573  
QY 480 NKTIKQWHEKKNNOVPYSVTRDCLBEGHRLV-MGSHCCFCFCMPCAGAGFLINTSEHTQ 538  
Db 574 ACDDGAWPDPLEGECPITLRLYLEWGNPESIVQVFACLGIVTSFVTEIFVLYR-DTPV 632  
QY 539 PGCTEEMAPEGSSACFSRIVEFLGHEPISLYLANTLTLLTISTAGLFA-WRLHTPV 597  
Db 633 VSSSRRELCTIILAGIFLGIQIP-FTLLIOPVYASCYLDRLVLGVSATGYSALVTKTR 691  
QY 598 VRSAGRCLCEFLMGLSVAG-SCSLYSFEGKPTVPACLLRPFLSIFAIETSLTIRSFQ 656

Db 692 IARIAGSKKKICTRRKPREMSAMQVLAGLVSYOLTLEVT-II-LE--PPMPKSP 747  
QY 657 LVITF-----KSTKVPFFHYHMAQNHAGIVYSSIVHLFLCLTWLAMPPTREIQ 711  
Db 748 SIRE-VFLIC-NTSTVGMVAPLGLNGLIMCTY-YAKTRVNPVNEAKIATMTYT 804  
QY 712 RPHVILIECTEVSNGVIFVAFHNLIS-TEFCSYLGEKLEPENYNEAKVFTSLIH 770  
Db 805 CLIMLAF--VP-ITYGSNKIITTSFSVSLSTVRLGCMFSPKIYIILAKPRENRSAT 861  
QY 771 FVSWIAFFTMSIYQGS-YLPAVNVLAGIATLDSGSGFYFLPKCYVILCRPELNTHEHQ 829  
Db 862 TS 863  
QY 830 AS 831  
RESULT 13  
ENTRY JH0561 #type complete  
TITLE metabotropic glutamate receptor 2 precursor - rat  
ORGANISM Rattus norvegicus #common\_name Norway rat  
DATE 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 13-Sep-1998  
ACCESSIONS JH0561  
REFERENCE JH0561  
#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.  
#journal Neuron (1992) 8:169-179  
#title A family of metabotropic glutamate receptors.  
#cross-references MUID:92110002  
#accession JH0561  
#molecule-type mRNA  
#residues 1-872 #label TAN  
#experimental\_source brain  
COMMENT This protein is coupled to a G protein and evokes a variety of  
functions by mediating intracellular signal transduction.  
CLASSIFICATION #superfamily metabotropic glutamate receptor 4  
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein;  
transmembrane protein  
FEATURE  
1-18 #domain signal sequence #status predicted #label SIG\  
19-872 #product metabotropic glutamate receptor 2 #status  
predicted #label MET\  
568-590 #domain transmembrane #status predicted #label TM1\  
605-625 #domain transmembrane #status predicted #label TM2\  
637-665 #domain transmembrane #status predicted #label TM3\  
680-700 #domain transmembrane #status predicted #label TM4\  
726-747 #domain transmembrane #status predicted #label TM5\  
761-782 #domain transmembrane #status predicted #label TM6\  
795-819 #domain transmembrane #status predicted #label TM7\  
203,286,338,402,  
547 #binding-site carbohydrate (Asn) (covalent) #status  
predicted\  
601,675,827,837,  
843 #binding-site phosphate (Ser) (covalent) #status  
predicted\  
832 #binding-site phosphate (Thr) (covalent) #status  
predicted  
SUMMARY #length 872 #molecular-weight 95773 #checksum 5740  
Query Match 12.1%; Score 769; DB 2; Length 872;  
Best Local Similarity 25.4%; Pred. No. 2,64e-120;  
Matches 210; Conservative 218; Mismatches 343; Indels 56; Gaps 43;  
Db 26 LILEGDLVIGGLFPVH----Q-KGCP-AEEGCPVVE-H-RGIQRLFAKIFALDRINRDPH 77  
QY 33 FSLPDPFLIAGLFSHADICQVRHRPDIYTSQDRSPSFGHGHYLPQAVRTVEENNSFA 92  
Db 78 LIPGVRLGHINDOSKDPHALDQALDVRASLSRGAQSGRIICPDGSAATSDAPATVAT 137  
QY 93 LIPNTILGELIDVCSSESNVYA-TL--RVPAQOGT-G--HL--EMQBDLRNHSKSYVA 143  
Db 138 GVIIGSYSDVSIVQVNLRLFOIPQISYASTAKLSDSKRYDYFARTVPPDFQAKAAE 197



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QY 144 -LIGPNDTHAVTAALLSPFLMPLVSYEASVYLSGKRRFSPSLTIPSDKYQVEIVR 202
DB 198 ILRFENWTVSTVASEGDYGETIEAFELARARNICVATSEKVGAMRAAFEGVVAL 257
QY 203 LQSFQFWMSISLVGSYDYGQALDELATPRGICVAFKQVPLS-AQAGDPRQRM 261
DB 258 LQPSAR--VANVLFPSDARELLAATQRLN-ASFTWASDGMGALESVAGSERAAEA 314
QY 262 LRLARATVVVVVFSNRHLAGVFFRSVLANLKGKWIASEDAIATYITNPAGIIGT 321
DB 315 I-TIELASTPISDFAYFOSLDPMNNSRNPWFREFEHFHCFRO--RDCAAHSRAVP 371
QY 322 YLGVAIQOQVPELKEFESESYVO-AVMGAP--RTCEGSM-CGTNQLCBECAFTTWNP 377
DB 372 FQESKIMEVNAVYAMAHAL--HNMHRAL-CPNTTHCDAMRPVNRRLTKDFVLNKP 429
QY 378 -ELGAFSMAAANYAVAYAVAHGLHQLGCTSGT--C-ARGVYVWQQLQ-ITYVNF- 431
DB 430 APPRPADTDEVRDFRFGGICGRYNTFTYLRAGSGR-YR-YQKVGYSWABGLTIDTSFIW 487
QY 432 L-LHK-KT--VAFDQKGPGLGYDIIAMDWNGPEWTFEYIGSASLSPYHLIDINKTIOM 486
DB 488 ASPSAGPLASRSEPCLONEVKSQPGEVCCMLICQPYEY-RIDEF-TCADGLGW 545
QY 487 HG-KNNQVAVSVCTRDCLSGHNLVYSGHCCFECPCCEGTFPLNTSELHCOPTCEEM 545
DB 546 PNASLTGCFELPOEYLRMGDAMAVGVTTIACIGALATLFLVGLGVFNHNPVYKASGREI 605
QY 546 AEGSSACSRVTEFEGWHEPISLVLLANTLILLLIGTAGIFARLHTPYRSAGRL 605
DB 606 CYLLGCVFLCYMTFVETAKPSTAVCTLRGLGTAFSVCSALLTKNRLARIFG-GA 664
QY 606 CCLMGSLVAGSCSLSTFEGKPTVPACLLRQPLFSGLGFALISCLTIRSFQVLIIFKST 665
DB 665 REGA-QRPPEFSPASOVALICLISGOLLIVAMLYVEAPGTKEAPERREVVYLRCHN 723
QY 666 KPTPTHTAQNNGAGIEYIVS-STVHLFLCTLWLMKMPRTREPQRPV-LVILECTE 723
DB 724 RDA-SMGLSLAVNVLIACTL-YAEKTRCPENENAEFIGTWTTCIIMLAFPIFY 781
QY 724 VMSVGLVAFANHLL-SISTFVCSYLGKELPENYENACVFESLLHRYSWAFTMS 782
DB 782 VMSDVRVQTTMCVSVSLSGSVLGLCPAPKIHILLFOPQKNVSH 828
QY 783 IYQSYLPAVNVLAGLATSIGFS-GY-FLPKCYILLCPRELNTBH 827

RESULT 14
ENTRY JH0562 #type complete
TITLE metabotropic glutamate receptor 3 precursor - rat
ORGANISM Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
ACCESSION JH0562
REFERENCE JH0561
#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glutamate receptors.
#cross-references WID:92110002
#accession JH0562
#molecule_type mRNA
#residues 1-879 #label TAN
#experimental_source brain
COMMENT This protein is coupled to a G protein and evokes a variety of
functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
FEATURE
1-722 #domain signal sequence #status predicted #label SIG\
23-879 #product metabotropic glutamate receptor 3 #status
577-599 #domain transmembrane #status predicted #label TRI\

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614-634 #domain transmembrane #status predicted #label TRI\
646-664 #domain transmembrane #status predicted #label TRI\
669-709 #domain transmembrane #status predicted #label TRI\
735-756 #domain transmembrane #status predicted #label TRI\
770-791 #domain transmembrane #status predicted #label TRI\
804-828 #domain transmembrane #status predicted #label TRI\
209,292,414,439 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
610,845 #binding_site phosphate (ser) (covalent) #status
predicted\

SUMMARY #length 879 #molecular_weight 98959 #checksum 5581
Query Match 11.9%; Score 759; DB 2; Length 879;
Best Local Similarity 25.8%; Pred. No. 2,56e-118;
Matches 206; Conservative 202; Mismatches 340; Indels 50; Gaps 44;

DB 57 GCRINE-D-RGQRELFAMFAIDELINKDNYLLPGKLGVLHIDTOSRQTYALEQLEVR 114
QY 63 CDRSDFNGHGHRLQARFVEELINNSTALLPNTLLEYLYDVS-BSSNYATLR-VP 120
DB 115 ASLTRYDEAEYVCPGSAIOENIPLLAGVIGSSVSIVQANLRLFOIPISTAST 174
QY 121 AQGGT-GHLE-X-Q-R-DLRHSSKYVA-LIGPNDTHAVTAALLSPFLMPLVSYEAS 173
DB 175 SAKLSDKSRDYFANTVPDPFYQAAMAEILRFENWTVSTVASEGDYGETIEAFQEA 234
QY 174 SVLSGKRKFPFLRTIPSDKYQVEIVRLQSFQWMSISLVGSYDYGQALGQALEELA 233
DB 235 RLNRICATAEYVGNISNRKISDSYIRELQKPNAR--VYVLFMSDSDSRELLAANRYN 292
QY 234 PRGICVAFKDVPLSA-QAGPRQRMRLARARTTVVFNFSNRHLAGVFFRSVLAN 292
DB 293 -ASFVWASDGMGAOESLYKSGEYVAGITELASHVRODFRQFOSLNPNNRNPMF 351
QY 293 LIGKWIASEDAIATYITNPAGIIGT-V-LGVAIQ-QRQPLKEFESESYVQAVMGAP 350
DB 352 RQFWBOKFOCSLQNF-RNHROYCDHLAIDSSNYQESKIMEVNAVYAMAHALHKMORT 410
QY 351 RCPREGSW-CGTNQLCBECAFTTWNP-ELGAFSMAAUN-VYBAVYAVAHGLHQLD-G 406
DB 411 LCPNTTKLQDANKILDGKLYEYLLKNTAPRPNKGASIVAFDFPGOGMKYXNPN 470
QY 407 -CTSGT-C-A-R--GP-VYPMQLQIYKVNFLHK-KTVA-FDQKGPGLGYDIIA 454
DB 471 LQOTGKSYLKVGHMA-ETLSLDV-D-S-IHW-SRNS-VPTSOCSDPAPNEMKMNOPGD 525
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DB 526 VCCWICICPEPEYEV-VDEF-TCMDCGPGQWFTADLSCYNLPEDYIKMEDAMAIQVYTI 583
QY 515 HCCFECMCEAGTFPLNTSELHCOGTEWAPDESSACFSRTVEFLGWHEPISLVLLA 574
DB 584 AGLGFLCTCIVITVRIKNNPPLVAKSGRELCTLLFVSVLSYCTTFEIKRPSVICAL 643
QY 575 NTLLELLIGTAGLAPMRHTPTVVSAGGRCLCELMGLSVAGSGSLYFEGPVPYACLL 634
DB 644 RLIGLTSFAICYALLTKTNCIARIP-GVYNGAQRKFI-SPSSQVFCIGLILVIV 701
QY 635 RQPLSLSGFAILSLTIRSPOLVILFKESTKVPFFHTHMQNHAGLFIYVSSR-VHLE 693
DB 702 MYSWLLIETP-GTRRYLPEKRETVILKC-NVQDSKEISITVDVVLVILCTVYAFETR 759
QY 694 LCLTWLAWMTPRPTREYQ-RFPH-LVILECEVNSVGLVAFANHLLISIFVCSYLGK 751
DB 760 KCPENPNAKFIGFMNTTCIWLAFILFYVTSDDYVQTTMKISLSGFFVLGCLF 819
QY 752 ELPEYNNKAKCYTFSLLHFVSWIAFTMSSLYQSYLPAVNVLAGLATSIGFS-GY-F 809
DB 820 APKVIHLEFOPQKNVYTH 837
QY 810 LPKCYVILLCPRELNTBH 827

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RESULT 15  
ENTRY 149142 #type complete  
TITLE metabotropic glutamate receptor 8 - mouse  
ORGANISM Mus musculus #common\_name house mouse  
DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Sep-1998

ACCESSIONS  
REFERENCE I49142  
#authors Duvoisin, R.M.; Zhang, C.; Ramonell, K.  
#journal J. Neurosci. (1995) 15:3075-3083  
#title A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb.  
#cross-references MIMD:95239344  
#accession I49142  
#status preliminary: translated from GB/EMBL/DBJ  
##molecule\_type mRNA  
##residues 1-908 ##label RES  
##cross-references EMBL:U17252; NID:g854728; PID:g854729

GENETICS  
#gene mGluR8  
CLASSIFICATION #superfamily metabotropic glutamate receptor 4  
KEYWORDS neurotransmitter receptor  
SUMMARY #length 908 #molecular\_weight 101413 #checksum 2996

Query Match 11.6%; Score 740; DB 2; Length 908;  
Best Local Similarity 24.6%; Pred. No. 1,51e-114;  
Matches 210; Conservative 246; Mismatches 332; Indels 66; Gaps 52;

Db 17 LIAKFWILTMORTHQOEYAHSLRDLIILGGLFPVHA---KG-ERG-V-PC--GDLK 68  
14 LAVAYCMAFSC-QRTES---SPGFSLPDGLAGLFLSHADCLQVRHRLPLTSCDRSDSF 69

Db 69 KKGIIHLEMLVAIDQTNKDPDLNITLGVRIIDTCSDRTALAEOSTIFVQALIEKDA 128  
70 NGCHYHLPQAMRFEVDINNSTALPLNITLGYELDYDVS--ESSNVAITLR-VPA--OQGT 125

Db 129 SDVKCANGDPPIFTKPKDISGVIGMAASVSIMVANIILFKIPQISYASTAPELSDNTR 188  
126 GHLE-MQRD--LRNHSSKVVALIGPDNTDHAVTALALSPFLMPLVGYEASSVILSGRK 182

Db 189 YDFFSRVPPDSYQAMVIVITAGLNIVSTLASGNYGSGVEAFTQISREIGVCIA 248  
183 FPFSLRTIPSDKYQEVIVRLQSFQWVWISYSGYQQLGVQALDELATPRG-ICVA 241

Db 249 QSQKIPREPRGEFEKIKRLTFPNARA--VIMEFANEDDIRGILEAAKKL--NOSGHFIW 305  
242 FKDVPLSAQAGD-PRQRMRLARARITVVVFSNRH--LAGVFRSVVLANITLTK-VW 298

Db 306 IGSDSWG-SK-IAPVYQOEIEAGAVTILPKRASIDGFRYFRSRTLANNRRNWFAPFS 363  
299 IASDEMAISTYITNPQIGIGYLGVAIQQR-VPL-KEFEESYQAVMGAPR-T-CP 354

Db 364 EGNFGCKSGSHGKRNHIKCTGLERIARDSSYEQSKVOFIDAVYSMAVALHMHKEL 423  
355 EGSW-C-GTNQLCRECHAF-T-WN-MPELGAFMSAAYN-VYEAVYVAHGLHQLL-G- 406

Db 424 CPQYIGLCPRMVITIDGKELGYIRAVNENSGAPVTENENGDAKGRDIFQYQINNKT 483  
407 CTS--GTCAH-GPYVPMQLLOQYKYNFLHAKKT-VAFDDGDPGLGYDITIAMDNQPEW 462

Db 484 EYKIIHMT-NOLHLKVED--MOMANREHTHPASVCSLPCKPGRKRTVKGVPCCMHGCR 540  
463 TFEVIGSASLPYHLDINKIKIQHGKKNQPVSVCTRDCLGHHRLVMGSHCCFECCMP 522

Db 541 CEGYNT-QVDEL-SCETCPLDQRPINRTGCGQIPILIKLEHSPAVVAVYLAIIIGIAT 598  
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Db 599 TFIYIVTFVRNDPTPIVASGRELIVLTGFLCYSTIFILMAADPTLICSFRRIIFGLG 658  
583 IGTAQLFAMRLHTPVVASAGRLCFMLGLSVAGSCSLYSPFGKPTVPACLLRQPLFSLG 642

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QY 702 WTPRPTREY--QR-F-P-HL-VIECTEVNSVGLVAFANILLISTFVCSYIGKEIPE 755

Db 776 TENEAKPIGFTMYTTCIWLAFPIFFGTAQSAEKMYIOTTTLVMS-LSASVSLGMLY 834  
QY 756 NYNDAKCVTSLLHFPVSWIAFTMS-SYQGS---YLPRAVNLGATLSGGS-G-YF 809

Db 835 MPKVYIIIFHPEQN 848  
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Search completed: Fri Mar 17 13:16:00 2000  
Job time : 48 secs.







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(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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\*\*\*\*\*  
MSEARCH protein - protein database search, using Smith-Waterman algorithm  
Run on: Fri Mar 17 13:22:47 2000; Maspar time 14.26 Seconds  
Tabular output not generated. 785.421 Million cell updates/sec

Title: >US-09-361-652-2  
Description: (1-842) from US09361652.pep  
Perfect Score: 6366  
Sequence: 1 MLFWAHLHLISLOLAAYCM.....NTEHFOASIDYTRRCGTT 842

Scoring table: PAM 150  
Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCR9\_COMB 5:backfiles1

Statistics: Mean 36.380; Variance 177.107; scale 0.205

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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2	1316	20.7	1085	1	US-08-485-Sequence 5, Applicatio	1.69e-100
3	1316	20.7	1085	2	US-08-480-Sequence 5, Applicatio	1.69e-100
4	1316	20.7	1085	2	US-08-943-Sequence 5, Applicatio	1.69e-100
5	1316	20.7	1085	3	US-08-353-Sequence 5, Applicatio	1.69e-100
6	1293	20.3	1078	2	US-08-943-Sequence 7, Applicatio	1.70e-98
7	1293	20.3	1078	3	US-08-353-Sequence 7, Applicatio	1.70e-98
8	1293	20.3	1078	1	US-08-485-Sequence 7, Applicatio	1.70e-98
9	1293	20.3	1078	1	US-08-484-Sequence 7, Applicatio	1.70e-98
10	1293	20.3	1078	2	US-08-480-Sequence 7, Applicatio	1.70e-98
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12	1282	20.1	1079	2	US-08-480-Sequence 8, Applicatio	1.54e-97
13	1282	20.1	1079	3	US-08-353-Sequence 8, Applicatio	1.54e-97
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## ALIGNMENTS

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DE	Sequence 5, Application US/08484565		
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CC	Sequence 5, Application US/08484565		
CC	Patent No. 5763569		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Edward M. Brown		
CC	APPLICANT: Steven C. Hebert		
CC	APPLICANT: James E. Garrett, Jr.		
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
CC	TITLE OF INVENTION: MOLECULES		
CC	NUMBER OF SEQUENCES: 20		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESS: Lyon 6 Lyon		
CC	STREET: First Interstate World Center		
CC	STREET: Suite 4700		
CC	STREET: 633 West Fifth Street		
CC	CITY: Los Angeles		
CC	STATE: California		
CC	COUNTRY: USA		
CC	ZIP: 90071		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: FASTSEQ		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/484,565		
CC	FILING DATE: 7 June, 1995		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	PRIOR APPLICATION DATA: Including application		
CC	PRIOR APPLICATION DATA: described below: 9		
CC	APPLICATION NUMBER: 08/353,784		
CC	FILING DATE: 9 December, 1994		
CC	APPLICATION NUMBER: PCT/US/94/12117		
CC	FILING DATE: 21 October, 1994		
CC	APPLICATION NUMBER: U.S. 08/292,827		
CC	FILING DATE: 23 August, 1994		
CC	APPLICATION NUMBER: U.S. 08/141,248		
CC	FILING DATE: 22 October, 1993		



















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ID	US-08-943-966-7		
AC	xxxxxx		
XX			
D7			
XX			
DE	Sequence 7, Application US/08943986		
CC	Sequence 7, Application US/08943986		
CC	Patent No. 5962314		

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CC CC GENERAL INFORMATION:
CC CC APPLICANT: Edward M. Brown
CC CC APPLICANT: Steven C. Hebert
CC CC APPLICANT: James B. Garrett, Jr.
CC CC TITLE OF INVENTION: CALCULOM RECEPTOR-ACTIVE
CC CC TITLE OF INVENTION: MOLECULES
CC CC NUMBER OF SEQUENCES: 20
CC CC CORRESPONDENCE ADDRESS:
CC CC ADDRESSEE: Lyon & Lyon
CC CC STREET: First Interstate World Center
CC CC STREET: Suite 4700
CC CC STREET: 633 West Fifth Street
CC CC CITY: Los Angeles
CC CC STATE: California
CC CC COUNTRY: USA
CC CC ZIP: 90071
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: FASTSEO
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/08/943, 986
CC CC FILING DATE: 03-OCT-1997
CC CC CLASSIFICATION: 530
CC CC PRIOR APPLICATION DATA:
CC CC APPLICATION NUMBER: 08/484, 565
CC CC FILING DATE: 7-June-1995
CC CC APPLICATION NUMBER: 08/353, 784
CC CC FILING DATE: 9 December, 1994
CC CC APPLICATION NUMBER: PCT/US/94/12117
CC CC FILING DATE: 21 October, 1994
CC CC APPLICATION NUMBER: U.S. 08/292, 827
CC CC FILING DATE: 23 August, 1994
CC CC APPLICATION NUMBER: U.S. 08/141, 248
CC CC FILING DATE: 22 October, 1993
CC CC APPLICATION NUMBER: U.S. 08/009, 389
CC CC FILING DATE: 23 February, 1993
CC CC APPLICATION NUMBER: U.S. 08/017, 127
CC CC FILING DATE: 12 February, 1993
CC CC APPLICATION NUMBER: U.S. 07/934, 161
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CC CC APPLICATION NUMBER: U.S. 07/834, 044
CC CC FILING DATE: 11 February, 1992
CC CC APPLICATION NUMBER: U.S. 07/749, 451
CC CC FILING DATE: 23 August, 1991
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Heber, Sheldon O.
CC CC REGISTRATION NUMBER: 38, 179
CC CC REFERENCE/DOCKET NUMBER: 213/006
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: (213) 489-1600
CC CC TELEFAX: (213) 955-0440
CC CC TELEX: 67-3510
CC CC INFORMATION FOR SEQ ID NO: 7:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 1078 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: Protein
CC CC SEQ SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
Db Db Query Match 20.3%; Score 1293; DB 2; Length 1078;
Db Db Best Local Similarity 31.8%; Pred. No. 1,70e-98;
Cc Cc Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;
Cc Cc 30 GDIIIGLGFPIHFG--VAAKDQDKSRPSEVEICIRYNGFRWLQAMIFALIEINSSPAL 88
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Cc Cc 89 PNLTIGRIIDTCNTYSKALEATLSFYAOKIKDSLNDCEHCNSEHIPSTIAYVGATGSG 148
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 QY 815 VILCREPLNTE 826

RESULT 10  
 ID US-08-480-751-7 STANDARD; PRT: 1078 AA.

AC xxxxxx  
 DE Sequence 7, Application US/08480751  
 CC Patent No. 5858684  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Edward F. Nemeth  
 CC APPLICANT: Edward M. Brown  
 CC APPLICANT: Steven C. Hebert  
 CC APPLICANT: Forrest H. Fuller  
 CC APPLICANT: James E. Garrett, Jr.  
 CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
 CC MOLECULES  
 CC NUMBER OF SEQUENCES: 20  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Lyon & Lyon  
 CC STREET: First Interstate World Center  
 CC STREET: Suite 4700  
 CC STREET: 633 West Fifth Street  
 CC CITY: Los Angeles  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 90071  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: FASTSEQ  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/480,751  
 CC FILING DATE: 7 June, 1995  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC PRIOR APPLICATION DATA: Including application  
 CC PRIOR APPLICATION DATA: described below: 9  
 CC APPLICATION NUMBER: 08/353,784

CC FILING DATE: 9 December, 1994  
 CC APPLICATION NUMBER: PCT/US/94/12117  
 CC FILING DATE: 21 October, 1994  
 CC APPLICATION NUMBER: U.S. 08/292,827  
 CC FILING DATE: 23 August, 1994  
 CC APPLICATION NUMBER: U.S. 08/141,248  
 CC FILING DATE: 22 October, 1993  
 CC APPLICATION NUMBER: U.S. 08/009,389  
 CC FILING DATE: 23 February, 1993  
 CC APPLICATION NUMBER: U.S. 08/017,127  
 CC FILING DATE: 12 February, 1993  
 CC APPLICATION NUMBER: U.S. 07/934,161  
 CC FILING DATE: 21 August, 1992  
 CC APPLICATION NUMBER: U.S. 07/834,044  
 CC FILING DATE: 11 February, 1992  
 CC APPLICATION NUMBER: U.S. 07/749,451  
 CC FILING DATE: 23 August, 1991  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Heber, Sheldon O.  
 CC REGISTRATION NUMBER: 38,179  
 CC REFERENCE/DOCKET NUMBER: 213/004  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (213) 489-1600  
 CC TELEFAX: (213) 955-0440  
 CC TELEX: 67-3510  
 CC INFORMATION FOR SEQ ID NO: 7:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 1078 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQ SEQUENCE 1078 AA; 120573 MW; 6153012 CN;

Query Match 20.3%; Score 1293; DB 2; Length 1078;  
 Best Local Similarity 31.8%; Pred. No. 1,70e-98;  
 Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

DB 30 GDIIIGLEPIHFQ-VAAKDDDKSRPESVEICIRNFGRFRLQAMIPALIEINSPALL 88  
 QY 37 GDPFLAGLFSIADCLQVRRHPLVTSRDS--FNGGHYLFQAMRTVEEINNSTALL 94  
 DB 89 PNLITGRIPTCNTVSKALEATLSFVAONKIDSINLDEFNCSEHPISTAVVATGSG 148  
 QY 95 PNLITGRIPTCNTVSKALEATLSFVAONKIDSINLDEFNCSEHPISTAVVATGSG 151  
 DB 149 VSTAAVNLGLFYIPQVSIASSSLSKNOFKSLRTIPNDEHQAATMADIIIEFRNMW 208  
 QY 152 HAVTTAALISPLMLPVSYEASVILSGKRFPSPFLRTIPSDKYOVEIVRLLOSFGWVW 211  
 DB 209 VGTIAADDDYGRPGIEKREAEEDICIDISELISQYSEDEE--IQHVEVIONSTAKV 266  
 QY 212 ISLVSYGDYGLQVQALDELATPGLICVAKRDVPLAQAGDPRMQMRLAARTTV 271  
 DB 267 IYVSSGPDLEPL-KEIVRRNITKILWASEVMASSLIAMPQYFHVVGITGPKLAG 325  
 QY 272 YVFSN-RHLGAVFRSYVLANLTGKWIASEDMA---IS-T-YITNVPQ-IQ-GI--G 320  
 DB 326 QIPGREFLAKYHPKRSVHNGFAKFEETFNCHIQDEAKGKPLPYDTLRGHEBGDFS 385  
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 DB 386 NSSTFRPLCTGDEMISSEVETPYIDYTHLRISYNYLVAVYSIAHLODIYCLPGRGLFT 445  
 QY 359 -CGTN-Q-LCRCHAFPTWNPDELGAFMSAANYEAVYAVAGLHDL---L-GC---T 408  
 DB 446 NSCADIRKVEAMQVLKHLRLNFTNNMGEOVTEDECGDLVGNYSIIMHLSPEDEGSIVF 505  
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 DB 506 KEVGYNYAKKGERLFINNEKILMSGFSREVPFNSCRDCLAGTRKGIIEGPTCCFEC 565  
 QY 465 EVIG--SA-SLSPVHLIDINKTIOMHGKNNOVPSVCTRDCLEGNHR-LVMSGHCCFEC 520



[illegible]

CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
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CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Heber, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/006  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 489-1600  
CC TELEFAX: (213) 955-0440  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1079 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 1079 AA; 120867 MW; 6054255 CN;

	Query Match	20.1%	Score 1282;	DB 1;	Length 1079;
	Best Local Similarity	31.2%	2rec. No. 1,54e-97;		
	Matches 269;	Conservative	240;	Mismatches 280;	Indels 73; Gaps 50.
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Db	89	PNNLIGRIEFTCTVSKALEPATLSEYVAKNKIDSLNIDFPCNSEHLPSTIAVVGATGSG	148		
QY	95	PNITGLGYELVYCESSSNVY-ATLRVPAQOGTGLEMR-PDLNHSKVALALGPNTD	151		
Db	149	VSTIAVNLGLFYIROYVYSSSSSLNKNKYSEFLTIPNDERQATAMADIIEFPWM	208		
QY	152	HAVTTALLSLFLMPLVSYEASSYILSGKKRFPBELTIPSDKYQVEVIRLLOSPFWW	211		
Db	209	VGIITAADDDYGRPIEKFREAEERDICIPISELSIQSYSDDEE--IQQVEVIONSTAKV	266		
QY	212	ISLVSGYGDYQQLVQALELALTRGICVAFKQVDPVLSAQAGDRQRMMLRLARATTV	271		
Db	267	IIVRSSGPDLEPLI-KEIVRRNITGRIMLASSEAMASSLLAMPBYHVGATIGFGIKAG	325		
QY	272	VVVSFN-RHNLGVEFFRSVLIANTLKGWIASDEWA---IS-T-YIINVG-IQ-GI-G	320		
Db	326	QIQPREFILOVHRKRVNHNSEAFKEEFEEFNCHLGQAGPLPYDFVFSHREGGRLL	365		
QY	321	TVLGV-A-IQ--Q-RQ--VP-GL-KEP-EEST--VO-AVNGA-P----PTCPGS-W--	358		
Db	386	NSSTAFLRLCTGDENINSVETPYVDYEHRLISYNNVLAVYSIMHALODITYCLPGRGLT	445		
QY	359	-CGIN-Q-LGCEHAFTTMNPELGARSMASAAVYVLAIVAHGHLQ---L-GC--T	408		
Db	446	NGSCADIKKYEAMOVLYKHLRLHNTNNAGQEVITFDECGDLVGNYSIINMHLSPDGIVF	505		
QY	409	SGTGA-RGPVPMQLLOQIYKVNFLHK-RTVAFEDDGDPGLGYDDIADAMNGE-W-T	464		
Db	506	KEVGYNNVYAKKGRRLINEKILMSEFSEVPVNSRPPCOGIRKGLIEGETOCFEC	565		
QY	465	EVIG--SH-SLSPVHLIDINKTIQIMHKKNNQVPSVCIROCLBGNH-LVMSHHCCFEC	520		
Db	566	VECPDGEYSGEIADACDKCPDDEFSWNSNHTSLAKIEFLTMEPRGIALTFYAVIGIF	625		
QY	521	MPCAGFELNLSLHTQPGCTEEMAREGSACSRVELLGMHEPISTVLIANLITLL	560		
Db	626	LTAFLVGLFIKFR-NTPIYKATNBELSYLLFLSLCCSSSLF-FIGEPDWTICRLQRA	663		
QY	581	LLITAGIGFA-WRIHTFVVSAGRGLOCLWLGSLVAG-SCSLYSFGKFPVPACLLROPL	638		







0Y	698	WLAMWTPEPTREYQEPFLVILECTEVN- SVGFLVFAHNNILLSIFPWSYIGRKLPE	755
Db	800	NFNEAKFTTFESMLFIPIYIWISFIPYASTY- GKRVSAVEVJAIILASFGLIACIFENKVV	858
0Y	756	NYNEKACFTFLLSHFVIAFFFTM-SSYOGSYLPAVNVLAGLATLSGGSGFYFLPKY	814
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ID	US-08-353-784-8	STANDARD:	PRT: 1079 AA.
XX	xxxxxx		
Dt			
XX			
DE	Sequence 8, Application US/08353784		
XX			
CC	Sequence 8, Application US/08353784		
CC	Patent No. 6011068		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Edward F. Nemeth, Edward M.		
CC	APPLICANT: Brown, Steven C. Hebert,		
CC	APPLICANT: Bradford C. Van Wageningen, Manuel		
CC	APPLICANT: F. Balandin, Forrest H. Fuller,		
CC	APPLICANT: Eric G. Delmar, and Scott T. Moe		
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		
CC	TITLE OF INVENTION: MOLECULES		
CC	NUMBER OF SEQUENCES: 20		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESS: Lyon & Lyon		
CC	STREET: First Interstate World Center		
CC	STREET: Suite 4700		
CC	STREET: 633 West Fifth Street		
CC	CITY: Los Angeles		
CC	STATE: California		
CC	COUNTRY: USA		
CC	ZIP: 90071		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: FASTSEQ		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/353,784		
CC	FILING DATE: 9 December, 1994		
CC	CLASSIFICATION: 514		
CC	PRIOR APPLICATION DATA:		
CC	PRIOR APPLICATION DATA: including application		
CC	PRIOR APPLICATION DATA: described below: 8		
CC	APPLICATION NUMBER: PCT/US/94/12117		
CC	FILING DATE: 21 October, 1994		
CC	APPLICATION NUMBER: U.S. 08/292,827		
CC	FILING DATE: 23 August, 1994		
CC	APPLICATION NUMBER: U.S. 08/141,248		
CC	FILING DATE: 22 October, 1993		
CC	APPLICATION NUMBER: U.S. 08/009,389		
CC	FILING DATE: 23 February, 1993		
CC	APPLICATION NUMBER: U.S. 08/017,127		
CC	FILING DATE: 12 February, 1993		
CC	APPLICATION NUMBER: U.S. 07/934,161		
CC	FILING DATE: 21 August, 1992		
CC	APPLICATION NUMBER: U.S. 07/834,044		
CC	FILING DATE: 11 February, 1992		
CC	APPLICATION NUMBER: U.S. 07/749,451		
CC	FILING DATE: 23 August, 1991		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Heber, Sheldon O.		
CC	REGISTRATION NUMBER: 38,179		
CC	REFERENCE/DOCKET NUMBER: 209/069		
CC	TELECOMMUNICATION INFORMATION:		

CC	TELEPHONE: (213) 489-1600
CC	TELEFAX: (213) 955-0440
CC	TELEX: 67-3510
CC	INFORMATION FOR SEQ ID NO: 8:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 1079 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 1079 AA: 120867 MW: 6054255 CN:
Query Match	20.1%; Score 1282; DB 3; Length 1079;
Best Local Similarity	31.2%; Pred. No. 1,54e-97;
Matches 269; Conservative	240; Mismatches 280; Indels 73; Gaps 50;
Db	30 GDILIGLGFPHFG-VAAKDODLKSRDESEVCIRYNGRFGWQAMIFAEINSSPLL 88
Oy	37 GDFLLAGLSFSLHACLOVRRHPRPLVTSDDSDS--FNGHGHLFOAMRFTYEEFNSTALL 94
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Oy	95 PNITLGYELDVDCSSSNVY-ATLRVPAQOGGTGLEVR--DLRNHSSKVALIGPDND 151
Db	149 VSTAVANILGLFTYPOVSASSSKLSNKOYSFLFTPNDEHQATAMADITFYRMKM 208
Oy	152 HAVTTAALSLFELMPLIVSYEASVILSGKKRPFSLTIPSDKYOVEVIRLLQSGWVW 211
Db	209 VGTIAADDDYRPIEXFRRDEAEED:CIDPSELISQSDDEE-10QVVEVYQNSTAVY 266
Oy	212 ISLVGSYEDYQLOVQALSELATRGICVAFKDVPLSAQGPFRQRMRLIARARTIV 271
Db	267 IVFSSGPDLEPLI-KEIVRRNIGRIWALSEAWASSSLIAMPYEFHVVGITIGFLKAG 325
Oy	272 VVFSN-RHLAGVFRSSVLANLIGKWIASEDMA---IS-T-YITNPG-IQ-GI--G 320
Db	326 QIPGFRFLQVHRKRSVHNGFAKEMEELFNCHLODAGKPLVDTFYRSHDEGNRLI 385
Oy	321 TVLGV-A-IQ--Q-RO-VP-GI-KEF-EESEY---VQ-AVWGA-P-----RTCEGS-W-- 358
Db	386 NSTAFRLCLGDENINSVEEPYDYEHLISYVAVYSIAHALDITGCPGSLPT 445
Oy	359 -CGTN-Q-LCECAFTTMNPELIGAFSMAAIVNIEAVIAVHGHQL--L-GC--T 408
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Oy	455 EVIG--SA-SLSPHLDINKRKIQMHGKNNOVPVSVCTRCLEIGHNR-LVMSHHCCEFC 520
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Db	684 FGISFVLICISILVKNRVLVFE-AKIPDSFRKMWGINOLFVLCFTEFMQICII 741
Oy	639 FSLGFAIFLSCLTIRSPOLVIFKFSFKVPT-FYHMAQKHGAGIVIVSVTHFLCLT 697
Db	742 WLTYAPSSRYKNHLEDEIFITICBESLMALSLIGYTC-LLAALCFPP-AKSKAKPE 799
Oy	698 WLAWMTRPFRKYORFPHVLILECTEVN--SVGFLVAFANILLSTIVCSIGLEPE 755
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Oy	756 NYNNAKCVTSILIHFWSTIAFLTM-SSIQSGYIDAVNVLAGLATLISGFSGYFLPKCY 814
Db	859 ILFSPRNTIEVRSIAA 880



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RESULT 14  
 ID US-08-943-986-8 STANDARD; PRT; 1079 AA.  
 AC xxxxxx  
 XX  
 XX  
 XX  
 DE Sequence 8, Application US/08943986

Sequence 8, Application US/08943986  
 Patent No. 5962314  
 GENERAL INFORMATION:  
 APPLICANT: Edward M. Brown  
 APPLICANT: Steven C. Hebert  
 APPLICANT: James E. Garrett, Jr.  
 TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
 MOLECULES  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: First Interstate World Center  
 STREET: Suite 4700  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: FASTSEQ

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,986  
 FILING DATE: 03-OCT-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/484,565  
 FILING DATE: 7-June-1995  
 APPLICATION NUMBER: 08/353,784  
 FILING DATE: 9 December, 1994  
 APPLICATION NUMBER: PCT/US/94/12117  
 FILING DATE: 21 October, 1994  
 APPLICATION NUMBER: U.S. 08/292,827  
 FILING DATE: 23 August, 1994  
 APPLICATION NUMBER: U.S. 08/141,248  
 FILING DATE: 22 October, 1993  
 APPLICATION NUMBER: U.S. 08/009,389  
 FILING DATE: 23 February, 1993  
 APPLICATION NUMBER: U.S. 08/017,127  
 FILING DATE: 12 February, 1993  
 APPLICATION NUMBER: U.S. 07/934,161  
 FILING DATE: 21 August, 1992  
 APPLICATION NUMBER: U.S. 07/834,044  
 FILING DATE: 11 February, 1992  
 APPLICATION NUMBER: U.S. 07/749,451  
 FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:  
 NAME: Heber, Sheldon O.  
 REGISTRATION NUMBER: 38,179  
 REFERENCE/DOCKET NUMBER: 213/006  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1079 amino acids  
 TYPE: amino acid  
 TOPOLOGY: 1linear

CC MOLECULE TYPE: Protein  
 SEQ SEQUENCE 1079 AA; 120867 MW; 6054255 CN;

Query Match 20.1%; Score 1282; DB 2: Length 1079;  
 Best Local Similarity 31.2%; Pred. No. 1,54e-97;  
 Matches 269; Conservative 240; Mismatches 280; Indels 73; Gaps 50;

Db 30 GDIILGGLPFIHFQ-VAAKDQDLSKRPSESEICIRYFRGFRMLQAMIFAIEEINSSPSLL 88  
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 95 PNTLGEYELDYCVSESSNYV-ATLRPAQQTGHLEMR--DLRNHSSKVALIIPDNTD 151  
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 212 ISLVSYGQYGLQVGLAELELATPRGICVAFKDVYPLSQADPRQRMMLARATTV 271  
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 Db 684 FGISFVLCISCLVKNRVLVFE--AKIPTSFHRKMWGLNQFLVFCFPMOILCII 741  
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 QY 815 VILCRELNTEHFOASIDYDT 836

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 ID US-08-485-588-8 STANDARD; PRT; 1079 AA.  
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XX DE Sequence 8, Application US/08485588
XX CC Sequence 8, Application US/08485588
XX CC Patent No. 5688938
CC GENERAL INFORMATION:
CC APPLICANT: Edward M. Brown
CC APPLICANT: Steven C. Hebert
CC APPLICANT: Forrest R. Fuller
CC APPLICANT: James E. Garrett, Jr.
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
CC TITLE OF INVENTION: MOLECULES
CC NUMBER OF SEQUENCES: 20
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Lyon & Lyon
CC STREET: First Interstate World Center
CC STREET: Suite 4700
CC STREET: 633 West Fifth Street
CC City: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90071
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/485,588
CC FILING DATE: 7 June, 1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC PRIOR APPLICATION DATA: including application
CC PRIOR APPLICATION DATA: described below: 9
CC APPLICATION NUMBER: 08/353,784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292,827
CC FILING DATE: 23 August, 1994
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CC APPLICATION NUMBER: U.S. 07/749,451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hebert, Sheldon O.
CC REGISTRATION NUMBER: 38,179
CC REFERENCE/DOCKET NUMBER: 213/005
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1079 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1079 AA: 120867 MW: 6054255 CN:
SQ
Query Match 20.1%; Score 1282; DA 1; Length 1079;
Best Local Similarity 31.2%; Pred.No.1,54e-97;
Matches 265; Conservative 240; Mismatches 280; Indels 73; Gaps 50.

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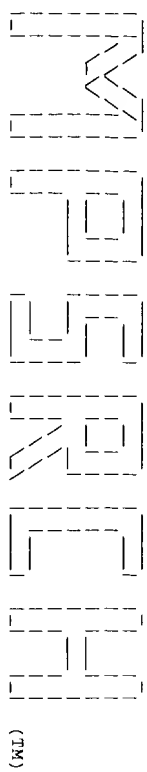
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Qy	37	GDFLAGLFSTHADLOVHRHPLVPTSCDRSDS--FNHGYSHLQAMFVTEINNSTALL	94
Db	89	PNMTIGRPIEDTCVTSKALBATLSPFAONKIDSLNDEFCNCSEHPTSLVAVGATSG	148
Qy	95	PNITIGLYLVYCESSSNVY-ATLRVAQOCTGHELQOR--DLRNHSSKVALIGPNTD	151
Db	149	VSTAVANLLGLFYIPQVSYASSSSLLSNKYQSFELTIPNDEHQATAMADIIEYRWN	208
Qy	152	HAVTAALSLPFMLPLVSYEASSVTLGKRKRFELTIPSDKQYEVIVRLQSFQWV	211
Db	209	VGTIADDDYRPRGLEKFEAEERDCLIDFELSISOYSDDEE--IQQVEVIONSTAKY	266
Qy	212	ISLVSYSDYDQOLGVOALEELATPRGICVAFKDVVP--SAQAGPRMQRMMLRLARATTV	271
Db	267	IVFSSGPDLEPLL-KELVRNITGRIMIASSEMASSSLAMPREYHVAGTIGFGKAG	325
Qy	272	VVFSN-RHLGVEFSSVLANLIGKMWISEDMA----IS-T-YITNPG-ID-GI--G	320
Db	326	QIPGREFLQYVHRKSVHNGFAKEFEETFNCHLOEAGPLPVDTVFVRSHEEGNRL	389
Qy	321	TVLGV-A-ID-Q-RQ-VP-GL-KEF-EESV---VQ-AVWGA-P-----RTPCBGS-W-	358
Db	386	NSSTAFRLCTGDNINSVETPYNDYEHRLSIVNVLAVYSIAHALODIYTCPLRGLETT	445
Qy	359	-CGIN-Q-LCRECHAFITMNPBELGAFSMAKNAVYEAVALAHGHOL---L-GC--T	408
Db	446	NGSCADIKYVAMQVLAHLRLNLTNNKMBGYTFDECGDLVGNYSILNHLSPEDGSIVF	505
Qy	409	SGTCA-RGPVPMOOLQOIKYVNLHLK-KTVAEDDGDGPLYDIIIAMWNGPE-WT-F	464
Db	506	KEVGYVNYAKGRGLFINEKILMISGFSREVPFNSRPOQATRKGIIEGEPTCFEC	565
Qy	465	EVIG--SA-SLSPYHLDNKTQIOMHKNQVPRVSVCTROCLBEHNR-LVMGSHCCFEC	520
Db	556	VECPDGEVSGETDASACDKCPDGFWSXENNTSCIAKCEFLPAMTEPGIALTLFAYLGIF	625
Qy	521	MPCEGATPLNTSELHQOPOCTSEMADEGSACSFVEFVGHWEPISTIVLLAANTLLL	580
Db	626	LTAFLVGFIFNR-NTPIVAKINNELSYLLFLSLCCFSSLP-FIEBPDMTCRLQOPA	683
Qy	561	LLIGTAGLFA-WRHTTPVVRAGGRLOCFLMGSLVAG-SCSLVSFEKPIVPACLLRQPL	638
Db	584	FGISFVLCISILVKNRNLVLFPE-AKIPFSFRKMMGNLQELVFLCTFMOLICII	741
Qy	639	FSLGAIATLSCTT-RSFOLVYTFEFSTKVP-FHTHAQNHGAGIPIVASYVHLLCLT	697
Db	742	WLYTAPSSYNNHELEDIIPITQEGSLMALGSLIYTC-LLAALCFP-AFKSRKLP	799
Qy	698	WLAMMTPRPTREYQRPFLVLLECTEVN--SVGLVFAFHILLISTIFVCSYGRKLP	755
Db	800	NFNNAKPTFSKULFFIYVLSFIDAVASTY-GKRVSAVEYVIAIILASFGLLACTFEKVV	858
Qy	756	NYNEKACTFESLLHFVSWIAFFTM--SSIYGSTYPAVNVNLAGLATLSGFSGYFLPKCY	814
Db	859	IIIFKPSRNTIEEVRSSATAHA 880	
Qy	815	VILCRPELNTNTEHFQASIDQY 836	

Search completed: Fri Mar 17 13:23:19 2000  
Job time : 32 secs.









(TM)

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MSearch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Fri Mar 17 13:13:13 2000; Maspar time 39.37 Seconds  
506.520 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-361-652-2  
Description: (1-842) from US09361652.pep  
Perfect Score: 6366  
Sequence: 1 MLFWAHLHLJSLQLAVAYCW.....NTEHFOASIDYTRCGTT 842

Scoring table: PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq36  
1:geneseqp

Statistics: Mean 38.664; Variance 175.009; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1316	20.7	1085	1	W89563	2.60e-107
2	1316	20.7	1085	1	W54844	2.60e-107
3	1316	20.7	1085	1	W38272	2.60e-107
4	1293	20.3	1078	1	W54845	3.67e-105
5	1293	20.3	1078	1	W89565	3.67e-105
6	1293	20.3	1078	1	W1889	3.67e-105
7	1293	20.3	1078	1	W38273	3.67e-105
8	1282	20.1	1079	1	W94928	3.91e-104
9	1282	20.1	1079	1	W54847	3.91e-104
10	1282	20.1	1079	1	W89565	3.91e-104
11	1282	20.1	1079	1	W38275	3.91e-104
12	1204	18.9	1068	1	W32059	7.44e-97
13	1204	18.9	1068	1	W38273	7.44e-97
14	1201	18.9	1068	1	W54845	1.14e-96
15	1201	18.9	1068	1	W89564	1.14e-96
16	1201	18.9	1068	1	W1888	1.42e-96
17	1069	15.6	1219	1	W25763	2.73e-84
18	993	15.6	1058	1	W25762	3.08e-77
19	974	15.3	779	1	W94921	1.77e-75
20	832	13.1	850	1	W94901	2.29e-62
21	814	12.8	1056	1	W25764	1.03e-60
22	810	12.7	906	1	R25081	2.41e-60
23	806	12.7	1180	1	R64253	5.63e-60

24	810	12.7	1199	1	R25080	GLU-G-R subtype 1a.	2.41e-60
25	807	12.7	1212	1	R64254	Human mcIUR5b.	4.55e-50
26	800	12.6	877	1	R64255	Human mcIUR5c.	2.00e-50
27	802	12.6	906	1	R64250	Human mcIUR1B.	1.31e-50
28	804	12.6	912	1	R82658	Human mcIUR4.	8.55e-50
29	801	12.6	912	1	R72092	Human mcIUR4.	1.62e-50
30	800	12.6	1056	1	W25765	Amino acid sequence of HSMGJUR1.	2.00e-50
31	800	12.6	1194	1	R42199	Amino acid sequence of HSMGJUR1.	2.00e-50
32	798	12.5	803	1	W94903	Mouse pheromone receptor	3.06e-50
33	785	12.3	866	1	W94920	Rat pheromone receptor	4.76e-50
34	778	12.2	872	1	R95052	Human metabotropic glu	2.10e-50
35	764	12.0	877	1	R82657	Human mcIUR3.	4.03e-50
36	757	11.9	872	1	R89580	Metabotropic glutamate	1.77e-55
37	760	11.9	879	1	R64252	Human mcIUR3.	9.39e-56
38	741	11.6	877	1	W01099	Metabotropic glutamate	5.16e-54
39	734	11.5	867	1	R72093	Human mcIUR4.	2.26e-53
40	732	11.5	915	1	R72097	Human mcIUR4.	3.44e-53
41	730	11.5	915	1	R80479	Rat metabotropic gluta	5.25e-53
42	734	11.5	922	1	R72098	Human mcIUR7b.	2.26e-53
43	727	11.4	667	1	W94919	Rat pheromone receptor	9.87e-53
44	718	11.3	908	1	W41568	Human metabotropic glu	6.56e-52
45	717	11.3	908	1	W49928	Human metabotropic glu	8.10e-52

ALIGNMENTS

RESULT 1  
ID W89563 standard; Protein: 1085 AA.  
AC W89563;  
DT 19-MAR-1999 (first entry)  
DE Bovine parathyroid calcium receptor BOPCAR 1.  
KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;  
KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;  
KW spinal cord injury; hypoxia induced nerve cell damage; cardiac arrest;  
KW neonatal distress; neurodegenerative disease; Alzheimer's disease;  
KW Huntington's disease; Parkinson's disease; dementia; muscle tension;  
KW depression; anxiety.  
OS Bos sp.  
PN US5658684-A.  
PD 12-JAN-1999.  
PE 07-JUN-1995; 480751.  
PR 23-AUG-1991; US-480751.  
PR 11-FEB-1992; US-749451.  
PR 21-AUG-1993; US-934161.  
PR 12-FEB-1993; US-017127.  
PR 23-FEB-1993; US-009389.  
PR 22-OCT-1993; US-141248.  
PR 19-AUG-1994; US-292827.  
PR 21-OCT-1994; WO-012117.  
PR 08-DEC-1994; US-353784.  
PA (BGM ) BRIGHAM & WOMENS HOSPITAL.  
PA (NPSD-) NPS PHARM INC.  
PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,  
PI Hebert SC, Nemeth EF, Van Wagenen BC;  
DR WPI: 99-119871/10.  
DR N-PDB: V82483.  
PT Screening for calcium receptor active compounds - by recombinant  
PT expression of nucleic acid encoding calcium receptor and determining  
PT the effect of compounds on calcium receptor activity  
PT Claim 1, Fig 47; 176pp: English.  
CC A method has been developed of screening for a compound able to affect  
CC one or more activities of a calcium receptor (CR) comprises: (A)  
CC contacting a recombinant cell with a test compound, where the  
CC recombinant cell comprises a recombinant nucleic acid expressing the CR,  
CC provided that the cell does not have functional CR expression from  
CC endogenous nucleic acid; (B) determining the ability of the test  
CC compound to affect one or more activities of the calcium receptor; and  
CC (C) comparing the ability with the ability of the test compound to  
CC affect the one or more CR activities in a cell not comprising the  
CC recombinant nucleic acid. The present sequence represents bovine  
CC parathyroid CR, designated a BOPCAR 1. The nucleic acid sequence of  
CC BOPCAR 1 can be used as part of the recombinant nucleic acid in the







[illegible]

Query Match	20.7%	Score 1316:	DB 1:	Length 1085:
Best Local Similarity	31.9%	Pred. No. 2,606-107:		
Matches	272:	Conservative	234:	Mismatches 273: Indels 73: Gaps 51:
Sequence	1085 AA:			
CC	activities, preferably disorders of calcium homeostasis, e.g.			
CC	hyperparathyroidism and osteoporosis.			
CC	Sequence			
DB	31 GDIIIGLGFPIIFG-VAAVDOLKSRPESVCIRNFRGFWLQAMFAEINSSPALL	89		
QY	37 GFPLLAGLFSILHADLOVRHRPLVITSCDRSS--FNGSGYLLPQAMRYVEINNTALL	94		
DB	90 PNMVLGRIFFDTQNTVSKALEATISYVAONKIDSLNDEPFCNSEHPISTIAYVATGSG	149		
QY	95 PIIITIGELYELDYCSSXVY-ATLRVPAQQTGHLEMR--DLNHSKVALIGPDNTD	151		
DB	150 ISTAANLGLFYTQVSYASSSRSLSKNPKFSFLRIPDDEQATAMADIIYFPMW	209		
QY	152 HAVTIAALISPLIMLVSEYASVYLSGKRFPFLRIPDKYQVEIYVRLQSFQMW	211		
DB	210 VETIADDDYGGPGEKFEFREAEEDDITDSELSQSDS-E-KIOQVNVIONSTAKY	267		
QY	212 ISLVSYGDYDGLGVQALEELATPRGIVAKRDVVPYSAQCDPRQMRRLRARTV	271		
DB	268 IVFSSGPDLEPLI-KEIVRRNITGRIMLASEMASSSLIMPEYFHYVGGTIGFGKAG	326		
QY	272 VYFEN-RHLGVEFRSVYLANLIGKWIASEDM---IS-T-YITNVP-Q-GI-T-G	320		
DB	327 QIPGRFELQVHPKSVHNGFAKEFWETTNCHLQZSAKQPLVDYDFLRGHEGGARLS	386		
QY	321 IYLGV-A-IQ-Q-RO-VP-GI-KEF-EESY--VQ-AVMKA-E-----RTCPDG-SM-C	359		
DB	387 NSPTAFRPLCTGEENISVETPYMDYTHLRTSYNWYLAIVYALADIDYTCIGRGFLT	446		
QY	360 -G-TN-Q-LCRCHAFFTTMNPELGAEFMSAIVYEVAVYVAAGLQDLGC-----T	408		
DB	447 NGSCADIKVEAMOVYLRHLNFTSNMGEOVIFDECGDLAGNTSIINHLSPEDGSIVF	506		
QY	409 SGTCA-RGVVYPMQDLQIYKVNFLHR-KIVARDKGDPLGYDIIILAMDNQPE-WT-F	464		
DB	507 KLVGYVNYAKKGELFINDEKILMSGFSREVPSSNSRDLACTRKGIIDGETCCFEC	566		
QY	465 EYIG--SA-SLSPVHLIDINKTKIQMGKNNOVPVSVCRDCLBGNHR-LVWGSRRCCFEC	520		
DB	567 VECPPGEVSEDFDASACKCPDPMNSNHRSCIAKEIEFELSMTEPGIALTEFAYVIGF	626		
QY	521 MPECEGTILNSELHTCOPCGTEEMAPRGSSACSRIYEEFGMEHPSLVYLAANTLLL	580		
DB	627 IIAVLGVGFIEKIR-NTPIVKATNRELSYLLFSLCLCFSSSLF-FIEPDQMTRLRQPA	684		
QY	581 LLIGTAGLFA-WRLHTPVYRSGAGLCLMGLSLVAG-SCSLYSFFQKPIYPAOLLQPL	638		
DB	685 FGISVLCIISCLVAKTNVLLVFE-AKIPFSFRKKMGNLQFLVFLCTPOIVICAI	742		
QY	639 FSLGPAIPLSCLTIISEFOLVIEEFSTVPT-FYHTAQNHGAGIPIVSVSTVHLFCLT	697		
DB	743 WNTNPSPSSYNHEDEDIIFITHEGSLMGLGLIYTC-LIAICOFF-AFSSRLPE	800		
QY	698 WIAAMTPPRIRIQCFPHLVLLCEEVN--SVGLVAFAENILISITFCOSYIGKELPE	755		
DB	801 NENAEKTFESKLFEFIWISFIPAYASTY-GKIVSAVEVPAIIAASFGGLACIFPKVY	859		
QY	756 NNNNAKCTFSLSLHFVSWIAFNTM-SSIIYGSLPRAVNYIAGIATISGGSGYFLPKCY	814		
DB	860 IILFKPSRNTIE	871		
QY	815 VILCRPELNTE	826		
RESULT	4			
ID	W54846 standard: Protein: 1078 AA.			
AC	W54846:			
DT	01-SEP-1998 (first entry)			







CC affect the one or more CR activities in a cell not comprising the  
CC recombinant nucleic acid. The present sequence represents human  
CC parathyroid CR, designated a pHPuCR 4.0. The nucleic acid sequence of  
CC pHPuCR 4.0 can be used as part of the recombinant nucleic acid in the  
CC method described above. The compounds identified can be used to treat  
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.  
CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
CC disorders. They can also be used for the treatment of diseases and  
CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures,  
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
CC diseases such as Alzheimer's disease, Huntington's disease and  
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
SQ Sequence 1078 AA:

Query Match 20.3%; Score 1293; DB 1; Length 1078;  
Best Local Similarity 31.8%; Pred. No. 3,67e-105;  
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

Db 30 GDIIIGLGFPIHFG-VAAKNODLKSRESVEICIRYNGRFRMLOAMFAEEINSSPALL 88  
QY 37 GDLULAGFLHADCLQVRRHPLVTSCDRSDS--FNGHGHLPOAMFYDEINNTALL 94  
Db 89 PNILGRIPTDNTVSKALEATLFSVAONKIDSLNDEFCNCEHPISTIAVVGATGSG 148  
QY 95 PNILGRIPTDNTVSKALEATLFSVAONKIDSLNDEFCNCEHPISTIAVVGATGSG 151  
Db 149 VSTRANALLDLEFIPOYSYSSSSRLSNKNOFKFLRTIPDEHQATAMDIIFEFKMW 208  
QY 152 HAVTATLALPFLMPLVSYSSSVLSGKRKFPFLRTIPDEHQATAMDIIFEFKMW 211  
Db 209 VGTIADDDGPRGIEKFEAREEDRICIDPSELSISQYSDDEE--IOHVEVIONSTAKY 266  
QY 212 ISLVSGIDGQLOVQLLELATPRGICVAFKDVVPLSAQAGDRMRMRMLKARATTV 271  
Db 267 IVVFSSPDLEPLI-KEIVRNITGKIWLASEAWASSLLIAMPQYFHVGGTIGFALAKG 325  
QY 272 VVVFESN-RHLAGVFFRSVLANLTGKWIASEDMA---IS-T-YITNVDPG-IG-GI- 320  
Db 326 QIGGFRFLKKNVHPRKSVNHGFAKEFEWETFNCHLOGACGPLPVDYFLGHESGGRFS 385  
QY 321 TVG--VA-IOOR-V-P-GL-KEF-EESY--VO-AVMGA-P-----RTCPG-GSM-- 358  
Db 386 NSSTAEPLCTGDENISSEVETPYDYTHLRISYVWYLAWSIAHALODITCLGREGLT 445  
QY 359 -CGTN-Q-LDRCHAFETTMKMPGLGATSKMAVYVAVAVAGLQOL---L-GC---T 408  
Db 446 NGSCADIKKVAANOVLKHLNLTNNMGEOVTFDECGDLVGNSTIINHLSPEDGSIVF 505  
QY 409 SGTCG-RGPVYPMOLLOQIKYVNFLLHK-KTVAFDDKGDPLGYDITIAMDNQGE-WT-F 464  
Db 506 KEVGYVWVAKKGERFLINEEKILMSGFSRVPVNSRCDLARTKGIIEGPTCCFEC 565  
QY 465 EVIG--SA-SLSPVHLIDINTKIQHMKNNQVPSVCTRCDECHNR-LVWGSHHCCFEC 520  
Db 566 VECPEGESETDASACNKPDPDEWSNENHTSCAKETIEFLSTPEPGIALTLPAVIGIF 625  
QY 521 MPCEAGFLTLTSELHTQCPGTEPMAREGSSACSRTEVERFEGHEDPISVILLANTLLIL 580  
Db 626 LIAFVLGVFIKFR-NPIVAKINBELSYLLFSLCCFSSSLF-FIGEPDWTORLROPA 683  
QY 581 LLIGTAGLFA-WRLHTPVVSAGRLCFLMGLVAG-SCSLYFFGKPYPAACLLNLOPL 638  
Db 684 FGISFVLCISCIYKTRVLVFE--AKIPISFRKMMWGLNLOPLVFLCFLNOVICVI 741  
QY 639 FSGGFAFLSCCLTIRSHQVLIIFEFSTKVPF-FYHTWAQNNGAIFIVISVTLFLCLT 697  
Db 742 WLVTAPSSYRNOLEDEIIFITCHEGSLMALGFLICYTC-LIAICFF-FAFRSKRLPE 799  
QY 698 WLAMMTPRPREYRPHVLVECTEVN--SVGPLVAFANHLLISITFYCSYIGKELPE 755  
Db 800 NFNDAKFTTSMCLFIWISFIPAYASTY-GKFSVAVEVIAIILASFGLLACIFENKIY 858

QY 756 NYNEAKCVTESSLHFWSWIAFFTM--SSIYQSYLPAVNVLAGIATLDSGFCGYFLPKY 814  
Db 859 IILFKPSPNTIE 870  
QY 815 VILORPEINTE 826

RESULT 6  
ID W1889 standard; Protein; 1078 AA.

DT 22-APR-1997 (first entry)  
AC W1889;  
DE Parathyroid calcium receptor encoded by clone pHPuCR4.0.  
KW Calcium receptor; human parathyroid gland adenoma tumour; pBOPCAR1;  
KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;  
KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;  
KW variant; untranslated region; alternative polyadenylation; probe;  
KW alternative transcription initiation; pHPuCR4.0;  
KW human CAR gene; isoform.  
OS Homo sapiens.  
PN W09612697-A2.  
PD 02-MAY-1996.  
PF 23-OCT-1995; U13704.  
PR 21-OCT-1994; WO-U12117.  
PR 08-DEC-1994; US-353784.  
PI (NPS-) NPS PHARM INC.  
PI Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;  
DR WPI: 96-230520/23.  
DR N-PSDB; T61882.

PT New di:arylalkyl amine cpds. useful for modulating inorganic ion  
PT receptor activities - esp. for modulating effect of extracellular  
PT calcium on cell surface calcium receptors; useful for treating e.g.  
PT hyperparathyroidism, Paget's disease or osteoporosis  
PS Example 1, Page 93-100; 231pp; English.  
CC The sequences given in W1888-89 represent functional calcium receptors.  
CC The cDNAs encoding these sequences were isolated from human parathyroid  
CC gland adenoma tumour using pBOPCAR1 as a hybridisation probe. mRNA was  
CC isolated from a 39 year old caucasian male diagnosed with primary  
CC hyperparathyroidism and two clones of approx. 5 and 4 kb were  
CC identified. These cDNAs were injected into Xenopus oocytes which were  
CC assayed for the presence of functional calcium receptors. Both clone  
CC types gave rise to functional calcium receptors as assessed by the  
CC stimulation of calcium-activated chloride currents upon addition of  
CC appropriate calcium receptor agonists, e.g. NPS R-467 and NPS R-568.  
CC Sequence analysis of the two cDNA clones indicated the existence of at  
CC least two sequence variants differing in the 3' untranslated region and  
CC which may result from alternative polyadenylation. Sequence variation  
CC also exists in the 5' end of the inserts. These sequence differences may  
CC have arisen due to alternative transcription initiation and/or splicing.  
CC Three additional sites of sequence variation occur within the coding  
CC regions of cDNA clones pHPuCR4.2 and pHPuCR4.0 demonstrating that they  
CC encode distinct proteins. Sequence analysis of the human CAR gene  
CC indicates that the additional 30 bp in clone pHPuCR4.2 as compared to  
CC pHPuCR4.0, results from alternative mRNA splicing. This alternative  
CC splicing is predicted to insert 10 additional amino acids into the CAR  
CC protein encoded by pHPuCR4.2 between residues 536 and 537 of the protein  
CC encoded by pHPuCR4.0. In addition pHPuCR4.0 encodes Gln at position  
CC 925 and Gly at position 990, whereas pHPuCR4.2 encodes Arg at both  
CC equivalent positions. The human CAR gene encodes for Gln and Arg  
CC respectively at these positions. These two receptor isoforms may be  
CC functionally and/or pharmacologically distinct. Pages 94-95 are  
CC missing from the specification, sequence information was obtained  
CC from the EPO.

SQ Sequence 1078 AA:  
Query Match 20.3%; Score 1293; DB 1; Length 1078;  
Best Local Similarity 31.8%; Pred. No. 3,67e-105;  
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

Db 30 GDIIIGLGFPIHFG-VAAKNODLKSRESVEICIRYNGRFRMLOAMFAEEINSSPALL 88  
QY 37 GDLULAGFLHADCLQVRRHPLVTSCDRSDS--FNGHGHLPOAMFYDEINNTALL 94  
Db 89 PNILGRIPTDNTVSKALEATLFSVAONKIDSLNDEFCNCEHPISTIAVVGATGSG 148



```
QY 95 PNTILGELVDVCESSSNVY-ATLRVPAQOQCTGHELMQR--DLRNHSSKVALLIGPNTD 151
DB 149 VSTRVANILGLFTIPQVYSSASSRLSNKNQKFFLRTIPNDEQATAMADIIEYFRMW 208
QY 152 HAVTTALLSPFLMPLYSEASSVILSGKRKFPFLRTIPSDKQVEYVRLLOSFGMW 211
DB 209 VGTIADDDYGRPGIEKFRFEAEERDIDSELSISQDEE--IQHVEVIONSTAKY 266
QY 212 ISLVGSYGDQGLQVQALEELATPRGICVAFKDYAPLSAQGDPRQRMRLARARTV 271
DB 267 IYVSSSPDLEPLI-KEIVRNITGKTWLSSEAAASSLLAMPYFHVVGITGFALKAG 325
QY 272 VVVFSSN-RHLAGVFRSVLANLTKWIASDEMA---IS-T-YITNVPQ-IG-GI--G 320
DB 326 QIDGFEFLKVVHPRKSVHNGFAKEFWEETFNCHLOEAKGPLEVDTFLRGHESSGDRS 385
QY 321 TVLG---VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPD-GSW-- 358
DB 386 NSSTAFRPLCTGDNISSEVETPYIDYTHLRISVNVLAVYSIAHALODIYTCLPGRLFT 445
QY 359 -CGTN-Q-LCRECHAFITWMPDELGAFSMSAAVNYEAVVAHAGHLQOL--L-GC---T 408
DB 446 NGSCADIKKYEAMQVYLKHLNFTNNMGEVTFDECGDLVGNYSIINMHLSPEDGSIVF 505
QY 409 SGTCG-RGPYPWQLQOQIKVNFLLHK-KTVAFDKGDPLGYDIIAMPNNGPE-WT-F 464
DB 506 KEYGVYNYAKKGERLFINEKILMSGFSEVPFNSCRDIACTRKGIIEGPTCCFEC 565
QY 465 EVIG--SA-SLSPVHLDINTKIQMHGKNNQVPVSVCTRCOLBEGHNR-LVMGSHCCFEC 520
DB 566 VECPDGEYSDETDASACNCPDDEFSNENHTSCIAKEIEFLSMTEPRGIALTFEVLGIF 625
QY 521 MPEAGTFELNTSELHTQCPGTEEMAEBSGACFSRTVEFGMEHPEISLVLAANTLL 580
DB 626 LTAFLVGLFIFKR-NTEPIVATNRELSTYLLLSLCCFSSSLF-FIGEPQDWCRLQOPA 683
QY 581 LLIGTAGLFA-WRLHFPVRSAGGRCLFELMGLSVAG-SCSLVSFFKRPVACLLRQPL 638
DB 684 FGISFVLCISCIIVKTRVLLVFE--AKIPTSFHRKMGMLQFLFELCTFMQIVCIV 741
QY 639 FSLGFAFLSCLTRSFQOLVIFEFKSKVPT-FYHTAQNQHGAGIPIVSVHLEFCLT 697
DB 742 WLYTAPSSYRNOLEDEIIFITCHEGSLMALGFLIYTC-LLAALGFF-AFKSRMLPE 799
QY 698 WLMAMPTRPREYORFPHLVILECTEYV--SVGFLVAFAHNILLISTFVCSYLKELPE 755
DB 800 NNEBAKITESMILFEIIVMISEIPAVASTY-GKPYSAVEYATILAAFGLLACFEFKIY 858
QY 756 NYNEAKCVTSLHLHFYSWIAFFTM-SITIGSTYLPVAVNLATLUSGGSGYFLPKCY 814
DB 859 IILFKPSRNTIE 870
QY 815 VILCRPELNTE 826
RESULT
ID W38274 standard; Protein: 1078 AA.
AC W38274;
DT 08-MAY-1998 (first entry)
DE Human parathyroid cell calcium receptor 4.0 (Hupcar 4.0).
KW Human parathyroid cell calcium receptor 4.0; Hupcar 4.0;
KW calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
PN US568938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
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PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGM ) BRIGHAM & WOMENS HOSPITAL.
PA (NPS-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
DR MPI: 98-008040/01.
DR N-PSDB: T95859.
PT DNA encoding calcium receptor polypeptide(s) - useful for
therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 20; Columns 125-134; 174pp; English.
CC The present sequence is human parathyroid cell calcium
receptor 4.0 (Hupcar 4.0).
CC The specification includes details of molecules that can modulate
one or more inorganic ion receptor activities, and antibodies and
antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
activities, preferably disorders of calcium homeostasis, e.g.
hyperparathyroidism and osteoporosis.
SQ Sequence 1078 AA;
```

Query Match 20.3%; Score 1293; DB 1; Length 1078;  
Best Local Similarity 31.8%; Pred. No. 3,67e-105;  
Matches 271; Conservative 234; Mismatches 274; Indels 73; Gaps 48;

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DB 30 GDIILGFLPIHNG-VAADQDCRSRESECTRYNFGFRMLOAMIFAEIINSSPALL 88
QY 37 GDIILGFLSILHADCQVRRPLVTCDSRDS--FNGHGLHFOARRVEELINSSALL 94
DB 89 PNTILGRIPTDCTNTYSKALEATLSFAQNKIDSLNDEFCNSEHPISTIYAVAGTSG 148
QY 95 PNTILGELVDVCESSSNVY-ATLRVPAQOQCTGHELMQR--DLRNHSSKVALLIGPNTD 151
DB 149 VSTRVANILGLFTIPQVYSSASSRLSNKNQKFFLRTIPNDEQATAMADIIEYFRMW 208
QY 152 HAVTTALLSPFLMPLYSEASSVILSGKRKFPFLRTIPSDKQVEYVRLLOSFGMW 211
DB 209 VGTIADDDYGRPGIEKFRFEAEERDIDSELSISQDEE--IQHVEVIONSTAKY 266
QY 212 ISLVGSYGDQGLQVQALEELATPRGICVAFKDYAPLSAQGDPRQRMRLARARTV 271
DB 267 IYVSSSPDLEPLI-KEIVRNITGKTWLSSEAAASSLLAMPYFHVVGITGFALKAG 325
QY 272 VVVFSSN-RHLAGVFRSVLANLTKWIASDEMA---IS-T-YITNVPQ-IG-GI--G 320
DB 326 QIDGFEFLKVVHPRKSVHNGFAKEFWEETFNCHLOEAKGPLEVDTFLRGHESSGDRS 385
QY 321 TVLG---VA-IQQRQ-VP-GL-KEF-EESY---VQ-AVMGA-P-----RTCPD-GSW-- 358
DB 386 NSSTAFRPLCTGDNISSEVETPYIDYTHLRISVNVLAVYSIAHALODIYTCLPGRLFT 445
QY 359 -CGTN-Q-LCRECHAFITWMPDELGAFSMSAAVNYEAVVAHAGHLQOL--L-GC---T 408
DB 446 NGSCADIKKYEAMQVYLKHLNFTNNMGEVTFDECGDLVGNYSIINMHLSPEDGSIVF 505
QY 409 SGTCG-RGPYPWQLQOQIKVNFLLHK-KTVAFDKGDPLGYDIIAMPNNGPE-WT-F 464
DB 506 KEYGVYNYAKKGERLFINEKILMSGFSEVPFNSCRDIACTRKGIIEGPTCCFEC 565
QY 465 EVIG--SA-SLSPVHLDINTKIQMHGKNNQVPVSVCTRCOLBEGHNR-LVMGSHCCFEC 520
DB 566 VECPDGEYSDETDASACNCPDDEFSNENHTSCIAKEIEFLSMTEPRGIALTFEVLGIF 625
QY 521 MPEAGTFELNTSELHTQCPGTEEMAEBSGACFSRTVEFGMEHPEISLVLAANTLL 580
DB 626 LTAFLVGLFIFKR-NTEPIVATNRELSTYLLLSLCCFSSSLF-FIGEPQDWCRLQOPA 683
QY 581 LLIGTAGLFA-WRLHFPVRSAGGRCLFELMGLSVAG-SCSLVSFFKRPVACLLRQPL 638
DB 684 FGISFVLCISCIIVKTRVLLVFE--AKIPTSFHRKMGMLQFLFELCTFMQIVCIV 741
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	Query Match	20.1%	Score 1282;	DB 104	Length 1079;
	Best Local Similarity	31.2%	Pred. No. 3.91e-104;		
	Matches 269;	Conservative	240;	Mismatches 280;	Indels 73; Gaps
Db	30	GDILGGLFPIHFG--VAAKODLKSRESEYECIYNNRGRFMDQAMFAEELINSSPLL	88	:    :	:    :
Qy	37	GDPLLAGLESLHADCLQVRRHRLPLVTSODRSDS--FNCHGHLQFMQFYELIINSSPLL	94	:    :	:    :
Db	89	PNMILGRIDTCTVSKALEATISLFAQNKIDSLNIDFECNCESEHPTSTIAVATGSG	148	:    :	:    :
Qy	95	PNILIGELDYVCSSENNY--ATLRVPAQQTGLHMQR--DLRNHSSKVAALIGDND	151	:    :	:    :
Db	149	VSIANVLNLGLEYPOVSYASSSFLNKKNYKSEFLTINDEHOATAMADIIEFFRMW	208	:    :	:    :
Qy	152	HAVTALLSFLMLPLVSYEASSVILSGKKRPFLATIPSDKYQVEVYRLLOSQGW	211	:    :	:    :
Db	209	VGLTAADDYGRPGIEKFFREAEPRDIDCFSELISQYSDEE--IQOQVEVYQNSTAKY	266	:    :	:    :
Qy	212	ISLVSGYGDYQGLTQVLALEELATPRGICVAFKDVPLVSAQAGPFRMDPMLRLARATTV	271	:    :	:    :
Db	267	IIVFSSGDPDEPLI--KEIVRNRINGRIWLASEAWASSLTAMDEYFHVGGTIGFGK	325	:    :	:    :
Qy	272	VYVESN--RHLGAVFRRSVLANLTGKRWIASBDMA-----IS-TYIINVG-IQ-GI--G	320	:    :	:    :
Db	326	QIPGFRFLQVHRPKSVHNGFANEETFNCHLQCGAGPLVPDITFVRSHEEGNRLL	385	:    :	:    :

RESULT 9  
ID W54847 standard: Protein: 1079 AA.  
AC W54847;  
DT 01-SEP-1998 (first entry)  
DE Rat kidney calcium receptor 3A protein 4xb fragment.  
KW Calcium ion concentration; parathyroid hormone; homeostasis; kidney;  
KW Calcium receptor; detection.  
OS Rattus sp.  
PN US5763569-A.  
PD 09-JUN-1998.  
PE 07-JUN-1995: 484565.  
PF 07-JUN-1995: US-484565.  
PR 23-AUG-1991; US-749451.  
PR 11-FEB-1992; US-834044.  
PR 21-AUG-1992; US-934161.  
PR 12-FEB-1993; US-017127.  
PR 23-FEB-1993; US-009389.  
PR 22-OCT-1993; US-141248.  
PR 19-AUG-1994; US-292827.  
PR 21-OCT-1994; WO-012117.  
PR 08-DEC-1994; US-353784.  
PA (BSHM ) BRIGHAM & WOMENS HOSPITAL.  
PA (NPSF-) NPS PHARM INC.  
PI Brown EM, Garrett JE, Hebert SC;  
PI WPI.: 98-347412/30.  
DR N-PSDB: V26965.  
PT Calcium receptor poly:peptide(s) - useful for drug screening or  
PT antibody production  
PS Claim 8; Fig 50; 174pp; English.  
CC The tissue from which the rat kidney calcium receptor and receptors from  
CC bovine parathyroid and rat kidney are derived, respond to changes, and  
CC control changes. In calcium ion concentration, e.g. parathyroid hormone  
CC regulates  $\text{Ca}^{2+}$  homeostasis in blood and extracellular fluid, and kidney  
CC function alters through changes in  $\text{Ca}^{2+}$  levels in juxtaglomerular and











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OY 756 NNEACVTFSLHLHFVSWIAFPTM--SSYOGSYLPAVNVLAGLATLSGGSGFYLPCKY 814
DB 859 IILFKPSRNTIEVRSSTAHA 880
OY 815 VILCRPELNTEHFQSIODYT 836

RESULT 12
W32059 standard; Protein: 1026 AA.
AC W32059.
DE 27-MAR-1998 (first entry)
DB Dogfish shark kidney calcium receptor related protein (SKCAR-RP).
KW Calcium receptor related protein; Car-RP; dogfish shark; SKCAR-RP;
KW polyclonal-sensing receptor; aquaculture; fish farming;
OS Squalus acanthias.
FH Key Location/Qualifiers
FT Region 351..395
FT /note="region in extracellular domain that is highly divergent from mammalian PVCR"
FT Region 870
FT /note="region in C-terminal domain that is highly divergent from mammalian PVCR"
FT Region 870
FT /note="region in C-terminal domain that is highly divergent from mammalian PVCR"
PD WO9735977-1.
PN 02-OCT-1997.
PF 27-MAR-1997: U05031.
PR 27-MAR-1996: US-622738.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI Brown E, Harris HW, Hebert S;
DR N-PSDB: T89290.
PT New isolated Aquatic polyvalent cation-sensing receptor - used to
PT develop products for increasing or decreasing the salinity tolerance
PT of fish for use in aquaculture.
PS Clam 9; Fig 5A-B; 5/PP: English.
CC This protein comprises dogfish shark kidney calcium receptor
CC related protein (SKCAR-RP), an aquatic polyvalent cation-sensing
CC receptor (PVCR). Its amino acid sequence was deduced from a kidney
CC cDNA clone (see T89290). It shows 74% homology to rat kidney
CC PCVR and bovine parathyroid PVCR and possesses general features
CC that are homologous to PVCR proteins, including a large
CC C-terminal domain, 7 transmembrane domains and a cytoplasmic
CC membrane of epithelial cells of elasmobranch fish particularly
CC from cells found in the collecting duct or late distal tubule in
CC the kidney, intestine, gill, rectal gland, gonad or brain; an
CC antibody that specifically binds to a PVCR; and a method of
CC screening for aquatic PVCR agonists and antagonists. Modulation of
CC the expression of the aquatic PVCR activates or inhibits aquatic
CC PVCR mediated ion transport and endocrine changes that permit fish
CC to adapt to fresh or salt water. The method facilitates the
CC aquaculture of marine fish and can provide for the development of
CC marine fish that are easily adaptable to fresh water aquaculture.
SQ Sequence 1026 AA;

Query Match 18.9%; Score 1204; DB 1; Length 1026;
Best Local Similarity 31.0%; Pired. No. 7.44e-97;
Matches 263; Conservative 237; Mismatches 273; Indels 76; Gaps 47;
DB 34 GDIIIGLPIIFHG--VAADQDLKSRPEATKIRYNGFRFMLOAMIFAIEINSMTEFL 92
OY 37 GDFLAGLGLSHADLCQVHHRPLVTSDD--RDSFNGHGTHLQFAARFVEEINNTALL 94
DB 93 PNITGGRIFDTCNTVSKALEATLSTVAQNKIDSLNLDFFCNSDHPITIAVVGATGSG 152
OY 95 PNITGGRIFDTCNTVSKALEATLSTVAQNKIDSLNLDFFCNSDHPITIAVVGATGSG 151
DB 153 ISAVANLGLFPIPOVYASSSRLLSNKREKAFRTIPNDEQQAATAEITEHQHNMW 212
OY 152 HAATVALLSPFLMPLVYSEASSVILSGRRKPFSLRIPSDKYQVEIVRLLQSGMW 211

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DB 213 VGLTAAADDYGRGIDKREKAVKRKIDICIDFSEMSIQY-T-QKOLEPIADYIONSSAKV 270
OY 212 ISLVSGYDGYGLGVQALBELATPRGICVAFKDVYPLSAQADPPMOQMLRAARTV 271
DB 271 IYVESNGDLEPLI-QEIVRNRITDRIMLASEAMSSLLIAKPEYFHVGGTIGFALRAG 329
OY 272 VYVFSN-RHLAGVFPRSVYLANLTGKWIASEDMALISTYITNVPISIQIG-TV--L-G 324
DB 330 RIGFKNFLKEVHPAGPPTMGSRSSGRLOLLHREDLQJLKNKVSHPGAGQDGSK 389
OY 325 -VA-10Q--ROY---P--GL-----K-EF--E-ESTYQ--A-VAG-ARTCPDGSW 358
DB 390 AGNSRTALRHPCTGEENITSYETPLDYTHLRISYNYVAVYSAHAADIDHSCPGTG 449
OY 359 GCTNQ---LCRCC---HAFTWMNELGAFSMAKYNYEAVYANAHLLHQLGCG---T- 408
DB 450 IFANSCADIKKVEAMQVNLHLHLKFTNSGEOVDPDQDGLKNTYITIMQLSAEDS 509
OY 409 --S-GTCA-RGFVYPMOQLQIKYVFLHR-KTVAFDKGDPLGYDIAMDWNGP-EW 462
DB 510 VLFHEGYNNAKPSDRLNINEKILMSGFSKYVPFSGNSRDCVPGTRKGIIEPTCC 569
OY 463 T-FEYIGS-ASLS-PV-HUDIKTKIOWHGKNOVPVSVCTRDCEGHR-LVMGSHHC 517
DB 570 FEOMACAESEFSDENDASACTKCPNDFWSENHTSCIAKELEYLSWTPEGIALTIIFAVL 629
OY 518 FEOMCEAGTFLNTSELHTCQPCGTEEMAPBESSACFRTEYFLOMHPISLVLAATL 577
DB 630 GLITSEVYLGVFIKFR-NPIYKATNRELSTYLLFSLICFSSSLI-FIGEDRDTCLR 687
OY 578 LLLLLIGTAGLFA-WRLHPVVRASGRLCFMLGSLVAG--SCSLYSPFGKPTVACILR 635
DB 688 OPAGFISFLICSLTNTNRYLVEE--AKPISLHKRWGLNQGLFVLCILYQVIT 745
OY 636 QLFSLGFAIFLSCLTINSFQVITFKSTKVT-FYTMQNHAGIFVYSSVTHLFL 694
DB 746 CIIWYTAAPPSSRYNHEDEVIPTCDGSLMAGFLIGYTC-LIAAICPEF-AFKSRK 803
OY 695 CIIWYTAAPPSSRYNHEDEVIPTCDGSLMAGFLIGYTC-LIAAICPEF-AFKSRK 803
DB 804 LPENNEAKFTFMSLIFFIYVISTIPAVSYI-GKYSANVEVILIASGGLACITFN 862
OY 753 LPENNEAKVTFSLHLHFVSWIAFPTM--SSYOGSYLPAVNVLAGLATLSGGSGFYLP 811
DB 863 KCIITLFRP 871
OY 812 KCYVILCRP 820

RESULT 13
W38273 standard; Protein: 1088 AA.
AC W38273.
DE 08-MAY-1998 (first entry)
DB Human parathyroid cell calcium receptor 5.2 (HUPCAR 5.2).
KW Human parathyroid cell calcium receptor 5.2; HUPCAR 5.2;
KW calcium homeostasis; hyperparathyroidism; osteoporosis.
OS Homo sapiens.
PN US5688938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 18-DEC-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PI (NESP-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;

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QY 571 LLAANTLLLLLIGTAGLFA-WRLHTPVVRSAGGRLCFLMLGSLVAG-SCSLYSFPGKPT 628  
Db 684 DWTCLROPAGISFVLCISCLIVKTNRLVFE--AKIPTSHRKWGLNLQFLLVFLC 741  
QY 629 VPACLRQPLFSLGFAIFLSCLIRSFQVLITFKESTKVPT-FYHTWAQNHGAGIFVIVS 687  
Db 742 TFMQIVICVIMLYTAPSSYRNOLEDEIIFITCHEGSLMALGFLIGYTC-LLAICFPF 800  
QY 688 STVHLEFLCLTWLAWTPRPTREYQRPRLVILECTEVN--SVGFLVAFANHILISTFV 745  
Db 801 -AFKSRLPENNEAKFITFSMLIEFIWISFIPIYASTY-GKEVSAVEVIAIILAAFG 858  
QY 746 CSYLGKELPENNYEAKCVTFSLHFEVSWIAEFTM-SIYQGSYLPANVYLAGIATLSGG 804  
Db 859 LACIFFNKIYIILFKPSRNTIE 880  
QY 805 FSGYFLPKCYVILCRPELNNT 826

Search completed: Fri Mar 17 13:14:52 2000  
Job time : 99 secs.







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 W O R L D  
 (TM)  
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MPearch\_pp Protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:31:21 2000; Maspar time 105.23 Seconds

Tabular output not generated.

Title: >US-09-361-652-3  
 Description: (1-777) from US09361652.pep  
 Perfect Score: 5838  
 Sequence: 1 RSCSFNEHGXYHLFQAMRLGV.....NSTEHFOASIDYTRRCGST 777

Scoring table: GAP 150  
 GAP 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database:

splembl12  
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human  
 5:sp-invertebrate 6:sp-mammal 7:sp-mmc 8:sp-oranelle  
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified  
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 51.690; Variance 98.585; scale 0.524

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	4587	78.6	840 11	0920R8	POTATIVE TASTE RECEPTO	0.00e+00
2	1848	31.7	843 11	0920R7	POTATIVE TASTE RECEPTO	0.00e+00
3	1293	22.1	848 13	093553	POTATIVE ODORANT RECEPT	1.23e-242
4	1286	22.0	868 13	073635	PEROMONE RECEPTOR.	4.21e-241
5	1270	21.8	864 13	073637	PEROMONE RECEPTOR.	1.33e-237
6	1271	21.8	880 13	073639	PEROMONE RECEPTOR.	8.07e-238
7	1217	20.8	844 13	093552	POTATIVE ODORANT RECEPT	5.15e-226
8	1216	20.8	940 13	073635	CALCIUM2+ SENSING RECEPT	8.51e-226
9	1197	20.5	856 13	073638	PEROMONE RECEPTOR.	1.20e-221
10	1066	18.3	875 13	073640	PEROMONE RECEPTOR.	3.95e-193
11	994	17.0	912 11	070410	POTATIVE PHEROMONE RECEPT	1.59e-177
12	946	16.2	855 11	070409	POTATIVE PHEROMONE RECEPT	3.72e-167
13	915	15.7	779 11	035269	POTATIVE PHEROMONE RECEPT	1.79e-150
14	844	14.5	983 11	062916	METABOTROPIC GLUTAMATE RECEPT	3.21e-145
15	838	14.4	458 13	093555	POTATIVE ODORANT RECEPT	6.20e-144
16	771	13.2	850 11	035189	POTATIVE PHEROMONE RECEPT	1.28e-139
17	765	13.1	408 13	093558	POTATIVE ODORANT RECEPT	2.42e-128
18	756	12.9	908 4	095945	METABOTROPIC GLUTAMATE RECEPT	2.00e-126
19	731	12.5	866 11	035268	POTATIVE PHEROMONE RECEPT	4.10e-121
20	718	12.3	803 11	035191	POTATIVE PHEROMONE RECEPT	2.35e-118

21	714	12.2	548 11	035265	POTATIVE PHEROMONE RECEPT	1.65e-117
22	711	12.2	667 11	035267	POTATIVE PHEROMONE RECEPT	7.13e-117
23	699	12.0	350 13	093556	POTATIVE ODORANT RECEPT	2.47e-114
24	703	12.0	758 11	035266	POTATIVE PHEROMONE RECEPT	3.53e-115
25	676	11.6	695 11	035272	POTATIVE PHEROMONE RECEPT	1.79e-109
26	648	11.1	852 11	035192	POTATIVE PHEROMONE RECEPT	1.41e-103
27	644	11.0	428 11	070413	POTATIVE PHEROMONE RECEPT	9.80e-103
28	643	11.0	723 11	035193	POTATIVE PHEROMONE RECEPT	1.59e-102
29	638	10.9	604 11	035195	POTATIVE PHEROMONE RECEPT	1.79e-101
30	619	10.6	339 11	035194	POTATIVE PHEROMONE RECEPT	1.72e-97
31	584	10.0	339 11	070411	POTATIVE PHEROMONE RECEPT	3.54e-90
32	521	8.9	250 13	073647	PEROMONE RECEPTOR (FR	4.03e-77
33	505	8.7	301 11	035364	CALCIUM SENSING RECEPT	7.89e-74
34	503	8.6	311 11	035363	CALCIUM SENSING RECEPT	2.03e-73
35	504	8.6	1267 5	093564	PEROMONE RECEPTOR.	1.27e-73
36	498	8.5	251 13	073655	PEROMONE RECEPTOR (FR	2.15e-72
37	490	8.4	250 13	073645	PEROMONE RECEPTOR (FR	9.38e-71
38	488	8.4	251 13	073653	PEROMONE RECEPTOR (FR	2.41e-70
39	483	8.3	250 13	073649	PEROMONE RECEPTOR (FR	2.53e-69
40	484	8.3	251 13	073656	PEROMONE RECEPTOR (FR	1.58e-69
41	479	8.2	250 13	073651	PEROMONE RECEPTOR (FR	1.66e-68
42	476	8.2	250 13	073646	PEROMONE RECEPTOR (FR	6.81e-68
43	480	8.2	251 13	073654	PEROMONE RECEPTOR (FR	1.04e-68
44	479	8.2	251 13	073652	PEROMONE RECEPTOR (FR	1.66e-68
45	477	8.2	808 11	035190	POTATIVE PHEROMONE RECEPT	4.25e-68

#### ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	840 AA.
AC	0920R8:			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	POTATIVE TASTE RECEPTOR TR1 (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
NC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-WISTAR;			
RX	MEDLINE: 99159821.			
RA	HOON M.A., ADLER E., LINDEMEIER J., BATTLE J.F., RYBA N.J.P.,			
RA	ZUKER C.S., "Putative mammalian taste receptors: a class of taste-specific GPCRs			
Rt	with distinct topographic selectivity."			
RL	Cell 96:541-551(1999).			
RD	EMBL: AF127389; AAD18059.1; -			
KW	Receptor.			
FT	NON_TER			
SQ	SEQUENCE	840 AA;	93496 MW;	B1F5F564 CRC32;

Query Match 78.6%; Score 4587; DB 11; Length 840;  
 Best Local Similarity 75.2%; Pred. No. 0.00e+00;  
 Matches 585; Conservative 99; Mismatches 93; Indels 1; Gaps 1;

Db	63	RPDSFNGHGXYHLFQAMRLGV.....NSTEHFOASIDYTRRCGST 777	122
Qy	1	RSCSFNEHGXYHLFQAMRLGV.....NSTEHFOASIDYTRRCGST 777	60
Db	123	FRRIEIKDLRNSSVYVAFIGPDNDHVTAAALGPIMLPLVSEASSVSAKRKP 182	
Qy	61	QHIEIDLGDLHISPLVLAVIGPDSINRAITTAALSPFLVH-ITRAASSETISVAKRQY 119	
Db	183	SFLRTVPSDRHQVEYVQVLQSGFQWVWISLIGSYG3QLGVQALAEELAVPRGICVAFPD 242	
Qy	120	SFLRTIPNDKYQVEYVWLLQKQGWVWISLVGSSDDYGLGVQALENQALVYGCIAFMD 179	
Db	243	IYFESRAGVDPRQSMQHLAQARTVVVVFNSRHLRAVFPSVLAINTGKVVASGDM 302	
Qy	180	IMFESQVODDERMOCLMRHLAQAGATVVVVFSSROLRAVFESVLTJNLTKGVWVASEAM 239	



D	b		303	AASFTITSTGIGIGTGVAVVOORVPGKKEEPESSVRATVPAPASCPGSMCSTNQL	362
Oy			240	ALSRHTGTGPGIQRIGMWLGAIQRAAIPGLKAFFBEARADRDKEAPRPRCHKSGMCSNQL	299
D	b		363	CRCCHTFTRNNPPTLGAFSMSAAHYEAUYAVAAGHLHQLLGCTSETICSRRPYPMWLQ	422
Oy			300	CRECOAFMAHMTPKAKFMSASSYANAYRAYVAAGHLHQLLGGACSELCSRRRYVPMWLE	359
D	b		423	QIKYNELLHEHTVAFDNDGDTLTGYDDLIAMDNGPEWTFFELIGSASISPVHLINKTKI	482
Oy			360	QIHAKHFLLHKDTVAFNNRPDLSSSYNTIAMDMGNPKPTFFVLGSSTWSPVOLINETKI	419
D	b		483	OMHGNNOPVSVCTDCLAGHHRVVSSHCCCEFCVCACEGTPLNMSELIQCPCTEE	542
Oy			420	OMHGNNHOVPKSVSCSDCLEGHQRRVVTHHCCEFCVCGAGTFLNKSELYRCOPCGTEE	479
D	b		543	WAPKSTTCFPPTVFEMLAHMEPISLVLIANAUTLLLLLIVTAGLFAMFHHTPPVRSAGR	602
Oy			480	WAPESOSICFPPTVFEMLRHRTSHVLLAANTLLLLLLGLTGRLFAWHLDTPVYRSAGR	539
D	b		603	LCFMLGSLVAGSCSFYSFFGEPTVPACLLNQPLEFSIGAFLSCLTIRSFOLYIFKFS	662
Oy			540	LCFLMGSLIAGSGSLYGFGCEPTRACILROLAFALGFTIFLSOLTIVRSQOLIIFKFS	599
D	b		663	TKVPFFYTMAONHAGLFYIVSSVVEHLICTLVMYMPRTPTREYQRFPHYLLECTEV	722
Oy			600	TKVPFFHYAWMONHAGLFVYMSSAOLLICTLWMYVVTLPAREYQRFPHVLMECTET	659
D	b		723	NSVGFLPAFTHHIILISTFPOCYSGKELPREYNEAKCVFSSLINFMSIAFTMASIY	782
Oy			660	NSUGTIILFVLINGLISIAFACSYIGKDPENYNEAKCVTSLSLFNFYSWAFTTASVY	719
D	b		783	OGSYLPAVNLAGLTTLTSGSGFYELPKCYIYLCPLELNTEHFOASIODYTRRCGTT	840
Oy			720	DOKYLPAAANNMAGSLSSSGFGGYTLPCROYILLCRPDLSNTEHFOASIODYTRRCGST	777
<hr/>					
	RESULT	2			
ID	O9ZOR7	PRELIMINARY;	PRT;	843 AA.	
AC	O9ZOR7;				
DT	01-MAY-1999 (TREMBLrel. 10, Created)				
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)				
DE	POTATIVE TASTE RECEPTOR TR2 (FRAGMENT).				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Euthelia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-WISTAR;				
RX	MEDLINE; 99159821.				
RA	HOON M.A., ADLER E., LINDEMAYER J., BATTERY J.F., RYBA N.J.P.,				
RA	ZUKER C.S.;				
RT	"Putative mammalian taste receptors: a class of taste-specific GPCR				
RT	with distinct topographic selectivity.";				
RL	Cell 96:541-551(1999).				
DR	EMBL; AF127390; AADI8070.1; -.				
KW	Receptor.				
FT	NON_TER	843	843		
SO	SEQUENCE	843 AA;	95799 MW;	6B0AE9EE CRC32;	
<hr/>					
	Query Match	31.7%;	Score 1848;	DB 11;	Length 843;
	Best Local Similarity	37.5%;	Pred. No. 0.00e+00;		
	Matches	293;	Conservative	193;	Mismatches 269;
					Indels 26;
					Gaps 22;

ID	RESULT	3	PRELIMINARY;	PRT:	848	AA.
AC	093553;					
DT	01-NOV-1998 (Tremblrel. 08, Created)					
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)					
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)					
DE	PUTATIVE ODORANT RECEPTOR.					
GN	GRB8.					
OS	Carassius auratus (Goldfish).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;					
OC	Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;					
OC	Cyprinoidae; Cyprinidae; Cyprininae; Carassius.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-OLFACTORY EPITHELIUM;					
Dp	190	ATHHEAMVQAMHFOKNMIVLVVSDDDYGRENHLSQRILKTSIDICIAFOEVLPIRES	249			
Qy	128	DKYEVETVVLLOQFGMTWISLVSSDSDYQOLGVQALENQ-ALVRGICIAFKIMPF--S	184			
Dp	250	SQVNRSEOROLDNIDILKRLRTSARVVVSP-ELSYFFHEVLRNFIAGFWINSEW	308			
Qy	185	AQV--GDE-R-MQIMHNLAAAGATVVVVSSROLAR-VFESVVLTNLIGKVVWASEAM	239			
Dp	309	AIDPVLHNLIELRHTGTFLGTIORVASIPGFSQFR--VRDRPGVVPPTNLRATCNQ	365			
Qy	240	ALSRHTIGVPDQIQIGVNLGVALIGRAVPGIKAFEEAYANADMEA-PRCHKSMCSNQ	298			
Dp	366	DCDACLN-TTKSENNIILISGERVYTSVSAVAVAHARHLGCRNVRCTOKQVYPMOL	424			
Qy	299	LCRCQAFMATMKELKAFSSMSA-YNAAYRAVVAAGHLQOLGCASELCSRRVYPMOL	357			
Dp	425	LREIWHNFTLLGRLEFFDQGGDPMIL-LDIIQOMDLSQNPQSTASYSPTRSKRLTYN	483			
Qy	358	LEQJLHKVHFLHKDTVAFNDNRD-PLSSYNIAMDMNGPMTFTVLGSSSTWSPVQLINE	416			
Dp	484	-NVSMYTPNNTPVPSMCSKSCOPGOMKSVGLHPCCFECDCDMPGTVLNRSADFNCLSC	542			
Qy	417	TKIQMHGKNHVPKSVSSDCLBEHQVNTVGFHHCECEPCAGATFLNKS-ELYRCQPC	475			
Dp	543	PGSMWSKYKNDITCFQRPRPFLMEHVEVTVIAVILAAIGFSTLALFIF-WRHFQTPMYR	601			
Qy	476	GTEMAPEGSGQTCPPRTVVFALREHNSWVLLAANTLLELLLGTAIGLAFMW-HLDPVYR	534			
Dp	602	SAGPMPGFLMVLVPLLLAFGAVPYVGVPPYFSCFCROAFTVCFSLCSTIYRSQIYC	661			
Qy	535	SAGRLCFLKMGSLAAGSGSLYGFEGEPTRPACOLLRLQALFGLFTIFSLCTIYRSQILII	594			
Dp	662	VFKARRLPSAYSPMMYHOPRYVFAVITAIKVALVGNLATTINPDIKGRTPDDDDNIMI	721			
Qy	595	IFKSTVPTPFYAAVYNBSAGLEFWMISSAQLICTLVLVTPLP-AREYQRPFLVW	653			
Dp	722	LSCHPNRNGLLFNTSMDLLSLVLSGFSAFMGKELPTNYNEAKFTILSMFSTSSISLC	781			
Qy	654	LEGRETNSLGFILAFNLGSLISAFRCSTGLGNDLPENYNEACVFFSLFNVSNIAPF	713			
Dp	782	TPMSVHDGVLITMDLIVLVNPLAIGLG-YFSPKCYMILEYERNTSAVNSMIGGYTM	840			
Qy	714	TTSVYVYGKRLPAPANNMAG-LSSLSGFGGYLPKCYVILICRDLNSTEHFQSIQDYTR	772			
Dp	841	R 841				
Qy	773	R 773				

[illegible]

CAO Y., OH B.C., SRRYER L.,  
RT "Cloning and localization of two multigene receptor families in  
goldfish olfactory epithelium."  
Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).  
DR EXBL/ AFO83081: AAC64076.1, "-  
PRAM: PF00003, 7tm-3, 1.  
DR PF01094, ANF-receptor, 1.  
PRINTS: PF00248; GPCRNGR.



[illegible]



Db 861 KHL 864  
Y 760 TEHF 763

RESULT 5  
ID 073637 PRELIMINARY: PRT: 864 AA.

AC 073637;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE PHEROMONE RECEPTOR.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
[1]

RM SEQUENCE FROM N.A.  
RP MEDLINE; 98226788.

RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,  
NAKANISHI S., BRENNER S.;  
"Putative pheromone receptors related to the Ca2+-sensing receptor in  
Fugu";  
Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

DR EMBL; AB008859; BAA26124.1; -.  
DR PFAM; PF00003; 7tm\_3; 1.  
DR PFAM; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.

KW Pheromone.  
SQ SEQUENCE 864 AA; 96216 MW; E26A0114 CRC32;

Query Match 21.8%; Score 1270; DB 13; Length 864;  
Best Local Similarity 30.6%; Pred. No. 1,33e-237;  
Matches 243; Conservative 216; Mismatches 287; Indels 48; Gaps 37;

Db 75 CTRFDLGFHMTAFMAVOEINKNPDLPLNLGLRGLYDNCGLVGFSGALALA-SGQ 133  
Y 3 CS-FNEHGHLFQMRGLVEEINNSTALPLNTLGLYQYDSCSANYATRLVSLRQ 61

Db 134 EEARLGGCGAG-SPPVLGIYGDLSSTTASAVLGKIKPMVSFYATCCLTRKQFP 192

Y 62 HH-TELQDHLHSPVLAIVIGPDSINRAATTAALSPFLVH-ISTYASSETLSVKRYP 119

Db 193 SFRPTIPSDDFOVAMIOILKHFQWTVGLVSDDYGLHYVASQSD-LVOSGGGCIAY 251

Y 120 SFLTIPDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALBNALYR-GI-CTAF 177

Db 252 LEVLPMDNYLSENR-R-IVHVIKESFANLVAFHOSHIMLM-BEYVRQVYGLQWLAS 308

Y 178 KDIMPFSQVGDERRMOCLMRHLAQAGATVVVSSR-QLARVFESVLTJLTKRVVVA 236

Db 309 EAMVGTFTLQ-TPDPMPLNLGLTGLAIRGELTGRLDLRLRPOSSNNTSYDVQFW 367

Y 237 EAMLSRHTGVPQIQR-IGVILGVALIQRAVPGKAFEEAYARADKAPRCHGGS--W 293

Db 368 EYSQKFGGASGAEACTGDNIOVDAEFLDVSNLREPNYKAYVALAYALDMLQCE 427

Y 294 -----CS-SNOLCRE-C-QAFMAHTMK-LKAPSSMSAAYNAYRAVVAAGLHRLGC- 342

Db 428 PGRPFSGGSCADILKLEPMQFVHLYQVNFVTGGDVSFDENDVLPIDYILMOWLP 487

Y 343 AS-E-L-----CS-RGRVPMOLLQIHVHFLH-KDTVAFNDNDPLSSNIILMDWG 394

Db 488 DGRVQVQVGVKSPSGEELQIHEDKIFNFESENKPRPHVSCSCSCEPGRMRMKKQOP 547

Y 395 PKMT-FTVLGSSVSPV--QLNINERKIQHGNHVPKSVSCSSDCEGQRVYT-CFH 449

Db 548 VCCPDLCSGKISNTDSMECTSCPEDFWSSPQDHCVPKRTBELSYHEPLG-ICLTA 606

Y 450 HCEPCVCGAGTFLNKSELRQPCGTEBMAPESSQTCFPTVYFLRLRETTSVLLAA 509

Db 607 ASLGTIVSVVVLGIFIHRRSTPVVRRANSELFLVLLSLKLCFLCSLL-FIGRRLWTC 665

Y 510 NTL-LILLGLTAGLTFAMHLDTPVRSAGRGCLFMGLSAGSG-SLYGFFGPTPAC 567

Db 666 QLRHAAGISIVLCVSCILTKMYLVAVFRASKGGGATLKRCAVQORGT-VLGLTSIQ 724

Y 568 LIRQALFALGFTIFLSCLTVRSFOLIIIFKSTVPPTFYHAMWON-IGAGIFVMISSAQ 626

Db 725 AALFAMLLSSPKPHKNIOYHKDKIVFECVSGTGVFAVLISYGLLAILFLPLAR 784

Y 627 LILCLTLVMTPLPAREYQRFHLVMECTETNSLGFILAFYLNGLISAFACSTLKG 686

Db 785 NLPDNEAKLITPSMDI-FCAYVAVFVPAYINSRGYADAVEFAILTSFGLLVAFG 843

Y 687 DLPENYDAKCVTSLFLNFVS-WIAFFTASYVDGYLPAANMAGLSSISGFGYFL 745

Db 844 PKCYILLFRPERNT 857

Y 746 PKCYILLCRPDLNS 759

RESULT 6  
ID 073639 PRELIMINARY: PRT: 880 AA.

AC 073639;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE PHEROMONE RECEPTOR.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
[1]

RM SEQUENCE FROM N.A.  
RP MEDLINE; 98226788.

RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,  
NAKANISHI S., BRENNER S.;  
"Putative pheromone receptors related to the Ca2+-sensing receptor in  
Fugu";  
Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

DR EMBL; AB008861; BAA26126.1; -.  
DR PFAM; PF00003; 7tm\_3; 1.  
DR PFAM; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.

KW Pheromone.  
SQ SEQUENCE 880 AA; 97464 MW; 91D72807 CRC32;

Query Match 21.8%; Score 1271; DB 13; Length 880;  
Best Local Similarity 30.6%; Pred. No. 8.07e-238;  
Matches 247; Conservative 214; Mismatches 298; Indels 48; Gaps 40;

Db 83 CTRSFRRFMOMTFAVEINNAELIPNLITGLYKTYDSCSPHOSIKRAIDL-MGSE 141

Y 3 CS-FNEHGHLFQMRGLVEEINNSTALPLNTLGLYQYDSCSANYATRLVSLRQ 61

Db 142 KDSQFEGKLRGGCGDNVAVIGDGSSTOSLVARFLGVFHPVQVSFYSSCACLSDKTOF 201

Y 62 HHIELQGLLH-YSPVYLVAVIGPDSINRAATTAALSPFLV-HISTYASSETLSVKRYP 118

Db 202 PAFLRMPDSLFOVQALVQYKFGMTWGVYIAGDDAYGRGAAIFANEVRRLLGACTALY 261

Y 119 PSFLRTIPDKYQVETWVLLQKFGMTWISLVGSSDDYQGLQVQALBNALYRGIACIAFK 178

Db 262 EMIR-KTQ-SQAAISIIISNRSSGAVLVFVNEQVYRLF-DEAYRQKITGLQWLASE 318

Y 179 DIMPFSAQVGDERRMOCLMRHLAQAGATVVVSSRQ-LARVFESVLTJLTKRVVVA 237

Db 319 AMSTAAILSTRKRYHILQSGMGFAIRRADIPGQDFLRLRHPSSAADDPFLIPWEE 378

Y 238 AMALSRTHTGVPQIQR-IGVILGVALIQRAVPGKAF-EAY-ARAD-KEAP--RPGHKG 291

Db 379 VFQCLDPHGSSEAKRCSGTEELRSVKNIYSDVSQILISYNYKAYVALAYAIKAMRSC 438



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OY 292 SW-CS--SN-OL-C-RECOAFMA-HIWPKL-KAFS-MSSAYNAYRAYAAHGLHOLLGC 342
Db 439 EKSGSPSOACPDLDNIHPMOLHHYIKOYNYTRFGEDEIKFDENDGPAAWYDLINMOLT 498
OY 343 ----A---SEL-CGR-GAVYWMOLLEOJHAKVFLH-KDYAFNDNRPLSSYNIANDWN 393
Db 499 PGDDMDFTVYKGEDDIAGTRKNIHIEEKIYVNGNTOVPLSVCSICPGTRKAIKRN 558
OY 394 -GRKMF-TV--LGS-STWSPVOLINETKIOWHGNHQVPKSVCSDDCLEGHORVY-TG 447
Db 559 YPLCHDCVYCTGGEISNQDIAECARCLEPFENSNADRTCKVROVEFLSFGDTIGALL 618
OY 448 FHHCECEVCGAGTFLNKSSELYRCQPCGTEWMAPECSQCFTPTVFLALREHTSVLL 507
Db 619 VV-SLIGSEFCAVALVEFHRTPSPIRANNSDSELLLSLICEFSLFISPPQWS 677
OY 508 AANTLLELLGLTAGL-FANHLDTPVRSAGRLCFMLGSLAAGSGLYGFGEPTRPA 566
Db 678 CMLRHTAFGITFVLICISLIGKTIIVLMAFRALPGSDVMK-WFGPKOKAILITFTLVQ 736
OY 567 CLRLQALFALGITFELSLCLVRSFOLLIFKSTKYPTFHAWQNGAGLFWISSAQ 626
Db 737 VYICTWLVV-APPTPOIYPRESAIIILLDCBSSTAFSLVGYIGVLAQKCFLAFLA 795
OY 627 LILCLTMLVWYTPDLPAREY-QREPHLWLECTEINSLGFLAFLYNGLLISAFACSYLG 685
Db 796 RKLPDNEARLLAFSLMI-FCAMVMAFVPAIYSSPGKYSTLITEIFALLS-SYGLLGI 853
OY 686 KDLPEINNEKCYTSLFLEFVS-WIAFFTASYDGKYLPAANMAGLSLSSGFGGY- 743
Db 854 FAPKCYIILMKSEKTRKHLMSKSEF 880
OY 744 FLPCYVILCRPDLNSTEHQASIQDY 770

RESULT 7
ID 093552 PRELIMINARY: PRT: 844 AA.
AC 093552:
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE PUTATIVE ODOURANT RECEPTOR.
GN GEBL.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OLFACTORY EPITHELIUM;
RX MEDLINE: 98426265.
RA CAO Y., OH B.C., STRYER L.;
RT "Cloning and localization of two multigene receptor families in
RT goldfish olfactory epithelium."
RL Proc. Natl. Acad. Sci. U.S.A. 95:11987-11992(1998).
DR EMBL: AF083080; AAC64075.1;
DR PFAM: PF00003; 7tm_3.1;
DR PFAM: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRNGR.
SQ SEQUENCE 844 AA: 94599 MW: 7A84F7AC CRC32:

Query Match 20.8%; Score 1217; DB 13; Length 844;
Best Local Similarity 29.2%; Pred. No. 5,15e-226;
Matches 227; Conservative 209; Mismatches 312; Indels 30; Gaps 30;

Db 67 SCSSVNLRFRLAQTIFAIOENKNEILLPNISIGYIIVDTGSSRLST-MTA-TMGIMN 124
OY 2 SCS-FNEHGYHLFOAMRLGVEEINNSTALLPNITLIGYQLDYVCSDSANYATLRLVSLPG 60
Db 125 SQDFG-PGNICNGHSPHAIIGSETSATYILSTTGPFKIPYISHSSCECLSNRKNYP 183
OY 61 QHIELOGDLHSPYLAVIDPSTNRATTAALLSPFLVH-ISTYASSETLSVKRQYP 119
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Db 184 SFFRTISSDYHOSRALASIVKHFHGWVWGANSDNDYGNNGMAIFLTVQEGICVEY-S 242
OY 120 SFLRTINDKXYQETWYLLQKFGWTKTISLVGSSDDYGGQGLVALENGALVRGICIFKD 179
Db 243 VK-PY-RTETEKLRKVVDTIKGTAKYVAFISFVENG-ILIEQLSIONITGQMIGVER 299
OY 180 IMFSAQVGDERRMQCLMRHLQAQATVYVYSS-RQLARVFESVYLTNLTKWMAVASEA 238
Db 300 WIANATFTKSLHMGSGIFAM-KK-?-NIGFAE-YAMKFPWDIAFCSSEGNYSK 355
OY 239 WALSRHTTGVPGIQRIGWLVGAIQKRAVGLAFEBAYR-RADKREPRCHHG-SWCS 296
Db 356 YALSCSYEEELAKXVYSEVYETERYSSVYKAVAAHSLKIKOEGCEKPIQ 415
OY 297 NOL-CRECOAFMAHTMKLAFMSKSSAYNAYRAYAAHGLHOLLGAS-ELCSRG-RVY 353
Db 416 PQOVETLKRKINFATKTDWTFDSTGTVALYEVVNMQDSQTYQKSVGYDASLPT 475
OY 354 PMOLLEQIHKVHFLHK-DYAFNDNRPLSSYNIANDWNGP-KMTFTVLGS-STWSPV 410
Db 476 YQNHILNVENTIYAGHLEPRASCSCEPGTRKA-CXGRPFCYCIICAGGEISNET 535
OY 411 -Q-LNINETKIOWHGNHQVPKSVCSDDCLEGHORVY-TGFHRCCEPCVCGAGTFLNKS 467
Db 536 RFINCKKCPMEYMSNAEKNKCVLKAVEFLSFTETMG-VLVFSLPGVGLLVAILFYN 594
OY 468 ELTRCOPCGIEENAPBESQCFRTVYFLALREHTSVYLAANTLLIL-LILGAGLFAW 526
Db 595 KDDTPYKANNSLSFLFLSLFCLSLFTIGRPTWSCMLCHAFGITFVLICISCVL 654
OY 527 HLDTPVRSAGRLCFMLGSLAAGSGSYGFGEPTRPACLLRQALFALGITFLISCLT 586
Db 655 GKTIIVLMAKATLPNGNINIK-WGPAQQLSLVAFETLVYCCVLMLTISPPPYNNMK 713
OY 587 VRSFOLLIFKSTKYPTFHAWQNGAGLFWISSAOLLICLTLVWYTPDLPAREYQ 646
Db 714 YXKEIILFECSLSTIGFWLVITYISLAFCLFLAFARTLPDKNEAKFITFSMLI-F 772
OY 647 RPHLWLEBETENSLGFLAFLYNGLLISAFACSYLGDLDBENYEAACVFFSLFNF 706
Db 773 CAVWITTFIPAYVSSPKFTVAVEIFAILSSFGLLGIFAPKCYIILKPEQNTKQHL 830
OY 707 VS-WIAFFTASYDGKYLPAANMAGLSLSSGFGGYFLPCYVILCRPDLNSTEHF 763

RESULT 8
ID 073635 PRELIMINARY: PRT: 940 AA.
AC 073635:
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE CALCIUM2+ SENSING RECEPTOR.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 98226788.
RA NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,
RA NAKANISHI S., BRENNER S.;
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
RT Fugu."
RL Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
DR EMBL: AB000857; BAA26122.1;
DR PFAM: PF00003; 7tm_3.1;
DR PFAM: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRNGR.
DR PRINTS: PR00592; CASENSINGR.
SQ SEQUENCE 940 AA: 105814 MW: 034CB09E CRC32:

Query Match 20.8%; Score 1216; DB 13; Length 940;
Best Local Similarity 30.7%; Pred. No. 8,51e-226;
```







RESULT	10	
ID	073640	PRELIMINARY: PRT: 875 AA.
AC	073640:	
DT	01-AUG-1998 (Tremblrel. 07, Created)	
DT	01-AUG-1998 (Tremblrel. 07, Last sequence update)	
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)	
DE	PHEROMONE RECEPTOR.	
GN	CA15.1.	
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;	
OC	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;	
OC	Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE: 98226788.	
RA	NAITO T., SAITO Y., YAMAMOTO J., NOZAKI Y., TOMURA K., HAZAMA M.,	
RA	NAKANISHI S., BRENNER S.;	
RT	"putative pheromone receptors related to the Ca2+-sensing receptor in	
RT	Fugu."	
RU	Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).	
DR	EMBL: AB008862; BAA26127.1; -	
DR	PFAM: PF00003; 7tm_3; 1.	
DR	PFAM: PF01094; ANF_receptor; 1.	
DR	PRINTS: PR00248; GPCRMR.	
KW	Pheromone.	
SQ	SEQUENCE 875 AA: 94934 MW: 8FC188F2 CRC32;	
Query Match 18.38; Score 1066; DB 13; Length 875;		
Best Local Similarity 31.08; Pred. No. 3.95e-193;		
Matches 246; Conservative 203; Mismatches 288; Indels 57; Gaps 45;		
Db	91 AMFEAVEINHSALLPGVKLYGHIRDSQA--LHPMTQALALVVGDSASCELTAPA-D 147	
Qy	15 AMFLGVEIINNSALLPNTITLGLYDVCSDSANVATLEVLSL-PEQHHT-ELQGDLLH 72	
Db	148 YSAETSEKGAASVPLIIGAGSSMAAKILGLTSLPISVSTASPCISDRHRYPTFERIM 207	
Qy	73 YSTVLAVIGPDSTN--RA-ATL-AA--LLSPF-LVHISVAASETSLSVKROGPSFLRTI 125	
Db	208 ASPTIYQAOLAVLRFNNTIGAVVANDYGVAAKVVEQIQGVCVLAFTETLORET 267	
Qy	126 PNDRYQVETMVLLOKFGWTWISLVGSSDDYQOLGVALENOALVAGICIAFDIMPFSA 185	
Db	268 IYVDA--VR-AARTIQASTARVILVFSWYPTDVGHLFRO-LOKINVTROQLFASMSSEV 324	
Qy	186 QYDEDMQCMRLAAGATVYVVFSS-RQLAVFESVYLTNLTKVWYASAMALSRH 244	
Db	325 LKPDPTSTVAGSVGVAIASQHPGFDRFLRGLNPSLRPSDKFLQEFWEFEFGCSPP 384	
Qy	245 ITGVPGIQRIGM-VLGVAIQRAVPGIKAF--E-EAVAR-ADK---E--APR-PCHKGS- 292	
Db	385 SSETSDNLNASLPPCGSAELEGVQHPTDTSRLRVTYNYLAVYAAANALHSLSCPIH 444	
Qy	293 WC--SSNQL--C-RECOAFMA-RTMPK-LKAFS--MSSAYNRAVYVAVAHOLHLLGC--- 342	
Db	445 NSPSGTSHTSPGKITTELOHLSKVNFTTPGKHLHYFGADIPAMYDINN-SDTGG 503	
Qy	343 -A-SEL--CSRGR-VYPMOLLEOIHKVFHLKADYAFNDNRPLSYNTIANDWNGPKW 397	
Db	504 TLQVLIGAV-AGFDQLNLESEMSAKYQNVVSVCSSESPGTRKANRKGHPLOCDFC 562	
Qy	398 TFL-VLGSSWSPVQININTKIQWHGKNHQVKSVCSSSCLLEGHQRYV-TGFHHCCFEC 455	
Db	563 IPCADSEINISGLQDCRPPFPFSDGRTACVPROLDLSTNELG-VALLAVAVSGA 621	
Qy	456 VPGAGTFLNKSFLYRCOPCGTEEMAPESQOTCFPRIVFLALREHISWILLANLILL 515	
Db	622 VVTAIVFVFLRHRTPMRANSELSEFLDLTLKLCFLCSLVEIGRPSWVSRCFOQAAF 681	
Qy	516 LILGTA-GLFAHMLDTPVYASAGRLCFLMLGLAAGSGGLYFEGEPTRPOLLRLQALF 574	
Db	682 GISFVLVCSLOYKTIIVLAAFRSARPGAGLMMKFGPSOORGSVCITFCVQARVILIIV 741	

Qy	575 ALGFTIFLSCLTVRSFOLLIEFKSTKVPFYHAW-QNNGAG-LFVIMSSAAQLLICLT 632	
Db	742 WLSLSPVPVQADLD-VPGLOYTIECAMASVGSVLGYIGLACTCLLAFIARLPDN 800	
Qy	633 WLWVWPLPARERYQRPPL-VMLECTEINSLGFIALFVNLGLSISAFACSYGKGLPEN 691	
Db	801 FNEAKLITFSMLI-FCVAVVAEVPAYISSPGKSVAVETFAIILAS-SYGLHFCIFAPKCF 858	
Qy	692 YNNAKCVTSLSLNFWS-MIAFTTASVYDGKATLPANMAGLSLSSGFGI-FLPKCY 749	
Db	859 ILLRPEKNTKML 872	
Qy	750 VILCRPDLNSTEHF 763	
RESULT	11	
ID	070410	PRELIMINARY: PRT: 912 AA.
AC	070410:	
DT	01-AUG-1998 (Tremblrel. 07, Created)	
DT	01-AUG-1998 (Tremblrel. 07, Last sequence update)	
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)	
DE	POTATIVE PHEROMONE RECEPTOR V2R2.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	TISSUE=VOMERONASAL NEURONS;	
RX	MEDLINE: 97436753.	
RA	RYBA N.J., TIRINDELLI R.;	
RT	"A new multigene family of putative pheromone receptors."	
RT	Neuron 19:371-379(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	TISSUE=VOMERONASAL NEURONS;	
RA	RYBA N.J.P., TIRINDELLI R.;	
RU	Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.	
DR	EMBL: AF053986; AAC08413.1; -	
DR	PFAM: PF00003; 7tm_3; 1.	
DR	PFAM: PF01094; ANF_receptor; 1.	
DR	PRINTS: PR00248; GPCRMR.	
SQ	SEQUENCE 912 AA: 102348 MW: 35AEE35A CRC32;	
Query Match 17.08; Score 994; DB 11; Length 912;		
Best Local Similarity 28.48; Pred. No. 1.59e-177;		
Matches 231; Conservative 224; Mismatches 291; Indels 68; Gaps 51;		
Db	77 CEGFNFRGRMKTMTHTIKETINERDILPNHTLGQIFDSCYTISKAMSSSL-VF-LTG 134	
Qy	3 C-SFNHGYLEPAMRLGVEIINNSALLPNTITLGLYQVLDVC-SDANVATILRVLSLG 60	
Db	135 QE--EFKPYERNSTGSTLALVSGSSSVAASTRILGLLYMPQVGYTSSCSILSKFOF 192	
Qy	61 QHHEILOGDLHNSPYVLA-VIGPDSTNPAATTAALLSPF-LVHISYASSETLSVKROY 118	
Db	193 PSYLRVLPDSNLOSEAIYVULIKHFQWYGAIAADDYQKYGKTKKEMESANLQVARS 252	
Qy	119 PSFLRTIPDKIOVETMVLLOKFGWTWISLVGSSDDYQOLGVALENOALVYRGICIAK 178	
Db	253 ETTP-KV-VSNEMKCAVAVKTSKAVIVLYVSDIDS-LFVLEMIHNITPRTIATE 309	
Qy	179 DIMPESAGQDEMQCMRLAAGATVYVVFSS-RQLAVFESVYLTNLTKVWYASAMALSRH 237	
Db	310 AMTSLIAKPEYFPYFGGTIGFAPRSVPIGKEFLYVUHNPKNDBNDVLTIEFWOTAFN 369	
Qy	238 AMALSHIITGVPIQIRIGWILGVAIOKRAVPGIKAFE-EAYARAD-KEA-PRPC-HKG-- 291	
Db	370 CTMPNSSVYVNDHRNMKGEKEDRLDMSDQOLCTGGEKLEDKNTYLDLSQRLITQOCO 429	
Qy	292 -SWC-SS--N-Q--LC-RECOAF-KA-H-T--TPKTK-AF-SMS--SAYNAYR- 327	
Db	430 AVYAIAHGIDHLSRCQEGGPFSGNOCAVIPTDFWQLMYVYKKEIKFKSHEDKWILDD 489	



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QY 328 AYAVAGLHQLGQC-ASE--LCSRRG-VY-P---WQLEQIHKVHFLHKDT-VAFND 377
D 490 NGDKNHYDVLMMHLDDEGEISFVTVGRFNFRSTNFEVLTPTNSTLFMTNTESSRRDSE 549
QY 378 NRDLSS-YN1IAMDNGP-KWITTVLGSSST-WSPV-QLN-NEFKIQMGKNQVRSV 432
D 550 CTOWCPGRTKRGNOGPICCFDCPCADGVSEKSGORECDPCGEDMWSNAGSKCVPK 609
QY 433 CSSDCEGHQRYVYGFHH-CQFECVPGAGVYFNKSELYRQPGCTEMAPESQOTCFPR 491
D 610 LVEFLAEGALGTLVLTSTFGALVYLAIVYVYIHRHTPLVYKANDRELSFLIOMSLVIT 669
QY 492 TVYFLALRETSVYLLAANLTLTLGLTGLFAMHLDTPVRSAGRLGFLMGSLIAG 551
D 670 VLSSL-FICKPCWMSMAROITLAGECLSLISLTKTISLEFARISVSKTRLI-S-M 726,
QY 552 S-GSLVGFEEPRPACLLKRALFALGTLTLFSLCTVRSFOLITIFRSTKVPFTYHMY 610
D 727 HPIFRKLIVCVYGEIGVCAAYLVLEPPRMFKNE-IONVKIIFECNE-GSYELCSIF 784
QY 611 QNAGAGLFWMISSAQLICLTWLVVWTPLPAREYQRFPH-VLLECTETNSLGFI-LAF 668
D 785 GFDVRLALFLTLTVARQLPDNTYBCKCTFGMLVFFIYVWISVPAYLSTGKFKYAVE 844
QY 669 LYNGLSLISAFACSYLCKDLPENYNEAKCVFSLFNFVSIAPFTASVYDKYLPAN 728
D 845 IFALIAS-SYLLGCLFLPFCFIILRPKRNTE 877
QY 729 MAGLSLSSGFGY-FLPKCYILCRDLNSTE 761

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RESULT 12
ID 070409 PRELIMINARY: PRT: 855 AA.
AC 070409:
DT 01-AG-1998 (Tremblrel. 07, Created)
DT 01-AG-1998 (Tremblrel. 07, Last sequence update)
DE 01-MAY-1999 (Tremblrel. 10, Last annotation update)
OS PUTATIVE PHEROMONE RECEPTOR V2R1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-VOMERONASAL NEURONS;
RX MEDLINE: 97436753.
RA RYBA N.J., TIRINDELLI R.;
RT "A new multigene family of putative pheromone receptors.";
RL Neuron 19:371-379(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-VOMERONASAL NEURONS;
RA RYBA N.J.P., TIRINDELLI R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF053985; AAC08412.1; -
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR SEQUENCE 855 AA; 96215 MW; C8389BJC CRC32;

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Query Match 16.2%; Score 946; DB 11; Length 855;
Best Local Similarity 28.3%; Pred. No. 3,72e-167;
Matches 223; Conservative 204; Mismatches 313; Indels 49; Gaps 45;

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D 79 YOHIAVFAIEKINKNDPILFNKSLGFFLVNFVIMKAEGSMAL-LGESPPIPNYS 137
QY 10 YHFOARLVEELINNTALPNTLTGLQYDVCSDSANVYATLRVLSFGQ-HHIELOG 68
D 138 CREPKTDKLVAVIGISTSIQISRYLSYXNPQISYAFPDQILGTQVLOQSPQFSMH 197
QY 69 DLHYSPTVLAIVGPDSTNAATTAALLSPVLY-HISYASSSELVSKRQYPS-FLATIP 126
D 198 TAAIYQ-GIVOLLV-FTWIVGLVDPDMRGELVLRDITREKIMSHGICFAFAKETEYS 255

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QY 127 NDK-YOYETVALLQKFGWTWISLVGSSDDYDGLGYOALENOALVIGICIAFKD-IMPFS 184
D 256 SMDTVMKH-FMERLTLT-PVITVGDTHSLRIYV-FVYFVLGSGWTTSDWTITTL 312
QY 185 AOVGDERMOCLMHLAQAGATVYVYVSSROLANVFESVYLTILTKRWYASAMLSRH 244
D 313 PFONLTYTHFGGSLFSFSEMEDILGFKDPLRSQVPRKYPHDFIRHVSLSFGCPHYQ 372
QY 245 ITGVPGI-QRIGVAVLQIKRAVPGLKAFEEAY-ARA-DKEA-PRPKHGSN-CSSN-Q 298
D 373 HRMLDSQCEPNSSITRPLHAMDANTSPYKYVYAAVYALAOALHEELSLREGSSNK 432
QY 299 -L-C-RECOFAHATMPKLAFSM-SS--AYNARYAVAVAGHLQ-L-L--GCASEL 346
D 433 CLLOAPLPWKLHPFOQKAO-IGRSTNEENTVNE-VSATKLDIFNYSQSLQSGTEAHVKG 490
QY 347 CSRGRTYPMOLLEQIHKVHFLHKDTVAENDNDPLSTNITAMDNGPRW-TFT-V-IG 403
D 491 EFVDSHVSQHLSLNDKILTW-GKHSQTPLSVCSQCFEFSKTAVEGKPFCCFCVPC 549
QY 404 SSTW-S-PVQ-LINNETKIQMGKNH-QYPKSYCSSDCLGHRV-VTGFHCCFCVPC 458
D 550 PDEIANKTDMHCCICPEQYFNKQKNOCLPKIITFLAHEDPLGVLYSLAISAFSA 609
QY 459 GAGTFNKSLEYLQCPQGEEMAPESQOTCFRTVYLAIRETSVYLLAANTLILL 518
D 610 MGLGFCYAREPIYVANNRNLSTYLLISLKLFCFSL-FIGQPRVYCVLRQIIFGIY 668
QY 519 GTAGLFRMHLDTPVVSAGRLCFMLGSLAAGSG-SLGFEEPRPACILRALFALG 577
D 669 FSIVISAILAKPIVYVAK-AIKPGSILKMGVTRLSNAYVCCSIIQVCIQAVLGTY 727
QY 578 FTIFLSCLTVRSFOLITIFRSTKVPFTYHAWQNGAGLFWISSAQLICLTWLVYW 637
D 728 PPPDDVMHSEFQIILM-CNEGSTIATFCVGLGFLASLILFLARLPDSNEAK 786
QY 638 TPLPARYOR-FPHVLWLEDETENSLGFIATLYNLSISAPACSYLCKDLPENYNEAK 696
D 787 TTFESMLV-FCSWISFVPAYISSKGTMYAVELISLAS-SAGLGCFLPFCYILAK 844
QY 697 CVFSLFNFVS-WIAFFTASYDCKYLPANMAGLSLSSGFGY-FLPKCYILCR 754
D 845 SGHSSRRK 853
QY 755 PDLNSTEHF 763

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RESULT 13
ID 035269 PRELIMINARY: PRT: 779 AA.
AC 035269:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-MAY-1999 (Tremblrel. 10, Last annotation update)
OS PUTATIVE PHEROMONE RECEPTOR.
GN GO-VNS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE: 97433086.
RA HERRADA G., DUDAC C.;
RT "A novel family of putative pheromone receptors in mammals with a
RT topographically organized and sexually dimorphic distribution.";
RL Cell 90:763-773(1997).
DR EMBL: AF016182; AAC53329.1; -
DR PFAM: PF00003; 7tm_3; 1.
DR PFAM: PF01094; ANF_receptor; 1.
DR SEQUENCE 779 AA; 88036 MW; B89CEAD5 CRC32;

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Query Match 15.7%; Score 915; DB 11; Length 779;
Best Local Similarity 25.5%; Pred. No. 1,79e-160;

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\*\*\*\*\*  
 W E S E L E  
 (TM)  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:29:20 2000; Maspar time 43.87 Seconds

Tabular output not generated. 528,906 Million cell updates/sec

Title: >US-09-361-652-3  
 Description: (1-777) from US09361652.pep  
 Perfect Score: 5838  
 Sequence: 1 RSCSFNHHGYHLFOAMRLGV.....NSTHFQASIDQYTRCGST 777

Scoring table: PAM 150  
 Gap 11

Searched: 82229 seqs, 29854856 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 53.443; Variance 92.251; scale 0.579

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1170	20.0	1085	1	CASR_BOVIN	1.05e-237
2	1160	19.9	1078	1	CASR_HUMAN	2.67e-235
3	1158	19.8	1079	1	CASR_RAT	8.09e-235
4	856	14.7	912	1	MGR4_RAT	9.24e-163
5	846	14.5	912	1	MGR4_HUMAN	2.13e-160
6	798	13.7	1203	1	MGR5_RAT	4.44e-149
7	796	13.6	1199	1	MGR1_RAT	1.31e-148
8	796	13.6	1212	1	MGR5_HUMAN	1.31e-148
9	789	13.5	872	1	MGR2_RAT	5.82e-147
10	787	13.5	1194	1	MGR1_HUMAN	1.72e-146
11	772	13.2	908	1	MGR8_MOUSE	5.74e-145
12	768	13.0	908	1	MGR8_RAT	4.99e-142
13	761	13.0	872	1	MGR2_HUMAN	2.19e-140
14	757	13.0	908	1	MGR8_HUMAN	1.90e-139
15	729	12.5	871	1	MGR6_RAT	6.82e-133
16	731	12.5	877	1	MGR6_HUMAN	2.32e-133
17	718	12.3	879	1	MGR3_RAT	2.54e-130
18	714	12.2	877	1	MGR3_HUMAN	2.18e-129
19	675	11.6	915	1	MGR7_HUMAN	2.64e-120
20	674	11.5	915	1	MGR7_RAT	4.50e-120
21	452	7.7	976	1	MGR_DOME	2.12e-69
22	333	5.7	999	1	MGR1_CAELI	2.05e-43
23	150	2.6	986	1	CYGR_ARBPU	1.21e-07

RESULT	1	STANDARD	PRT	1085 AA.	ALIGNMENTS
ID	CASR_BOVIN				
AC	P35384				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR).				
GN	CASR OR PCAR1.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
OC	Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;				
OC	Bovinae; Bos.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PARATHYROID.				
RX	MEDLINE: 94077182.				
RA	BROWN E.M., GAMBA G., RICCARDI D., LOMBARDI M., BUTTERS R., KIFOR O., SUN A., HEDIGER M.A., LYTON J., HEBER S.C.;				
RT	"Cloning and characterization of an extracellular Ca(2+)-sensing receptor from bovine parathyroid."				
RL	Nature 366:575-580(1993).				
CC	-1- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL: S67307; AAB29171.1; -.				
DR	PIR: S40476; S40476.				
DR	GCORDB: GCR_0900; -.				
DR	PROSITE: PS00979; G-PROTEIN RECP_F3.1; 1.				
DR	PROSITE: PS00980; G-PROTEIN RECP_F3.2; 1.				
DR	PROSITE: PS00981; G-PROTEIN RECP_F3.3; 1.				
DR	PRAM: PF00003; 7tm_3; 1.				
DR	PRAM: PF01094; ANF_receptor; 1.				
KW	G-protein coupled receptor; Transmembrane; glycoprotein; signal.				
FT	SIGNAL 1 19				



























FT VARSPLIC 876 907 MISSING (IN ISOFORM 5A).  
 SQ SEQUENCE 1203 AA; 131885 MW; 2955EA33 CRC32;

Query Match 13.7% Score 798; DB 1; Length 1203;

Best Local Similarity 26.4%; Pred. No. 4,44e-149; Matches 212; Conservative 207; Mismatches 329; Indels 55; Gaps 51;

Db 55 RKGAVREOYGIORVEAMLTLELRINSPTLLPNTLTCCELDSCWMSVALEDSIEFIR 114  
 1 RSC-SFNH-GYHLFOARLGYEELNNSTALLPNTLITGLDVCSDSANYA-TLR-VL 56  
 Db 115 DLSISEEEGLVRCVDSRSSRKKPIYGVIGPSSSAIOVONLLEPNIPQIAYSAT 174  
 57 -SL-PGOHHEIL-Q-GD-LLHY-SEPT-VLAVIGPSTNAAATALLSPFLV-HISYAS 108  
 Db 175 SMDSDKTLFKFMVYSDAQAARAMDIVRYKMTVYSAVHTEGANGESMEAFKMS 234  
 109 SETLSVKQYPSFLKTPIDKXQVETWVLLLOKFEWMTWISLSSDDDGQGLVQALEMOA 168  
 Db 235 AKEGICIA-HSYKIXSN-AGESEFDLKLKLSHPKARVAVACEGEMTVRGLAMRRL 292  
 169 LVRGICIAFKDIMPFSAGVDERMOCILMRHL-AQ-AGATVVVVFESSRLARVFEFSVYL 226  
 Db 293 GLAGEFLLGSDGMA-DRYDV-TDGYORA-VGITT-KLOSPDYKWPDDYLYLRPETN 348  
 227 NLTKR-VWVASEAMALSHHITGVPGIORIGWLVGAIOKRAVPGIKAFEEAAYA--RADKE 283  
 Db 349 LRNPFOFQWOFRO-CLEGEFAOENSKYKNTKCNSSLTRTHVODSKMGFINAYGMA 407  
 284 APRPHKSKWSSNOLCR-E--CO--A-F-MA-HTMPKIKASMSASATNA--RAVAVAA 333  
 Db 408 YGLHNMWMSLCPGYAGLDDAMKPIDGRKLLSLMKTNFTVSGMDILPDENGDSRGREI 467  
 334 HGLHLQ-LG-CAS-E-LCSRGR-VYPMQLEQIKHVHFL-LKQIVAFANDNDPLSYNI 387  
 Db 468 MAFKMGADY-FDIYVNGSWNGELKADDEY-W-SKNNITRVSCEPCEGQITVIRK 524  
 388 IAMDNGKRWTFYVYSSSTWSPVQNLINETKIQMHGKNHVKYSVCSCLLEGHORVY-T 446  
 Db 525 GEVSCWMTCPCKENEYAF-DE-YTCRACQQLGSWPTDLDLPGVYLRMGDEPIAA 582  
 447 GFHHCFCPCVPGAGTFLLKSELKYLKQPCGTEEMAPESQTCFPTTVFLLARETTSWL 506  
 Db 583 VYFACIGLALTLFVVFILYRDPFVYVSSSRELQYIILAGICGLYCFCLIAKPKOY 642  
 507 LAANTLTLTLGLTAGLFAMHLDPTVVSAGRGLCFIMGLSLAAGSGLYGFEPTRA 566  
 Db 643 CYLORIGIGLSPAMYSALVTKTNRIARILLAGSKKIKCTKPRFMSACAQVIAFILCI 702  
 567 CLLRQALALGFTIFLSCILTVASFQIIFRSTK-VPTFYHAMVONHGAGLFVMISSAA 625  
 Db 703 OGIIVAFLEPPDLMHDYSIRE-VYLICNTN-LGVVPLAGYNGILLISCFE-VAFK 759  
 636 OLLILTLWVWTPLPAREYORFPLVMECTETSLSGLITLFLYNGLLIS-ARACSL 684  
 Db 760 TRNPANFENAKYIAFTYTCIWLAF-VPIY-FGSNYKIITMCFVSLSA-TVALGCM 816  
 685 GKDLPEINENAKCVFSLFLNFVSMIAFTTASVYDGR-LPAAMMAGLSLSSGFGY 743  
 Db 817 FVPKYITILLAPERNVRSALFTTS 839  
 744 FLPKYVILCRDLNSTEFOAS 766  
 RESULT 7  
 ID MGR1-RAT STANDARD; PRT: 1199 AA.  
 AC P23385;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-DEC-1999 (Rel. 39, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.  
 GN GRM1 OR MG1UR1.  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGE-DAMLEY; TISSUE-BRAIN;  
 RX MEDLINE; 91156047.  
 RA MASU M., TANABE Y., TSUCHIDA K., SHIGEMOTO R., NAKANISHI S.;  
 RT "Sequence and expression of a metabotropic glutamate receptor.";   
 RL Nature 349:760-765(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 92022526.  
 RA HOUVAMED K.M., KUIJZER J.L., GILBERT T.L., HALDEMAN B.A., O'HARA P.J.,  
 RA HOUVILL E.R., ALMERS W., HAGEN F.S.;  
 RT "Cloning, expression, and gene structure of a G protein-coupled  
 glutamate receptor from rat brain.";   
 RL Science 252:1318-1321(1991).  
 RN [3]  
 RP ALTERNATIVE SPLICING (1B).  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 92110002.  
 RA TANABE Y., MASU M., ISHII T., SHIGEMOTO R., NAKANISHI S.;  
 RT "A family of metabotropic glutamate receptors.";   
 RL Neuron 8:169-179(1992).  
 RN [4]  
 RP ALTERNATIVE SPLICING (1C).  
 RC TISSUE-BRAIN;  
 RX MEDLINE; 93066232.  
 RA PIN J.-P., WAEBER C., PREZEAU L., BOCKAERT J., HEINEMANN S.F.;  
 RT "Alternative splicing generates metabotropic glutamate receptors  
 inducing different patterns of calcium release in Xenopus oocytes.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10331-10335(1992).  
 CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS  
 MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
 CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL  
 ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM DEPRESSION IN  
 THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS: 1A (SHOWN HERE), 1B AND 1C;  
 ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY  
 TRUNCATED FORMS OF 1A.  
 CC -1- TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR  
 PURKINJE CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE HIPPOCAMPUS, AND  
 MITRAL AND TUFTED CELLS OF THE OLFACTORY BULB.  
 CC -1- MISCELLANEOUS: ACTIVATED BY OUTSULATE > GLUTAMATE > IBOTENATE >  
 TRANS-1'-AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY  
 2-AMINO-3-PHOSPHONOPROPIONATE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGURS.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X57569; CAA40799.1; -;  
 DR EMBL; M61099; AAI19497.1; -;  
 DR EMBL; S48085; AAB24138.1; -;  
 DR PIR; S15362; S15362.  
 DR PIR; A41939; A41939.  
 DR GCRDB; GCR\_0216; -;  
 DR PROSITE; PS00979; G\_PROTEIN\_RECEPTOR\_F3\_1; 1.  
 DR PROSITE; PS00980; G\_PROTEIN\_RECEPTOR\_F3\_2; 1.  
 DR PROSITE; PS00981; G\_PROTEIN\_RECEPTOR\_F3\_3; 1.  
 DR PFAM; PF00003; 7tm\_3; 1.  
 DR PFAM; PF01094; ANF\_receptor; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Multigene family; Alternative splicing.  
 FT SIGNAL  
 1  
 18



FT	CHAIN	19	1199	METABOTROPIC GLUTAMATE RECEPTOR 1.
FT	DOMAIN	19	592	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	593	615	I (POTENTIAL).
FT	DOMAIN	616	629	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	630	650	II (POTENTIAL).
FT	DOMAIN	651	661	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	662	680	III (POTENTIAL).
FT	DOMAIN	681	706	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	707	727	IV (POTENTIAL).
FT	DOMAIN	728	750	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	751	772	V (POTENTIAL).
FT	DOMAIN	773	785	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	786	808	VI (POTENTIAL).
FT	DOMAIN	809	814	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	815	840	VII (POTENTIAL).
FT	DOMAIN	841	1199	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	1014	1034	GLN/PRO-RICH.
FT	DOMAIN	1074	1080	GLN/PRO-RICH.
FT	DOMAIN	1126	1135	ASP/GLU-RICH.
FT	DOMAIN	1140	1199	SER-RICH.
FT	CARBOHYD	98	98	POTENTIAL.
FT	CARBOHYD	223	223	POTENTIAL.
FT	CARBOHYD	397	397	POTENTIAL.
FT	CARBOHYD	515	515	POTENTIAL.
FT	CARBOHYD	87	906	NSNKSYSWSPPGGRAPKG -> KRKPFPSPSQPSAH
FT	VARSPPLIC	887		AOL (IN ISOFORM 1B).
FT	VARSPPLIC	907	1199	MISSING (IN ISOFORM 1B).
FT	VARSPPLIC	888	897	SNKGSYSMS -> FALDRONTYV (IN ISOFORM 1C).
FT	VARSPPLIC	898	1199	MISSING (IN ISOFORM 1C).
SO	SEQUENCE	1199 AA:	133235 MW:	EB21AF2 CRC32;

Query Match	13.6%	Score 796;	DB 1;	Length 1199;
Best Local Similarity	27.1%	Pred. No. 1,31e+18;		
Matches	219;	Conservative 210;	Mismatches 318;	Indels 61;
				Gaps 51.
Db	65	KRCGEIREOYGIOQVEAMFHTLKDINADPVLTPNTLTSEIRSDSCMHSVVALEQISFIR	124	
Oy	1	RSCS-FNH-GYHLEQAMRLGVEEINNSTALLPNTLTQYLDVCSDBA-NVY-AT--LR	54	
Db	125	DSLIRIBKBOGLNKLCDGOTLPFGFKKRIAGYIGFGSSVAIOYONLLQFLDIPOLA	184	
Oy	55	-VL-SLPGQH-IE--L-QGDLHSP--VLAVIGDSTIRATTAALSP-LVHIS	104	
Db	185	YSATIDSDKTLKYLEFLRVPDILQARALDIVKRRMTYVSAVHEGNGESGDAF	244	
Oy	105	YAASETLISVRQYPSFIRITPNKQYQVETVLLQKRGWIMISLWSSDDYQGLQYAL	164	
Db	245	KELAAQBELCAHSDKT-YSN-AGEKSFDRLLKRLRELPKARYVVCFCBGATVGLISA	302	
Oy	165	ENQALVRCICAFIDIMFSAQVODERMOCIMRHL-AQ-ACATVYVFFSSROLARVFFES	222	
Db	303	MRLRGVGEFSLIGSDGA-DRDEV-IEGYE-VEANGGIT-KQSPFVRSFDYFLKL	358	
Oy	223	VLLNLITGKW-VASEAMALSRHILITGVQIDRIGIMLOVALQKRAVGLKAFEEAYN-R	279	
Db	359	LDTRNRNWFEEFNQHRQ-CRLDGHLENNFKVCTGNDSLEENTYQDSKMGFVINA1	417	
Oy	280	ADKCAPRCHKSGWCSSNQLQRECAFAAH-MPKL-KAF-SMGSAY--NA--Y--RAV	329	
Db	418	YAMAAGLQNMHALCPGHVGLCDAMKPRDGRKLLDFLTKSSFVSGSEVFEDEGDGAP	477	
Oy	330	YAAVHGHLQL-G-CASE--LCSNGR-VYPMQLLEQIHKVHFL-LHNDYAFNNRPLS	383	
Db	478	RYDLMNLOYTANR-YDVVHGVTGHEGVNLNDYKIQ-MKSGMY-RSVCSEFLKQOIK	534	
Oy	384	SYNTIIMWNGPKMTFTVLGSSITSPVOLNTEKIKIMHGKNNHVPKSVSSDCLDEHOR	443	
Db	535	VIRKGEVSCCMITACKENEFVQ-DE-FTCRADLG-WMPAELTGCEPIPVRYLEWSDI	591	
Oy	444	VV-TGFHNHCFCYCPGAGTFLNKSEIYRQCPGTEWAPRGSGT-CFPRVYVLAUREH	501	
Db	592	ESIIAIAASCGLIVTLFVTLIFVLYKRTPVYKSSSRELCTIILAGFLGYVCFI1IAK	651	

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QY 502 TSNVLLAANTLTLTLLLLLTGTAAGLFAHHDLPVVRSAOGRCLFCLMSLAAGSSGIVCFEE 561
Db 652 PTTTSCYQRLDIVGSSAMCYALVTKTNRIARIAGSKKICTRRPRFMSAAQVIAS 711
QY 562 PTPRACILRLQALFALGFTTFLSCLTVRSPQILIIKFS-T-K-VPTFYHAAWQNHGAQL 620
Db 712 ILISVQLIVLVLLIMEPPMLPSPIKE-VYLIC-NTSNAGVAPVQVNGLLIMSCIV 769
QY 621 ISSAQLICLILWLVWVWTPLPAREQREPHVLMECTETNSGFLIAFLYNGLLIS-AF 679
Db 770 -AAFTNRPANPANEAKYIAFTMYTCIIWLAF-VPVY-FGSGNYKIITCFVAVSLV-VAV 825
QY 680 ACSYGLKDLPEYNNAKCYTFESLLNPNYSWIAFFTTASVYDGI-LPAAHMAAGLSSSS 738
Db 825 ALGCMFTPRXIIIAKPERNVRSAFTTS 853
QY 739 GEGYFLPRPCVYILCRPDLNSTEHRQAS 766

RESULT 8
AC MGR5_HUMAN STANDARD: PRT: 1212 AA.
P41394;
Dt 01-NOV-1995 (Rel. 32, Created)
Dt 01-OCT-1996 (Rel. 34, Last sequence update)
Dt 15-DEC-1999 (Rel. 39, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR MGUR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94197696.
RA MINAKAMI R., KATSUKI F., YAMAMOTO T., NAKAYURA K., SUGIYAMA H.:
RT "Molecular cloning and the functional expression of two isoforms of
RT human metabotropic glutamate receptor subtype 5."
RL Biochem. Biophys. Res. Commun. 199;1136-1143(1994).
RN [2]
RP REVISIONS.
RA KATSUKI F.:
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 860-952 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 93343913.
RA MINAKAMI R., KATSUKI F., SUGIYAMA H.:
RT "A variant of metabotropic glutamate receptor subtype 5: an
RT evolutionally conserved insertion with no termination codon.";
RL Biochem. Biophys. Res. Commun. 194;622-627(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CC CHLORIDE CURRENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: 5A (SHOWN HERE) AND 5B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
CC 32 RESIDUES.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGUR1.
CC -----
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CC -----
DR EMBL: D28538; BAA05891.1; -
DR EMBL: D28539; BAA05892.1; -
DR EMBL: S64316; AAD13954.1; -

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EMBL: D28538; BAA05891.1; -.  
EMBL: D28539; BAA05892.1; -.  
EMBL: S64316; AAD13954.1; -.  
.....











FW	Signal	1	18	POTENTIAL.
FT	CHAIN	19	1194	METABOTROPIC GLUTAMATE RECEPTOR 1.
FT	DOMAIN	19	592	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	593	615	I (POTENTIAL).
FT	DOMAIN	616	629	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	630	650	II (POTENTIAL).
FT	DOMAIN	651	661	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	662	680	III (POTENTIAL).
FT	DOMAIN	681	706	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	707	727	IV (POTENTIAL).
FT	DOMAIN	728	750	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	751	772	V (POTENTIAL).
FT	DOMAIN	773	785	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	786	808	VI (POTENTIAL).
FT	DOMAIN	809	814	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	815	840	VII (POTENTIAL).
FT	DOMAIN	841	1194	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	1014	1035	GLN/PRO-RICH.
FT	DOMAIN	1067	1081	GLN/PRO-RICH.
FT	DOMAIN	1095	1130	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	1142	1194	SER-RICH.
FT	CARBOHYD	98	98	POTENTIAL.
FT	CARBOHYD	223	223	POTENTIAL.
FT	CARBOHYD	397	397	POTENTIAL.
FT	CARBOHYD	515	515	POTENTIAL.
FT	VASAPPLIC	887	906	POTENTIAL.
FT	VASAPPLIC	907	1194	NSNKRYSWSPGGGQYPKG -> KKRQPEFSPSSQCPSAH
FT	VASAPPLIC	887	906	AOL (IN ISOFORM BETA).
FT	VASAPPLIC	887	906	MISSING (IN ISOFORM BETA).
FT	VASAPPLIC	887	906	NSNKRYSWSPGGGQYPKG -> KKRQPEFSPSSQCPSAH
FT	VASAPPLIC	887	906	VOL (IN ISOFORM BETA, REF. 2).
FT	VASAPPLIC	887	906	P -> S (IN REF. 2).
FT	CONFLICT	593	593	P -> S (IN REF. 2).
FT	SEQUENCE	1194 AA;	132376 MM;	6ACDFE3 CRC32;
Query Match		13.5%;	Score 787;	DB 1; Length 1194;
Best Local Similarity		26.9%;	Pred No. 1,72e-146;	
Matches		217;	Conservative	211; Mismatches 319; Indels 61; Gaps 51
Db	1	RSCS-FNEH-GYHLEQARLGEVEENINSTALPNTITLGYLYDCPSDA-NVY-AT--LR	54	
Db	125	DSLSIRBKEKGINCLPDGQSLPPGRKKPRLAGYIGGSSVAIQVONLQLEDPDIA	184	
Qy	55	-VL-SLPQNH-IE--L-QGDLLHSP--V-LAYIGDSINRATTAALISPF-LVHIS	104	
Db	185	YSATSIDSDTKLYYFLRVPSPDLQARAMDYKRNMTYVSATHEGNYGSGMDAF	244	
Qy	105	YAASETLSVAKRQPSFLRTIPNDKYQVEYVLLQKRGWISLSYSSDDYQGLQVAL	164	
Db	245	KELAAQEGCLIAHSDKI-YSN-AGEKSFDRLLKRLERLPARVYVCFCEGMTYGLISA	302	
Qy	165	ENQALVRGICIAFKIKIMPFSAOVGERMQCLMRHL-AQ-AGATVYVVSRRQLARVPES	222	
Db	303	MRRLGVGEFELIGSDGA-DRDEV-IGYE-VELANGSIT-ILQSPYRBFDFYFLKL	358	
Qy	223	VVLNLNLGKVM-VASEAVALSRHITLTVGDIQIGVGLAVALQKRAVPGLKAFEEYA--R	279	
Db	359	LDLTNRNPFEPFNOHRQ-CRLPCHLENNFKIKCTGNSELEENYQDSKMGFVIAI	417	
Qy	280	ADKEPRFRCCHGSMSSQQLQRECOAFMAH-MKVL-KAF-SMSAT--NA---Y--RAV	329	
Db	418	YAMAAGLONMHALCPGHVGLCDANKPIDGSKLLDFLAKSSFYIGVSGEVEFDEKGA	477	
Qy	330	YAVAHGLHQLL-G-CASE--LCSRRR-VYPMQLLEQIKHVEFL-LHKQTVAFNRRDLS	383	
Db	478	RYDMLNLOYTANR-YDYVHVGTWHEGVNLIDYKIQ-MNKS-GVYRVSCEPCLQGIK	534	
Qy	384	SYNIILAMQNPCKMTFTYLGSSWSPVQNLININETIKIWHGKNHQPKVSCSSDCLE	443	
Db	535	VIRKEVSCMCTACRKENEVQ-DE-FTCAACDGL-WMPAADLTGCEPIIVYRLIEMNI	591	
Qy	444	VV-TGFHHCCCEVPYCGAGTFLNINSELYRCQPCGTEENAPRGSQT-CPRPVVLA	501	

Dd	592	EPIPLASMCGLIYVTELTIFLYLRDPVWSSRELCTIIAGLFGVCFETIAK	651
Oy	502	TSMVLANTLLILLILLAGTACLFAMHNDTPVVRBAGGCLCTLMGSIAAGSGSLXGPGE	561
Dd	652	PTTSCYLQRLLVGLSSACMSALVTIKTNRIARILAGSKKICTRKPFSMAQVIAS	711
Oy	562	PTRPACLRLQALFALGFIEFLSCLTVRSEFOLIIFKESTK-VPTFYHAMVNHGAGLEVM	620
Dd	712	ILISQLTLVYTLIMEPPMILSPSIKE-VYLIC-NTSNLGVAAPLGVNGLIMSTY	769
Oy	621	ISSAQOLICTLFWVWPPELPAREYORPHMLDECTENSLGELFLAFLNYGLLISIS-AF	679
Dd	770	-YAFTNRVPANPENAKAIATMYTCITLMAF-VPIY-FGSNKITTCRAVSLS-VTV	825
Oy	660	ACSIGNRDLPENYNDAKCVTSLFNYSWAIFTTASVYDGI-LPRANMAQLSSLSS	738
Dd	826	ALGCMTPKMTIILAKPERNVRSAPTS	853
Oy	739	GFGGYFLPKCYVILCRPDNLSTEHPQS	766

RESULT	11	STANDARD;	PRT;	908 AA.
ID	MGR8.MOUSE			
AC	P47743;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, last sequence update)			
DT	15-JUL-1998 (Rel. 36, last annotation update)			
DE	METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.			
GN	GRM8 OR MGLUR8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
RC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6; TISSUE=RETINA;			
RX	MEDLINE; 95293944.			
RA	DIVOISIN R.M., ZHANG C., RAMONELL K.;			
RT	"A novel metabotropic glutamate receptor expressed in the retina and olfactory bulb".			
RL	J. Neurosci. 15:3075-3083(1995).			
CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE ACTIVITY.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN OLFACTORY BULB, ACCESSORY OLFACTOR BULB, AND NASALLARY BODY. WEAKER EXPRESSION IN THE RETINA, AND IN SCATTERED CELLS IN THE CORTEX AND HINDRAIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL: U17252; AAA68149.1; .			
DR	GCDB: GCR_1712; --			
DR	MGD; MG1:109600; GRM8.			
DR	PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.			
DR	PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.			
DR	PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.			
DR	PFAM; PF00003; 7tm_3; 1.			
DR	PFAM; PF01094; ANF_receptor; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; signal;			
FT	MultiGene family; Olfaction.			
FT	SIGNAL	1	33	POTENTIAL.
FT	CHAIN	34	908	METABOTROPIC GLUTAMATE RECEPTOR 8.
FT	DOMAIN	34	583	EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	584	608	I (POTENTIAL).
FT	DOMAIN	609	620	CYTOPLASMIC (POTENTIAL).











Accession	Species	Gene	Protein	Length	Score	E-value	Bit Score	Identities	Positives	Gaps	Conserved Domains	Annotations
QY 59	P-GQHIIHQD	DL-H-VSP7VLA-VICPDS	TNNATTAALSSFLV-HISYMASSFTLS	113								
Db 174	DKSRDYIAFATVPDP	FOAKAAEILREFNNTYV	STASEGDEGTETIEAFEARANI	233								
QY 114	VKROYPSFLRTIPNDKY	OVETIMVLLIQFGTWISL	VSSSDYQGLQVLAENQALVGI	173								
Db 224	CVATISEKVG-RA-MSRAF	EGVVARALLOKSPARAVLFT	REDKARELLASQRLN-ASFT	290								
QY 174	CIAFKNDIMFSAOVD	ERMOCMLRRLAQ-ACATVAVV	FSSQLRAFFEESVTLNLTGV	232								
Db 291	WVASGMCALSVASG	EGCAE-GAI-TIELASPISD	FAFQSDLPNNNSRNPWFREF	348								
QY 223	WVASAM-ALSRHIT	GVGICRIGWLCVALIQKA	VPOLKA-FEAYARADKEAP--RPC	268								
Db 349	WEORFCSFRC-RDCA	HSLSRAP-FEESKI-MFVY-NAVY	AMAHLMHRALCPNT	403								
QY 289	HKGSWCSNQLCR	COQAFMAHTPKLAFS	MSSAYNAVAVAHGLHQL-G-CA-S	344								
Db 404	TRLCDAMPVNGRLYK	CFVLYNVKFDAPRADTHNE	YRDPEDGIGRINIFTYLAGS	463								
QY 345	E-LSRGR-VYPWQ	LLEO-IKHVF-L-LHK-DT--VAF	NDNDPLSYNIIMDWNGP	399								
Db 464	GR-YRQVGVWABE-LT	DFTSLPMASPSAGPLASR	CSPCIONEWSYQPEVCWL	521								
QY 396	KWTFVLCSSWSPVQ	LININTKIQMHCKN-QVPSK	YSCDCEGHQAVTGFHCCFE	454								
Db 522	CIPC-Q-PYEYRLDE	FTADGCLGYM-PNASLTGCFEL	POEYIR-WGDA-NAVGPVLIAC	576								
QY 455	CVPGCAAGFLMKSE	LYRQCPGTEEMAEQSQT-CFPR	TVFLALREHTSM-V-LIANT	511								
Db 577	LGALATFLVLCV	EVARNHATPVKASGRELCYLLG	CVLYCMTFIFIAKSTAVCTLR	636								
QY 512	LLLLLLTGALFL	FMHLDTPYVRASGGRCLCLM	SLAAGSGSLYGFGEPTRAPCLLR	571								
Db 637	LGIGFAEVCVCSA	LTKNRIARIFG-CARGAQRPF	IFSPASQVALCLALISQILLIV	699								
QY 572	ALFALGFETFL	ISCLTVRSFOLLIFKSTIKVPT	YHAMVONHGGLVMISSAOLLICL	631								
Db 696	AMLVEAGTGKET	APERREVTLRCHNRDA-SMIS	LAVVLIATCLTVAENTRCP	753								
QY 632	TMLVMTPLPARE	YORFPH-LYMECHETNSL	GLIFLNYGLL-SISAFACSLGDL	689								
Db 754	ENFNEAKFIGT	YTTCTIIMALLPIFYVTS	SDRYOTTMCVSLSGSVLQCLFAPK	813								
QY 690	ENYNEAKCVT	STSLFENFWSIAFFTAS	YVDGY-LPANMMAGLS-SLSG	FGCYFLPK	747							
Db 814	LHILIFQOKNV	SH	828									
QY 748	CYVILCRPDL	NSTEH	762									
RESULT 14												
LD	MGR8_HUMAN	STANDARD:	PRT:	908	AA.							
AC	000222;	015493;										
DT	01-NOV-1997	(Rel. 35, Created)										
DT	01-NOV-1997	(Rel. 35, Last sequence update)										
DT	15-DEC-1999	(Rel. 39, Last annotation update)										
DE	METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.											
GN	GRM8 OR MGLUR8.											
OS	Homo sapiens (Human).											
OC	Eukaryota; Metazoa; Chordata; Ctenidata; Vertebrata; Mammalia;											
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.											
RA	SEQUENCE FROM N.A.											
RX	MEDLINE; 9811892.											
RA	WU S., WRIGHT R.A., ROCKEY P.K., BURGETT S.G., ARNOLD J.S.,											

```

RX SEQUENC FROM N.A.
RA MEDLINE: 97446143.
RA SCHERRER S.W., SODER S., DUVOISIN R.M., HUIZENGA J.J., TSUI L.C.:
RT "The human metabotropic glutamate receptor 8 (GMR8) gene: a
RL disproportionately large gene located at 7q31.3-q32.1.";
RL Genomics 44:232-236(1997).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U92459; AAB51764.1; -.
DR EMBL: U95025; AAB72040.1; -.
DR GCRDB: GCR_18894; -.
DR GCRDB: GCR_2604; -.
DR MIM: 601116; -.
DR PROSITE: PS00979; G-PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G-PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G-PROTEIN_RECEP_F3_3; 1.
DR PFM: PFM0003; 7tm_3; 1.
DR PFM: PFM1094; ANF_receptor; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 33
FT CHAIN 34 908
FT CHAIN 34 583
FT TRANSSEM 584 608
FT DOMAIN 609 620
FT TRANSSEM 621 641
FT DOMAIN 642 647
FT TRANSSEM 648 668
FT DOMAIN 669 695
FT TRANSSEM 696 716
FT DOMAIN 717 746
FT TRANSSEM 747 768
FT DOMAIN 769 781
FT TRANSSEM 782 803
FT DOMAIN 804 818
FT TRANSSEM 819 843
FT DOMAIN 844 908
FT CARBOHYD 95 95
FT CARBOHYD 298 298
FT CARBOHYD 452 452
FT CARBOHYD 480 480
FT CARBOHYD 565 565
FT CONFLICT 194 194
FT CONFLICT 460 460
FT CONFLICT 642 642
FT CONFLICT 768 768
FT CONFLICT 904 904
SQ SEQUENCE 908 AA; 101741 MW; 18865C0F CRC32;
Query Match 13.0%; Score 757; DB 1; Length 908;
Best Local Similarity 26.2%; Pred. No. 1,90e+139;
Matches 209; Conservative 218; Mismatches 307; Indels 65; Gaps 53;
D6 69 KKKIHRLEAMLAIVADINKDPDLLSITLGVRIIDTCSQSDIYALAEOSLTFVQALIEKDA 128
QY 6 NENHYHFLQARLGEVEINNSTALPNITGYOLYDVC-DSANVYATLR-VLSPGOH- 62
D6 129 SDVGCANGDPPIETFKPKXIGSIVGAASIAWVNLRFKIPQISVASTAPELSDNTR 188
QY 63 -HIE-LOGDILHYS-P-TVLAIVIGPDSINRAATTAALSLPFLV-HISVASESTLSVKRO 117

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Db 189 YDFSRVVPDPSYQAQAVDITVATLGMNVTSLASEGNGSGVEATQISREIGVCIA 248  
 QY 118 YPSFRTIPNDKYQVETWVLLQKFGMTWISLVGSSDDYGLQVATLBNQAL-VGICICIA 176  
 Db 249 OSQKIPRPRPREPEKFI--IKRLLETTPNARAVIMANEDDILRIIEAAKLNQSHFEMI 306  
 QY 177 FKDIPEFAQVGD-ERMOCILMRHLAQATVAVVSSRQLAKVFESVLTNLTKG-VWV 234  
 Db 307 GSDSWG-SK-LAPVYQOEELIAGAVTILPKRA--SIDGDFRFRSRTIANNRRWFAEF 362  
 QY 235 ASEAMALRHITGVPCIGRIGVNLGVALOKRAVPLKAFEEAY-ARAKKAPRRC-HKGS 292  
 Db 363 W-EENFGCKLGGHGRNSHIKKCTGLERLARDSSYDEGKVOYIDAVYSMAVALHNHK 421  
 QY 293 WCSSNQLCR-ECQAFM-AHTMP-K-LKAFSSSAYN--A--Y-R-AVYAAVHGHQLL- 340  
 Db 422 DLCPGICLPRMSTIDKELLGYIRAVNPNSSACTPYTPENNGAPRDIPOVQ-ITN 480  
 QY 341 G-CAS-ELCSR-GVNYWQLEQIHKVFLHKDT-VAFNDRDPLSSYNITIAMDNMP 395  
 Db 481 KSTERKIGH--WTN-QLHLKVEDQMAHREHTHPASVCSLPCKGKERKTVKGV-CCW 536  
 QY 396 KWT-FTVAGSSWSPVQNLINETKIQMGKNQYKSVSSDCLG-HQRYVTGFHCCF 453  
 Db 537 HCEGCEGYNY-QVDEL-SCELCPIDQRPNMFTGCOLIPIKLE-W-HSPAAVPEVAI 592  
 QY 454 ECVPGAGCTFLNKSSELYKQPCGTENAPESGOTCFPRIVFALEHREHSHWLLAANTLL 513  
 Db 593 LGIATTVITVYFVRYNDTPYRAGRELSYLLGIFLCISITPLMAADPTICRR 652  
 QY 514 LLLLGTT-AGL-FAMHLDTPVRSAGRGICFLMGLSLAGSSIXIGFGEPRACILLRQ 571  
 Db 653 VFLGCMCFSYAALLTKNRIHRIFEQKKSVTA-PKEI-SPASQVLTFTSLISVOLGV 710  
 QY 572 ALFALGFIILFSLCLVRSFQILLIFKSTKVTFTYHAWQNHGALFWMIS-SAAQLLIC 630  
 Db 711 FVWEVVDPRHIIIDYGEORTLDPERAGVLC-DISDISLCSLGSILLVAVCTVYANK 769  
 QY 631 LTMELVMTPLPAREX--OR-F-PHLY--MLECTENSLGFIILAFYNGLLISAFACSYL 684  
 Db 770 TRGVETFEENKPIGFTMYTTCIILAFIPIFFGTAQSAEKYIOTITLLYMSLSAHSV 829  
 QY 685 GKIDPEENTENKCVTFSLTFNVSW--TA-FTTASVYDGKYLPAANMAGLS-SLSSG 739  
 Db 830 LGMLYMPKVIILIFHEON 848  
 QY 740 FGYYFLPKCYVILCRPDLN 758

RESULT 15  
 ID MGR6\_RAT STANDARD: PRT: 871 AA.  
 AC P35349;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.  
 GN GRM6 OR MGLUR6.  
 OS Rattus norvegicus (Rat).  
 OC Eutheria: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:  
 NN Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINA;  
 RX MEDLINE: 93280152.  
 RA NAKAJIMA Y., IMAKABE H., AKAZAWA C., NAWA H., SHIGEMOTO R.,  
 "Molecular characterization of a novel retinal metabotropic glutamate  
 receptor mglur6 with a high agonist selectivity for L-2-amino-4-  
 phosphonobutyrate";  
 RT J. Biol. Chem. 268:11868-11873(1993).  
 CC -I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR  
 IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE  
 ACTIVITY.

CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR  
 CC LAYER OF THE RETINA.  
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC STRONGEST, TO MGLUR4.  
 CC -----  
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 CC -----  
 DR EMBL: D13963; BAA03066.1; -  
 DR PIR: A46742; A46742.  
 DR GCRDB: GCR\_0623; -  
 DR PROSITE: PS00979; G\_PROTEIN\_RECP\_F3\_1; 1.  
 DR PROSITE: PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.  
 DR PROSITE: PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.  
 DR PFAM: PF01094; ANF\_receptor; 1.  
 DR PFAM: PF01094; ANF\_receptor; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW Multigene family; Vision.  
 FT SIGNAL 1 18  
 FT CHAIN 19 871  
 FT DOMAIN 19 579  
 FT TRANSSEM 580 602  
 FT TRANSSEM 603 616  
 FT TRANSSEM 617 637  
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 FT TRANSSEM 649 667  
 FT TRANSSEM 668 691  
 FT TRANSSEM 692 712  
 FT TRANSSEM 713 742  
 FT TRANSSEM 743 764  
 FT TRANSSEM 765 777  
 FT TRANSSEM 778 800  
 FT TRANSSEM 801 813  
 FT TRANSSEM 814 839  
 FT TRANSSEM 840 871  
 FT DOMAIN 290 290  
 FT CARBOHYD 445 445  
 FT CARBOHYD 445 445  
 FT CARBOHYD 473 473  
 FT CARBOHYD 561 561  
 SQ SEQUENCE 871 AA; 95089 MW; 81A229E4 CRC32;

Query Match 12.5%; Score 729; DB 1; Length 871;  
 Best Local Similarity 26.5%; Pred. No. 6.82e-133;  
 Matches 215; Conservative 219; Mismatches 308; Indels 70; Gaps 56;

Db 49 RACGLKKEGVHLEMTALDRVNDPPELLPGVRLGRLTCSRDYALBOALSFG 108  
 QY 1 RSC-SFN-EHYHFLQMRIGVEEINNSTALLPRITIGLYDYCS-DSANVATILR-VL 56  
 Db 109 ALINGRDXGDEASVRCGPVPLRSAPPERVAVVSGASASSIMAVNLRFLAIPDISY 168  
 QY 57 SL--PqG-HHIEQ--GDL--LHYSPT--VIAVIGDSINRAATATLSPFLV-HISY 105  
 Db 169 ASTPELSDSTRIDFESRVVPPDSYQAQAVDITVATLGMNVTSLASEGNGSGVEAFY 228  
 QY 106 AASETSLSVKQYPSFLRTPNDKYQVETWVLLQKFGMTWISLVGSSDDYGLQVATL 165  
 Db 229 QISREAGVCIAGIKIPREKPGPEFIK-VIRRLMEPNRAGIIFANEDDIRVLEATR 287  
 QY 166 NQAL-VGICIAFQDIPEFAQVGDERMOCILMRHLAQATVAVVSSRQLARVFESVY 224  
 Db 288 QANLTGFHLWSDSWG-SK-ISPIINLEEEA-VGATILPKRA--SIDGDFQYFMTSL 342  
 QY 225 LTNLTGR-VWVASAWMLSHITGVPCIGRIGVNLGVALI-QRAVAPGLKAFEEAY-ARAD 281  
 Db 343 ENNRNIRWFAEFW-EENFNCKLTSSGGQSDSTRCKTGEEIRIGQSDASVDEGKVOYIDA 401















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QY 276 AYA-R-AD-KEA-P-----RPCHKG-SMCSNOLC-RE-C-QAFNAHTMPKLAFS-M 319
Db 416 RISYNYLAVYSIAHALODIYTCIPGRGLFTNGSCADIKKVEANOVKHLRHLNFTSMG 475
QY 320 SSAYNAIRAYAVAHGHOLLGC-AS-EL-----CS-RGRVYPMQLDQIKHVFLLHK- 370
Db 476 EGYTFDECGDLGAGNYSIINMHLSPEDGSIVFEVGYVYAKKGERLFINDEKILMSGFS 535
QY 371 DTVAFNDNRDPLSSYNIITAMDNGPK-WT-FTVLGS-STWSP-VQ-LININETKIOMHGKN 425
Db 536 REVPFNSCSDCLAGTRKGIIEGPTCCFEVCEPDEYSDETDASACDKCPDDFMSNEN 595
QY 426 HOVPKSVCSDDCLEGHOR-VVTGFHCCFPCVPCAGTFLNKSSELYRQPCGTBEMAREG 484
Db 596 HTSCIAKEIEFLSWTEPFG-IALTFLAVLGIFLTAFLVGFIRKFNTPYKATNELSYL 654
QY 485 SGTCFPRVTVFALREHTSVLLAANTLLILLG-TAGLFAMHLDTPVYSAGRGCLFL 543
Db 655 LLEFSLCCFSSSLF-FIGEPDWTCLRQAPFGISFVLCISCLIVKTNRLVFE-AKI 711
QY 544 MGLSLAAG-SGSLYGFGEPTRPACLLRQALFALGFTIFLSCLTVRSFOLIIKFKSTKV 602
Db 712 PTGFHRKMWGLNLOFLVLCFTFMQIVICAIWNTAPSSYRNHEDELIIFITCHE-GS 770
QY 603 PT-FYHAWQNHGAGLEFVMSAQLLICLTWLVMTPLPAREYQRPHPHVMECTETNS 661
Db 771 L-MALGFLIGYTCLLAICFFFAFKSRKLPENFEAKITFMSLIFITWISFIPAVAST 829
QY 662 LGFLIAPL--YNGLLISAFACSYLGKDLPENYNKACVTFSLFNFVSMIAFTTT-ASY 718
Db 830 Y-GREYSAVEVIALIA-SFGLLACIFENKYYIIIFKPSRTIE 871
QY 719 YDKKYLPAANMMAGLSLSSGFGGY-FLPKCYVILCRPDINSTE 761

RESULT 2
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TITLE calcium-sensing receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 16-Feb-1995 #sequence_revision 12-May-1995 #text_change
03-Aug-1995

ACCESSIONS
S49341; A49419; B49419; C49419
REFERENCE
#authors Pearce, S.H.S.; Thakker, R.V.
#submission submitted to the EMBL Data Library, August 1994
#accession S49341
#status preliminary
#molecule_type DNA
#residues 1-1078 #label PEA
#cross-references EMBL:X81086

REFERENCE
#authors Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, T.; Seidman, C.E.; Seidman, J.G.
#journal Cell (1993) 75:1297-1303
#title Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism.
#cross-references MVID:94094324
#accession A49419
#status preliminary
#molecule_type DNA
#residues 178-180, 'K', 182-192 #label POL
#experimental_source family N
#note sequence inconsistent with nucleotide translation
#note sequence modified after extraction from NCBI backbone
#note 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism
#note sequence extracted from NCBI backbone (NCBIN:142453)
#accession B49419
#status preliminary
#molecule_type DNA
#residues 289-303 #label PO2

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#experimental_source family E
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#status preliminary
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#note 796-Tip mutation is associated with familial hypocalciuric hypercalcemia and neonatal severe hyperparathyroidism
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#accession #length 1078 #molecular_weight 120672 #checksum 8159
SUMMARY

Query Match 19.9%; Score 1163; DB 2; Length 1078;
Best local Similarity 31.9%; Pred. No. 1,42e-201;
Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

Db 60 CIIYNRGRFMDQAMFAIBEINSPALLPNTLGRIFRDTCTVSKALEA--TISFVAQ 117
QY 3 C-SFNEHGYHLFQAMRLGVEEINNSTALLPNITLIGQYLDVCSDSANVATLRLVSLPQ 61
Db 118 NKIDSLNDFCSCSHISTAVVATGSGVSTAVANILGLFIPOVYASSRLLSK 177
QY 62 HMLE-IQ-GDLHYS--PVLAVIPDSTNRATTAALISPLV-HISASSETLSVK 115
Db 178 NOPQSLRTIPNDEHQAAMADIEYFRNWWGTIAADDYGRGFEKREAEEDICI 237
QY 116 RQPSFLRTIPNKQYQVETMVLILQKFGMTWISVSSDYDGLQVALENQALVAGICI 175
Db 238 DESELIQSDE--EE-IQHVETIONSTAKYIVVSSGDLEPLIKE-IYRNITGKIM 293
QY 176 AFKDIMP-FSAQYDDEMOCKLHRLAQAATVAVVSS-ROLARVFESVLTNLGKYW 233
Db 294 LASEANSSSLIMPYPHYVGTIGFALKAGIIPFRSEFLKVKHRRKVVHNGFAKEME 353
QY 234 VASEANA---L-S--R--HITGP-GIQ-RIGWVLGV-A-IQK--R-AVP-GL-KAF-E 274
Db 354 ETENCHLOEGAKPLVDFTLRGHESGDRFNSSTAPRLTGDENISVETPYIDYTH 413
QY 275 EAVA-R-ADKE-APRCH--KSMCSNOLCRECAF--M-A--HTMPKLA---FS- 318
Db 414 LRISYNYLAVYSIAHALODIYTCIPGRGLFTNGSCADIKKVEANOVKHLRHLNFTNM 473
QY 319 MSSAYNAIRAYAVAHGHOLLGC-AS-EL-----CS-RGRVYPMQLDQIKHVFLLHK 370
Db 474 GEQVTFDECGDLGAGNYSIINMHLSPEDGSIVFEVGYVYAKKGERLFINDEKILMSGF 533
QY 371 DTVAFNDNRDPLSSYNIITAMDNGPK-WT-FTVLGS-STWSP-VQ-LININETKIOMHGKN 424
Db 534 SREVPFNSCSDCLAGTRKGIIEGPTCCFEVCEPDEYSDETDASACDKCPDDFMSNE 593
QY 425 NHQVPKSVCSDDCLEGHOR-VVTGFHCCFPCVPCAGTFLNKSSELYRQPCGTBEMARE 483
Db 594 NHTSCIAKEIEFLSWTEPFG-IALTFLAVLGIFLTAFLVGFIRKFNTPYKATNELSYL 652
QY 484 GSQTCFPRVTVFALREHTSVLLAANTLLILLG-TAGLFAMHLDTPVYSAGRGCLFL 542
Db 653 LLEFSLCCFSSSLF-FIGEPDWTCLRQAPFGISFVLCISCLIVKTNRLVFE--AK 709
QY 543 LMGSLAAG-SGSLYGFGEPTRPACLLRQALFALGFTIFLSCLTVRSFOLIIKFKSTK 601
Db 710 IPTSFHRKMWGLNLOFLVLCFTFMQIVICAIWNTAPSSYRNHEDELIIFITCHE-G 768
QY 602 VPT-FYHAWQNHGAGLEFVMSAQLLICLTWLVMTPLPAREYQRPHPHVMLEBTEIN 660
Db 769 SL-MALGFLIGYTCLLAICFFFAFKSRKLPENFEAKITFMSLIFITWISFIPAVAS 827
QY 661 SLGFLIAPL--YNGLLISAFACSYLGKDLPENYNKACVTFSLFNFVSMIAFTTT-AS 717

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RESULT	ENTRY	3
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Oy	718	YVDGKYLTPAANMAGSLSSSGFEGY-FLFKCYVILCRPLDNSTE 761
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ORGANISM	Calcium receptor (clone pHPAR-4.0) - human	
DATE	#format_name Homo sapiens #common_name man	
DATE	19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999	
ACCESSIONS	A56715	
REFERENCE	A56715	
#authors	Garrett, J.E.; Capano, I.V.; Hammerland, L.G.; Hung, B.C.P.	
#journal	Brown, E.M.; Hebert, S.C.; Nemeth, E.F.; Fuller, F.	
#title	J. Biol. Chem. (1995) 270:12919-12925	
#cross-references	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs.	
#accession	MU01:95279439	
##status	A56715	
##molecule_type	preliminary	
##residues	1-1078 ##label GAR	
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Oy	3	C-SENEHGYHLFQMRIGVEINNSTALPLNLTIGQLDYVSDSANVATLRVLSPEQ 61
Db	118	NKIDSLNLEDFCNCESEHPISTIAVAGTSGSVTAANVLGLTFPIYQVSASSRLSNK 177
Oy	62	HHIE-LQ-GDLHRS---PTVLAVIGPDSINRAATTALLSPLYL-HISYAASSETLSX 115
Db	178	NQKFSFLTINDSHQATAMADIEFRKMWVGTIAADDYGAPGLEKTRFEAEEDICI 237
Oy	116	ROYPSFLETTINDRYQYETVLLQKKGWMTISLVGSSDDYQGLQVQALENQALVNGICI 175
Db	238	DFSELSIQSPD--EE-IQHVVEYIQNSTAKVIVYSSGDEPLIKE-IIVRNINIGKI 293
Oy	176	AFKQMDP-FSAQVQDDEKQCLMRLLAQAGITVVVSS-RQLARVFESVYLTNLGKW 233
Db	294	LASEMAWSSLIAMPQYFHVYVGTIGFALAKAGIPIGFERFLKRVPRKSYHNGFAKEWE 353
Oy	234	VASEMAA--L-S--R--R-HITGVV-GIQ-RIGWLVG-A-IQK--R-AVP-GL-KAF-E 274
Db	354	ETPNCHLOEAGKGLPVDTPLRGHEBSGDPFSSNSTAFRLCTGDENISSVETPIYDIYH 413
Oy	275	EAYLA-R-ADKE-APRPH---KGSWCSSNOLCREQCAF-M-A--RTMKRLXA---FS- 318
Db	414	LRISVNYVLAJAHALODIYICLPGRGFTNGSCADIKKYAAQOVLLHLRLTNM 473
Oy	319	MSASVNAVRAVYVAHGLHQILGC-AS-EL-----CS-RGRVYLPQOLLQIKHVFHLHK 370
Db	474	GEQYTFDECGDVLGNSYIIMNHLSPEDGSIVFEVEGYNYAARKGERLFINETKILMSGF 533
Oy	371	-DTVAENNDNRPLISYSYNIAMDWNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIOWHGK 424
Db	534	SREVPFNSGSDCLAGRKGIIEBEPIFCCECEVCECPDGEVSDETDASACKKCPDDEWSE 593
Oy	425	NHOVPKSVCSDDCLGEHOR-VVTGFHHQCEVCPVCGAGFLNKSSELYRQPCGTETMAE 483
Db	594	NHTSIAKEIEFLSMTEPEG-IALTFAVIGIFLTAFLVGFIFKFNTPPIVAKTNELSY 652
Oy	484	GSQGTFFRTVVFALRHEITSVYLLAANTLLLLLLLG-TALFLAMHMDITPYVRASAGRLCF 542
Db	653	LLLSLLOCSSSLF-FIGEPQDMTCFLQPAFGISVILCISCIILVKNRVLLVEF--AK 709

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Oy      543 LMTSLAAG-SGSIYGFGEPTRCALRALATGTTITLSQTVRSPLIITFFKFNK 601
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Oy      602 VPT-FYHAWQNHGAGFGFWMISSAQILICITLWLVTPIPARERYORPHTWLECTETN 660
Db      769 SL-MALGFLICYTOLLALICEFFAFKRKPENPNNEKFTTEEMLFIFYIWISFIAYAS 827
Oy      661 SLGFLIAFL-YNGLSISAFAVSGLKKDIPENVNKCKVTSITSLFNFSWIAFEFTT-AS 717
Db      828 TY-KFWSAVEAVIALAA-SEGLLACIFFEKYIIITFKPSRNITE 870
Oy      718 YVDGRYLPAANMAGLSISSGPEGY-FLPKCYVIICRPDLNSTE 761

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ORGANISM        #formal_name Rattus norvegicus #common_name Norway rat
DATE            02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                01-May-1998
ACCESSIONS     I59362; A55594
REFERENCE       I59362
#authors        Ruat, M.; Molliver, M.E.; Snodman, A.M.; Snyder, S.H.
#journal         Proc. Natl. Acad. Sci. U.S.A. (1995) 92:3161-3165
#title          Calcium sensing receptor: molecular cloning in rat and
                localization to nerve terminals.
#cross-references MIMD:95241465
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#cross-references EMBL:U02089; NID:g790578; PID:g790579
##experimental_source striatal
REFERENCE        A55594
#authors        Ricciardi, D.; Patk, J.; Lee, W.S.; Gamba, G.; Brown, E.M.;
                Hebert, S.C.
#journal         Proc. Natl. Acad. Sci. U.S.A. (1995) 92:131-135
#title          Cloning and functional expression of a rat kidney
                extracellular calcium/polyvalent cation-sensing receptor.
#cross-references MIMD:95116508
#accession      A55594
##molecule_type mRNA
##residues      1-133; 'X', 135-1079 ##label RIC
#cross-references GB:U0354
##experimental_source kidney
KEYWORDS         calcium; glycoprotein; phosphoprotein; transmembrane protein
FEATURE
1-20            #domain signal sequence #status predicted #label SIG\
187-212         #region hydrophobic\
613-635         #domain transmembrane #status predicted #label TM1\
650-670         #domain transmembrane #status predicted #label TM2\
683-700         #domain transmembrane #status predicted #label TM3\
725-744         #domain transmembrane #status predicted #label TM4\
770-790         #domain transmembrane #status predicted #label TM5\
806-828         #domain transmembrane #status predicted #label TM6\
841-860         #domain transmembrane #status predicted #label TM7\
90-261,287,386,456,
488,594,893,1005 #binding_site carbohydrate (Asn) (covalent) #status
                    predicted\
794             #binding site phosphate (Ser) (covalent) (by protein
                    kinase C) #status predicted\
899,901         #binding site phosphate (Ser) (covalent) (by protein
                    kinase A) #status predicted
SUMMARY          #length 1079 #molecular_weight 120867 #checksum 8153

Query Match      19.8%; Score 1158; DB 2; Length 1079;
Best Local Similarity 31.4%; Pred. No. 1,51e+200;
Matches          262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;

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QY      3 C-SFNEHGHLFOAMRLGVEEINNSTALPNITLGLQYLDVDCSDSANVATLRYLSLPGQ 61
DB      118 NKIDSLNDEFCNCEHIFSTIAVVGATGSGVSTAVANLGLFIYPOVYASSSRLLSNK 177
QY      62 HHE-LQ-GDLHYS---PVLAVIGPDSINRAITTAALSPFLY-HISTAASSETLSVK 115
DB      178 NOYKSLRTIPNDEHOATAMADIEFRNMVGTIAADDYGRPGIEKREAEEDICI 237
QY      116 ROYPSFLRTIPNDKYQVETWLLQKFGMTWISLVGSSDDYQGLQVQALENLAVRGICI 175
DB      238 DFEELISOYDE--EEIQQ-VVEYIONSTAKYIVFSSGDLPLIKE-IVRRNITGRW 293
QY      176 AFQDIMP-FSAQYGDERMOCIMRLAQAGATVYVFS--ROLARVFESVYLTNLGKW 233
DB      294 LASEAMASSLLAMPYFHYVGTIGFGLAKAQIPGREFLOKHPRKSVHNGFAKEWE 353
QY      234 VASEAMA--L-SR---HITGP-GIQ-RIGWLVG-A-IQK--R-AVP-GL-KAF-E 274
DB      354 ETNCHLQEGAKGPLVDFTVRSHEGSGNRLNSSTAFRPLCTGDNENISVETP-YMDYE 412
QY      275 EAVA-R-AD--KEA-P-----RPHKGS-W---CSSN-Q-LCREQAFMAHTMPLKAFS 318
DB      413 HLISVNYLAVYSIALADIDITCLPRGLFTNGSCADIKKYEAMOVHLRLNNTNN 472
QY      319 -MSATNAYAVYAVAGLQGLGC-AS-BL-----CS-RGRYPMQLQIKHVLHLH 369
DB      473 MGEQVTEDECGDLVGNYSIINWELSPEDGSIVKEGYVNVYAKKGERLFINKEKILMSG 532
QY      370 K-DTAVFNDRDPLSSNIIAMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINEKTIQWHS 423
DB      533 FSEVFPNSNCRCCQAGTRKGIIEGPTCCFEVCEPDGEYSGEYSDTASACDPCDDEWSN 592
QY      424 KNOQVRSVSSDCLBHQH-VYGFHHCCEVCPCAGGTFLNKSELYRQCPGTEEMAP 482
DB      593 ENHTSCAKIEFLAWTEPRG-IALTFAVIGIFLFAVGVFIKFNTEIVAKTINELS 651
QY      483 EGSQTCPRVIVLALREHTSWVLANITLILLIG-TAGLFAWHLDTVVSAGGRIC 541
DB      652 YLLFSLFCSSSLF-FIGEPDWTCLRQPAFGISFVLISCIIYKTRVLVEE--A 708
QY      542 FLMLGSLAAG-SSLYGFGEPRPACLLRQALFALGFTIFLSGLYRSQLIIFRST 600
DB      709 KIPTSFRKRWGINTLOPLVFLCTFMQILCIITWLYTAPSSYRNHELEDEIIFITCHEG 768
QY      601 KVPY-FYHAWQNHGAGLFWMISAAQLLCLTFLVWVTPLPAREYORFPHLVLETER 659
DB      769 SLAALSLIGYTLAALICFFAFKSRKLPENNEAKEIFSMILFIYVISPAAST 828
QY      660 NSLGFILAFIYNGULISAFACSLGKDPENNEAKCVFSLFNFSVIAFFTT-ASV 718
DB      829 Y-GKFVSAVEVIAIIAA-SFGILACIFFNKYIILFKPSNTEIEVVSSTAHA 880
QY      719 YDKYKIPAAWMAAGLSLSSGFGGY-FLPKCYILCRDLNSTEHQASIODYT 771

RESULT      5
ENTRY      B56715      #type complete
ENTRY      calcium      receptor (clone pNpCAR-5.2) - human
ENTRY      #formal name Homo sapiens #common name man
ORGANISM    19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
DATE      17-Mar-1999

ACCESSIONS
REFERENCE    B56715
#authors      Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.;
#journal      J. Biol. Chem. (1995) 270:12919-12925
#title        Molecular cloning and functional expression of human
#             parathyroid calcium receptor cDNAs.
#cross-references MIMD:95279439
#accession    B56715
#status       preliminary
#molecule_type mRNA
#residues     1-1088 ##label GAR

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#cross-references GB:U20760; NID:g683746; PID:g683747
KEYWORDS    glycoprotein; receptor; transmembrane protein
SUMMARY     #length 1088 #molecular-weight 121799 #checksum 5263

Query Match      18.2%; Score 1063; DB 2; Length 1088;
Best Local Similarity 31.6%; Pred. No. 4,26e-181;
Matches 264; Conservative 231; Mismatches 250; Indels 90; Gaps 59;

DB      60 CIRRNGFRWLOAMFALFEINSSPALLPNTLIGRIDTONTVKALDEA--TISFVAQ 117
QY      3 C-SFNEHGHLFOAMRLGVEEINNSTALPNITLGLQYLDVDCSDSANVATLRYLSLPGQ 61
DB      118 NKIDSLNDEFCNCEHIFSTIAVVGATGSGVSTAVANLGLFIYPOVYASSSRLLSNK 177
QY      62 HHE-LQ-GDLHYS---PVLAVIGPDSINRAITTAALSPFLY-HISTAASSETLSVK 115
DB      178 NOYKSLRTIPNDEHOATAMADIEFRNMVGTIAADDYGRPGIEKREAEEDICI 237
QY      116 ROYPSFLRTIPNDKYQVETWLLQKFGMTWISLVGSSDDYQGLQVQALENLAVRGICI 175
DB      238 DFEELISOYDE--EEIQQ-VVEYIONSTAKYIVFSSGDLPLIKE-IVRRNITGRW 293
QY      176 AFQDIMP-FSAQYGDERMOCIMRLAQAGATVYVFS--ROLARVFESVYLTNLGKW 233
DB      294 LASEAMASSLLAMPYFHYVGTIGFGLAKAQIPGREFLOKHPRKSVHNGFAKEWE 353
QY      234 VASEAMA--L-S--R--HITGP-GIQ-RIGWLVG-A-IQK--R-AVP-GL-KAF-E 274
DB      354 ETNCHLQEGAKGPLVDFTVRSHEGSGNRLNSSTAFRPLCTGDNENISVETPIDYTH 413
QY      275 EAVA-R-ADKE-APRCH--RGSWCSNOLCRECAF--M-A--HTMPLKLA---FS- 318
DB      414 LRISVNYLAVYSIALADIDITCLPRGLFTNGSCADIKKYEAMOVHLRLNNTNN 473
QY      319 -MSATNAYAVYAVAGLQGLGC-AS-BL-----CS-RGRYPMQLQIKHVLHLH 370
DB      474 GGEVTEDECGDLVGNYSIINWELSPEDGSIVKEGYVNVYAKKGERLFINKEKILMSG 533
QY      371 -DTAVFNDRDPLSSNIIAMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINEKTIQWHS 423
DB      534 SREPLFLVSLVQVPPNSNCRCLAGTRKGIIEGPTCCFEVCEPDGEYSGEYSDTASACN 593
QY      424 -KNH-----QVPRSVSSDCLBHQH-VYGFHHCCEVCPCAGGTFLNKSELYRQ 473
DB      594 KCPDDEWSNENHTSCAKIEFLAWTEPRG-IALTFAVIGIFLFAVGVFIKFNTEIVAKTINELS 651
QY      474 PCGTEEMAPBGSTCPRVIVLALREHTSWVLANITLILLIG-TAGLFAWHLDTV 532
DB      653 VKATNELSYLLFSLFCSSSLF-FIGEPDWTCLRQPAFGISFVLISCIIYKTR 711
QY      533 VRSAGGRILCFIMLGSLAAG-SSLYGFGEPRPACLLRQALFALGFTIFLSGLYRSQ 591
DB      712 VLVFE--AKIPTSFRKRWGINTLOPLVFLCTFMQIVCIITWLYTAPSSYRNQLEDE 769
QY      592 LIIFKSTKVPY-FYHAWQNHGAGLFWMISAAQLLCLTFLVWVTPLPAREYORPH 650
DB      770 IIFITHE-GSL-MALGFIYGYTLAALICFFAFKSRKLPENNEAKEIFSMILFIY 827
QY      651 LVVLECTEINSLGFIILAF--YNGLLISAFACSYGRKLPENYNAKCVTSILFNFS 708
DB      828 WISFIPAVASTY-GKFVSAVEVIAIIAA-SFGILACIFFNKYIILFKPSNTE 880
QY      709 WIAFFTT-ASVYDGYKLPAAWMAAGLSLSSGFGGY-FLPKCYILCRDLNSTE 761

RESULT      6
ENTRY      JH0563      #type complete
ENTRY      metabotropic glutamate receptor 4 precursor - rat
ENTRY      #formal name Rattus norvegicus #common name Norway rat
ORGANISM    30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
DATE      13-Sep-1998

ACCESSIONS
REFERENCE    JH0563
#residues     JH0561

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#authors Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
#journal Neuron (1992) 8:169-179
#title A family of metabotropic glutamate receptors.
#cross-references MIMD:92110002
#accession JH0563
#molecule-type mRNA
#residues 1-912 #label TAN
#experimental-source brain
COMMENT This protein is coupled to a G protein and evokes a variety of
functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
FEATURE
1-32 #domain signal sequence #status predicted #label SIG\
33-912 #product metabotropic glutamate receptor 4 #status
588-610 #domain transmembrane #status predicted #label TR1\
625-645 #domain transmembrane #status predicted #label TR1\
657-675 #domain transmembrane #status predicted #label TR1\
700-720 #domain transmembrane #status predicted #label TR1\
751-772 #domain transmembrane #status predicted #label TR1\
786-807 #domain transmembrane #status predicted #label TR1\
822-847 #domain transmembrane #status predicted #label TR1\
98,301,454,484, #domain transmembrane #status predicted #label TR1\
569 #binding-site carbohydrate (Asn) (covalent) #status
621,689,695,859, #binding-site phosphate (Ser) (covalent) #status
870 #binding-site phosphate (Ser) (covalent) #status
SUMMARY #length 912 #molecular-weight 101818 #checksum 808
Query Match 14.7% Score 856; DB 2: Length 912;
Best Local Similarity 27.3%; Pred. No. 4,92e-139;
Matches 219; Conservative 225; Mismatches 289; Indels 68; Gaps 54;
Db 72 KEGGIRLEAMFLADRIINDDPDLPIITGARIIDCSRDTHALEOSLTFVALIENKDG 131
6 NEHYHLFOAMRGLVEEINNSTALPITLIGQLDYCS-DSANVATLR-VLSLPQGH 63
132 TEVRCGSGGPIITKPRVGVIGASGSSIVMANTLRFKIPQIYSTAPDLSNSR 191
64 IELO---GDL-LHYSPT-VLAVIGPDSINRAATTAALSPFLV-HISYASSETLSVKRQ 117
192 YDFSRVPSDTYQAOAMVDIVALKWNYSTLASSEGSYGSEVATIQKRENGVCIA 251
118 YPSFLRTIPNDKQVETWVLLQKFGMTWISLVGSSDDYQGLQVLENOALVRG-ICIA 176
252 QSVKIPREPKTGEFDKI--IKRLLETSNAGIIIFANEDDIRVLEAARANOTGHEFM 309
177 FKDIIMPSSAOGD-ERMOCMLRHLAGAGATVYVVFSSRLQARVFESVLTNLTKGV-WV 234
310 GSDSWG-SKS-APVLRLEEAAG-AVTILPKRMS-VGDFRYESSRLDNNRNIMFAEF 365
235 ASEAMALSRHTIGVPGIORIGMVGLVAIQKRAVPGKAKFEBAVA-RADKEAPRC-HKGS 292
366 W-EDNEHCKLSRAHLKKGSHIKCTNERNRIGODSAVEQEGKVOFIDAVYAMGALHAMH 424
293 WCSSNQLCREC-QAFM-AHTMP-KLKA-FSMSSAYN-A---Y-R-AVVAAGHGLHOLL 340
425 RDLCPGAVGLCPMDPDVDTOLTKYIRNVNFSAGNPTFENEGDAPGRDIOYOLRN 484
341 -G-CAS--ELCSR-GRVYPMOLLEQIKHVT-LHKDTVAANDNRDPLSINITIAMD-CC 393
485 GSA-EYVVGIS--WTD-HLHRIERKQMPGSGQOLPRSICGLPCQPGRRKTVGMA-CC 539
394 GPKMTFTVLGSGTSPVQOLNINETKIQMHGKNHQPVSVCSSDLEG-HQHVYGVGFHHC 452
540 WHCPRC-TG-YOYOVDRYTKCTCYDMAPRTNRTSCOPIPYKLE-WD-SWAVLPLFLA 595
453 FECPVCGAGFTLNKSEIRQCPCTEEHAPGSGOTCPRTVYFALRHISW-VL-LAAN 510
596 VVGIAATLVVTVFVRVNDPVRKASGRELSEYVLLAGIFLCYATTFIMIAEPDGTGSLR 655

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511 TLLILLGLTAGLFAWHLDPVVRASAGRCFLMGLGSLGSGFGEPRPACLLR 570
656 RIFPLGMSISYALLTKRIRIRIFEOGKRSVSAPRFISPAQOLATITFLIS--LQLLG 713
571 QALFALGFTIFLSCLTVRSPQOLIIKFFSIRK-VPIYHANVQNHGAGLFLMISNAOLL- 628
714 ICV-MFVVDSSHVSVDPODRTIDPREPARGLKC-DISDLSICLLGYSMLMVTCTVYA 771
629 ICLTWLVWTFPLPAREQ--R-F-PHLY--MLECTERNISGIFLAPLYNGLSISAFCS 682
772 IKRGVPEIENEAKPIGFTWITCIWLAFFIPFGISQSDADRLXIQTTLTVSYSLAS 831
683 YLGKDPENYENAKCVTFSLFNFVSWIAF---FTIASVYDGR-YLPANMAMAGLS-SLS 737
832 VSLGMLTPKPVYITLHPEDN 852
738 SGEGGYFLPKCYVILCRPDLN 758
RESULT 7
ENTRY 158149 #type complete
TITLE metabotropic glutamate receptor - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
13-Sep-1998
ACCESSIONS 158149
REFERENCE 158149
#authors O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.;
Haldeman, B.A.; McGrane, V.; Houamed, K.M.; Thomsen, C.;
Gilbert, T.L.; Mulvihill, E.R.
#journal Neuron (1993) 11:41-52
#title The ligand-binding domain in metabotropic glutamate receptors
#cross-references MIMD:93352699
#accession 158149
#status preliminary; translated from GB/EMBL/DBJ
#molecule-type mRNA
#residues 1-912 #label RES
#cross-references GB:M90518; NID:g205400; PID:g205401
GENETICS
#gene GLUR4
#classification #superfamily metabotropic glutamate receptor 4
#keywords neurotransmitter receptor
SUMMARY #length 912 #molecular-weight 101846 #checksum 818
Query Match 14.6% Score 854; DB 2: Length 912;
Best Local Similarity 27.3%; Pred. No. 1,25e-138;
Matches 219; Conservative 225; Mismatches 289; Indels 68; Gaps 54;
Db 72 KEGGIRLEAMFLADRIINDDPDLPIITGARIIDCSRDTHALEOSLTFVALIENKDG 131
6 NEHYHLFOAMRGLVEEINNSTALPITLIGQLDYCS-DSANVATLR-VLSLPQGH 63
132 TEVRCGSGGPIITKPRVGVIGASGSSIVMANTLRFKIPQIYSTAPDLSNSR 191
64 IELO---GDL-LHYSPT-VLAVIGPDSINRAATTAALSPFLV-HISYASSETLSVKRQ 117
192 YDFSRVPSDTYQAOAMVDIVALKWNYSTLASSEGSYGSEVATIQKRENGVCIA 251
118 YPSFLRTIPNDKQVETWVLLQKFGMTWISLVGSSDDYQGLQVLENOALVRG-ICIA 176
252 QSVKIPREPKTGEFDKI--IKRLLETSNAGIIIFANEDDIRVLEAARANOTGHEFM 309
177 FKDIIMPSSAOGD-ERMOCMLRHLAGAGATVYVVFSSRLQARVFESVLTNLTKGV-WV 234
310 GSDSWG-SKS-APVLRLEEAAG-AVTILPKRMS-VGDFRYESSRLDNNRNIMFAEF 365
235 ASEAMALSRHTIGVPGIORIGMVGLVAIQKRAVPGKAKFEBAVA-RADKEAPRC-HKGS 292
366 W-EDNEHCKLSRAHLKKGSHIKCTNERNRIGODSAVEQEGKVOFIDAVYAMGALHAMH 424
293 WCSSNQLCREC-QAFM-AHTMP-KLKA-FSMSSAYN-A---Y-R-AVVAAGHGLHOLL 340
425 RDLCPGAVGLCPMDPDVDTOLTKYIRNVNFSAGNPTFENEGDAPGRDIOYOLRN 484
341 -G-CAS--ELCSR-GRVYPMOLLEQIKHVT-LHKDTVAANDNRDPLSINITIAMD-CC 393
485 GSA-EYVVGIS--WTD-HLHRIERKQMPGSGQOLPRSICGLPCQPGRRKTVGMA-CC 539
394 GPKMTFTVLGSGTSPVQOLNINETKIQMHGKNHQPVSVCSSDLEG-HQHVYGVGFHHC 452
540 WHCPRC-TG-YOYOVDRYTKCTCYDMAPRTNRTSCOPIPYKLE-WD-SWAVLPLFLA 595
453 FECPVCGAGFTLNKSEIRQCPCTEEHAPGSGOTCPRTVYFALRHISW-VL-LAAN 510
596 VVGIAATLVVTVFVRVNDPVRKASGRELSEYVLLAGIFLCYATTFIMIAEPDGTGSLR 655

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RESULT	8
ENTRY	
TITLE	A42916 #type complete
ORGANISM	metabotropic glutamate receptor mGluR5 - rat
DATE	#formal_name Rattus norvegicus #common_name Norway rat 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999
ACCESSIONS	A42916
REFERENCE	A42916
authors	Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
#journal	J. Biol. Chem. (1992) 267:13361-13368
#title	Molecular characterization of a novel metabotropic glutamate receptor mGluR5 coupled to inositol phosphate/Ca <sup>2+</sup> signal transduction.
#cross-references	MU054:92317054

[illegible]

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RESULT      9
ENTRY
TITLE      JC2132      #type complete
ORGANISM   metabotropic glutamate receptor 5 A - human
DATE       28-Aug-1985 #formal_name Homo sapiens #common_name man
          05-Jan-1996 #sequence_revision 07-Oct-1994 #text_change
ACCESSIONS
REFERENCE   JC2132
            JC2131
            Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.;
            Sugiyama, H.
            Biochem. Biophys. Res. Commun. (1994) 199:1136-1143
            Molecular cloning and the functional expression of two
            isoforms of human metabotropic glutamate receptor subtype
            5.
            #cross-references MUID:94197596
            #accession      JC2132
            ##molecule_type RNA
            ##residues      1-1180 ##label MIN
COMMENT     This protein is coupled to guanine nucleotide binding proteins.
KEYWORDS    glycoprotein; neurotransmitter; receptor; transmembrane
            protein
FEATURE
580-604     #domain transmembrane #status predicted #label TM1\
617-637     #domain transmembrane #status predicted #label TM2\
644-664     #domain transmembrane #status predicted #label TM3\

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	domain	status	predicted	label	TM5
694-714	transmembrane			label	TM5
738-759	transmembrane			label	TM5
773-794	transmembrane			label	TM5
803-827	domain			label	TM7
SUNMARY	transmembrane	status	predicted	label	TM7
	molecular-weight	129053	#checksum	237	
	#length	1180			



Db	652	PTTSCYORLRLVSSSSMCSSALVTKNRIARLAIAGSKICGRKPRPMSAMQVITIAS	711
Qy	562	PTRPCALRLQALFALGFITFLISCLTVRSFOLLIIKFEETK-VPTFFAAWVONHEAGLFLVM	620
Db	712	ILISVQLTLVLTLMIEPPMILSYPSIKE-VYLIC-NTSNLGVAPVGYNGLLIMSCY	769
Qy	621	ISSAOLLCITLWVWPLPAREYQRPFPPLVMECTETNSLFIPLAVLYGLLIS-AF	679
Db	770	-YAFIRVAVPNPNEAKXIAFTMYTCLIMLAF-VPII-PESNKKIITTCRAVLS-VTV	825
Qy	660	ACSYLGGKLPENYNAKCVTSLFLENFWSIAFTTASVYDGKY-LPAAANMAGLSLSS	738
Db	826	ALGCMFTPKMYIIIAKPERNVRSAPFTS	853
Qy	739	GFGGYFLPKCYVILCRPDLNTEHROAS	766
RESULT	11		
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TITLE		metabotropic glutamate receptor 5 B - human	
ORGANISM		#formal name Homo sapiens #common name man	
DATE	28-Aug-1985	#sequence_revision 07-Oct-1994	#text_change 05-Jan-1996
ACCESSIONS	JC2131		
REFERENCE	JC2131		
authors	Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.		
#journal	Biochem. Biophys. Res. Commun. (1994)	136:1136-1143	
#title	Molecular cloning and the functional expression of two isoforms of human metabotropic glutamate receptor subtype 5.		
#cross-references	MUID:94197696		
#accession	JC2131		
#molecule_type	RNA		
##residue_type	1-1212	##label MIN	
COMMENT	This protein is coupled to guanine nucleotide binding proteins.		
KEYWORDS	glycoprotein; neurotransmitter; receptor; transmembrane protein		
FEATURE			
	580-604	#domain transmembrane #status predicted #label TM1\	
	617-637	#domain transmembrane #status predicted #label TM2\	
	644-664	#domain transmembrane #status predicted #label TM3\	
	694-714	#domain transmembrane #status predicted #label TM4\	
	738-759	#domain transmembrane #status predicted #label TM5\	
	773-794	#domain transmembrane #status predicted #label TM6\	
	803-827	#domain transmembrane #status predicted #label TM7	
SUMMARY		#length 1212	#molecular-weight 132579 #checksum 3155
Query Match	13.6%;	Score 796;	DB 2; Length 1212;
Best Local Similarity	26.7%;	Pred. No. 6,00e-127;	
Matches	215;	Conservative	204; Mismatches 329; Indels 56; Gaps 49;
Db	55	RKCGAVRQYQIQRYEALHTLERINSPTLPLNITLACEIRDCSMHSAVALQEISFIR	114
Qy	1	RSC-SFNH-GYHLEQARLRGVEELNNSTALLPNTITLGQYLDVDCSSANYYA-TLR-VL	56
Db	115	DSLISSEEBELVKRCVDSSSSFSKSKPIYGVIGPGSSVAIQVNTLLQFNIPQIAYSA	174
Qy	57	-SL-PCGHIEHL---QGLDLHY-SPT-VLAVIGPDSYRNAAATTAALLSPFLV-HISYAA	107
Db	175	TSMDLSDTLTKKMYRVRVPSDAQARAVVDYKRYNMTYGAVTEEGNYESGSEAKKD	234
Qy	108	SSETLSVAKRQPSPLRTIPNPKYQETVWVLLQFGMTWISLVSDDYQGLQVQALENQ	167
Db	235	SAKEGICIA-HSYKLYSN-AGEQFDKILKLTGSLPARVAVAFCEGMYRGLMMRR	292
Qy	168	ALYRGICIAFDIMPFSAQVDEDMQCLMRLLA-Q-AGATVYVVYSSRQLARVFESEVYL	225
Db	293	LGALGEFLILGSDGMA-DRYDV-TDGVOREA-VGGITL-KIQSPDVAKFPDYLIKIPET	348
Qy	226	TNLTKG-YVVAISEAMALSRHITGVPGLDRIQMLGVAIQKRAVAPGLKAFEEAYA--RADK	282
Db	349	NHRNPWFQEPNQHRPQ-CRLGPGFQENSKYKNTGSSILTLKTHVQDSKMGFYINALYSM	407

QY 283 EAPRPHCKGSSCNÖLCR-E--CÖ--A-F-MA-HIMPLKAFMSSANNAI--RAVAV 332  
 Db 408 AYLGNQMOMSLCPQYAGLCADMPKPIDGRKLLESIMKNTFGVSGDTILFDENGDSFGRYE 467  
 QY 333 AHGHLQ-LG-CAS-E-LCSGR-VYPMÖLBQIKHVFL-LHKDVAFNDRDPLSYN 386  
 Db 468 IMNFKEGKXDY-EDYIIVGSMNGELKAMDDY-W-SKSNITRYSVCSPCKQIKYIR 524  
 QY 387 IIAWMNGPKWTTVYLGSSSTWSPVÖINIFETKIÖWMGKHQWPKSSCSDDLGEHQRYV- 445  
 Db 525 KGEVSCCMTÖPCKENEVYF-DE-YTCRACÖLGSMPTDÖLTCDDILPÖYULRWGPREPIA 582  
 QY 446 TGFHHCCECVPGAGTFLNKSELKYCÖCGTEBNAPBESÖCPRFYVFLALREHTSV 505  
 Db 583 AVEFACGLLATTFTVIVTFIYRDPYVAKSSSHELICYIIAGICLGYLCTECLAKPKÖI 642  
 QY 506 LLANTLILLILLIGTAGLFEMHJDTFVVSAGRGLOF.LXGLAAGSGSLYGFGEPTRP 565  
 Db 643 YCYLÖRIGIGLSPAMSSALVYTKNINAILIANGSKKICÖTKKPRMSACÖLYVIFILIC 702  
 QY 566 ACLRLÖMFLMGLFTILSCLTIVRSFÖLIIIFKSTK-VPEFYHAWÖNHGAGLFWISSA 624  
 Db 703 IÖLGIIVALEFIMEPPDIMHDYPSIRE-VYLICNTYH-LGVYPLAGYNGLLISTCF-YAF 759  
 QY 625 AÖLLICLTLVYMTPLPAREYÖRFLVMECEHTSSLOFILAFYNGLLIS-AFASY 683  
 Db 760 KTRNVPANENEAKYIAFTMTTCIILWAF-VPIY-FGSNYKIIYMGFVSSLSA-TVALGC 816  
 QY 684 LKGKDLPENYENACVTFSLFENFVSIAIEFTTASVYDGKY-LPAANMAGLSSLSGFGG 742  
 Db 817 MEVPKYIITIAKPERNVRSAFTS 840  
 QY 743 YLDPKCYILLCRDPLNSTEHFÖAS 766

```

RESULT      12
ENTRY
TITLE      JH0561      #type complete
ORGANISM   metabotropic glutamate receptor 2 precursor - rat
DATE       30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
13-Sep-1998
ACCESSIONS JH0561
REFERENCE   JH0561
AUTHORS    Tarabe, Y.; Yasu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
JOURNAL    Neuron (1992) 8:169-179
TITLE      A family of metabotropic glutamate receptors.
CROSS-REFERENCES NCID:92110002
ACCESSION  JH0561
FEATURE
#molecule_type mRNA
#residues      1-872
#label TAN
#experimental_source brain
COMMENT      This protein is coupled to a G protein and evokes a variety of
functions by mediating intracellular signal transduction.
CLASSIFICATION #superfamily metabotropic glutamate receptor 4
KEYWORDS     G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
FEATURE
1-18      #domain signal sequence #status predicted #label Sig\
19-872    #product metabotropic glutamate receptor 2 #status
predicted #label MEN\
568-590   #domain transmembrane #status predicted #label TR1\
605-625   #domain transmembrane #status predicted #label TR1\
637-655   #domain transmembrane #status predicted #label TR1\
680-700   #domain transmembrane #status predicted #label TR1\
726-747   #domain transmembrane #status predicted #label TR1\
751-782   #domain transmembrane #status predicted #label TR1\
795-819   #domain transmembrane #status predicted #label TR1\
203,286,338,402,
547        #binding site carbohydrate (Asn) (covalent) #status
predicted\
601,675,827,837,
843        #binding_site phosphate (Ser) (covalent) #status

```



```
832      predicted\
      #binding-site phosphate (Thr) (covalent) #status
SUMMARY      #length 872 #molecular-weight 95773 #checksum 5740

Query Match      13.5%; Score 789; DB 2; Length 872;
Best Local Similarity 27.8%; Pred. No. 1,53e-125;
Matches 221; Conservative 195; Mismatches 322; Indels 56; Gaps 51;

Db 54 NEHGRGIORLEAMFLADRIKRDHLLPGVRLGAIHIDSCSDKHAEQALDFVAKASISRG 113
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6 NEH-GYHLFGQAMRLGVEINNSTALLPNIILGYQLYDVCSDSANVYA-TL--RV-LSL- 58

Db 114 ADSSRHICPGPSYATSHDAPTAATGAVIGSGYSDVISQVALLRFLQIPQISYASTSKLS 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 P-GQHHELEOGDLL-HF-SPT-VLAIVGPDSINRAATALLSFTLV-HISYAASSSTLS 113

Db 174 DKSRDYFAITVPPDFQAKAMAEILFEFMYVYVSVASGSDYGETIEAFEELEARANT 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 VKRQPSFLRTIPNDKYQVETWLLQKFGMTWISLVGSSDDYQGLQVQALEMQLVRGI 173

Db 234 CVATSEKVG-RA-MSRAEFGVVRALLQKPSARAVLFTSEDAARELLATQRLN-ASFT 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 CIAFKDIMPESAQVGERMQLMRHLAQ-AGATVYVVFSSRQLARVFEESVLTNLTGKV 232

Db 291 WVASDGMG-ALE-SVAGSERAEG-AITIELASYP-ISDFASYFQSLDPMNNSRNPFR 346
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 233 WVASAMALSRHITGVPGIDIRIGWLGVALQKRAVPGIKAFPEEYAAADR-EAPR-PCR 290

Db 347 EFWEERFH-CSFRORDCAHSLRAV-PFEQESKIMFVYNAVYMAHALHMHRAICPNT 404
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 GSWCSSWQLORECO-AFMAHITMKLKAFSMSAYN-AYRAVYVAHQLQLL-C-C--AS 344

Db 405 HLDAMRPVGRRLYKDFVNVNKFDAFRADDDDEFRPFGDGRIRYVIFITLRAAGSG 464
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 ELCSRGR-VYPMQLLEQ-IHKVHF-L-LHK-DT--VAFNDNRDPLSSYNIIMDMNGPK 396

Db 465 R-VRYQGVGWAEG-LTLDTSFIPMASPSAGPLPASRCSPECLONEKVSQVPGVCCMLC 522
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 397 WTTVLGSSWNSVOLNINTEKIQMHGKNH-QYPKSVCSDDCLEGHORVYTGHHCCFEC 455

Db 523 IPC-Q-PYEXRLDEFTCADCGLYW-PNASLIGCFELPOEYIR-WGDA-WAVGPVTIACL 577
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 456 VPGAGATFLKKSSELYRQPCGTSEMAPEGSGT-CFPRTVFVFLAREHISM-V-LLANTL 512

Db 578 GALATLFLGVFRRHNAIPVYKASGRELCYILGVPFLCMTFVFIKASTAVCTIRL 637
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 513 LLLLLGTAGLFAWHMDTPVYRASAGRLCFMLGSLAAGSGSLYGFGEPTRPACILROA 572

Db 638 GLGTAFSVCSALLTKNRJARIFG-CAREGAQRPRFISPASQVAIGLALISGOLLIVAA 696
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 573 LFLAGFIIFISCLTVRSFQLIIFKFKSTKPTTYHAMVQHGAGLFWISSAOLLCIT 632

Db 697 WLVEAPGTKETAPERRREVYVLRCHNRDA-SMGLSLAVNVLIALCTL-YAEKTRKCP 754
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 633 WLWVMPPLPAREYORPH-LVMLECTEINSLGFLATLYGDL-SIAFAFCSYLGKDLPE 690

Db 755 NNEEAFIGTWTTCIWIALFPIFYVTSYDVVOTTMCVSVSYLGLCLAPKL 814
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 691 NYNEAKCVTFSLLENFYSWIAFETIASVYDGY-LPAAHMMAGLS-SLSGFGYGLPKC 748

Db 815 HILFOPOKNVVSH 828
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 749 YVILCRPDLNSTEH 762

RESULT 13      149142      #type complete
ENTRY      149142      #metabotropic glutamate receptor 8 - mouse
TITLE      metabotropic glutamate receptor 8 - mouse
ORGANISM   Mus musculus #common_name mouse
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
           13-Sep-1998
ACCESSIONS 149142
```

```
REFERENCE      149142
#authors      Duvoisin, R.M.; Zhang, C.; Ramonell, K.
#journal      J. Neurosci. (1995) 15:3075-3083
#title        A novel metabotropic glutamate receptor expressed in the
              retina and olfactory bulb.
#cross-references MVID:9529344
#accession    149142
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues    1-908 ##label RES
##cross-references EMBL:U17252; NID:9854728; PID:9854729
GENETICS
#gene          mGluR8
#classification superfamily metabotropic glutamate receptor 4
#keywords      neurotransmitter receptor
SUMMARY      #length 908 #molecular-weight 101413 #checksum 2996

Query Match      13.2%; Score 772; DB 2; Length 908;
Best Local Similarity 25.8%; Pred. No. 3.95e-122;
Matches 205; Conservative 221; Mismatches 311; Indels 59; Gaps 51;

Db 69 KEGRIHLEAMLYAIQOTNKDPLDLSNITGVRIJLJCCSDYALQSLTFVQALIEKDA 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 6 NEHGYHLFGQAMRLGVEINNSTALLPNIILGYQLYDVCSDSANVYATLR-VLSLPGQH- 62

Db 129 SDVKCANGDPIFTKPKDKISGVIGAAASSYIMVAVNILRFKIPQISYASTAPELSDNR 188
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 -HIE-IQGLDLHYS-P-VLAIVGPDSINRAATALLSFTLV-HISYAASSSTLSVKRO 117

Db 189 YDFESRYVPPDSYQAOAMVDIVTALGMVNYSTLASEGNGEVEAFQTSIRIGVCIA 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 YPSFLRTIPNDKYQVETWLLQKFGMTWISLVGSSDDYQGLQVQALEMQL-VRICIA 176

Db 249 QSQKIPREPRPGFEKTI--IKRLLETPNARAVLTFANEDDINGILDAKKLNSGFHWT 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 FKDIIMPESAQVGD-ERMQCLMRHLAQAGATVYVVFSSRQLARVFEESVLTNLTGKV 234

Db 307 GSDSWG-SK-IADVYQOEELAEBAVTLIPKRASIDGDFRFRSRLTANNRRNWFAPFSE 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 ASBAMALSRHITGVPGIDIRIGWLGVALQKRA-VPLG-KAFPEYAIRADAEAPR-P-CHK 290

Db 365 GNFQXSGSGEGRKNSHKKCTGLERIARDSYBOEKVQVVIDAVYSMAVALHMKKEIC 424
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 GSM-C-SSNQLCREQQAFAHMTPKL-K-AFESMSAYN-AYRAVYVAHQLQLL-G-C 342

Db 425 PGYIGLCPKRVITDGEELCYIAVNPNSAGTPV-FENEGDAPGRYDFQYIYN-KST 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 AS--ELCSR-GRVYPMQLLEQIHKVHFLLHKDT-VAFNDNRDPLSSYNIIMDMNGPKWT 398

Db 484 EYKLIIGH-WTN-QLHLKVEDMOMANREHHPASVCSLCPKPEERKKYGV-CCMHG 539
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 399 -FTVLSSSTWSVOLNINTEKIQMHGKNHQPVSVCSSDCLB-HQRYVYTGHHCCFECV 455

Db 540 RCEGVYV-QVDEL-SCLEPLDQRPINRTGC-QR-IPIIKLEMHSPMAVVPYLAIIIGI 595
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 457 PCGAGFIKKSSELYRQPCGTSEMAPEGSGTCEPRVFLALREHISWVLANTLIDLL 516

Db 596 IATFYIVFVRVNDPVRASGRELSYVLGIFLCYSTIFLMAAPDTITICSPRRIFL 655
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 517 LIGT-AGL-FAMHLDTPVYRASAGRLCFMLGSLAAGSGSLYGFGEPTRPACILQALF 574

Db 656 GLMGCSYVALTKNRHHRHFEQKKSVTA-PKFI-SPASQVLIIFSLISYOLLLEVFW 713
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 575 ALGFTTIFLSCLYRSFQLIIFKFKSTKPTTYHAMVQHGAGLFWIS-SAAOLLICLW 633

Db 714 FVVDPPHTIIDYGEQRTLPDENAGVLC-DISDLSJCSLGSILMAYCTVYAIKTRG 772
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 634 LVVMTPLPAREY--QR-F-P-HL-VMLECTEINSLGFLATLYGDLSSIAFACSLGMD 687

Db 773 VPETPENAKFICTWTTCIWIALFPIFFGTAQSEKMTIQCTITLVSKSLASVSLGM 832
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 688 LPENYNEAKCVTFSLLENFYSW--IA-FFTASVYDGYRLPAAHMMAGLS-SLSGFGG 742
```



Db 833 LYMPKVIITFHPEON 848  
: : : : :  
QY 743 YFLPKCYIICRPDLN 758

RESULT 14  
ENTRY S71376 #type complete  
TITLE glutamate receptor homolog - cherry salmon  
ORGANISM #formal\_name Oncorhynchus masou #common\_name cherry salmon  
DATE 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 01-May-1998

ACCESSIONS  
REFERENCE S71376  
#authors Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.  
#journal FEBS Lett. (1996) 392:71-76  
#title Cloning and characterization of a bifunctional metabotropic receptor activated by both extracellular calcium and glutamate.

#cross-references M0ID:96354880  
#accession S71376  
#status not compared with conceptual translation  
#molecule\_type mRNA  
#residues 1-1128 #label KUB

KEYWORDS  
FEATURE glycoprotein; phosphoprotein

603-625 #domain transmembrane #status predicted #label TM1\  
640-660 #domain transmembrane #status predicted #label TM2\  
672-690 #domain transmembrane #status predicted #label TM3\  
717-737 #domain transmembrane #status predicted #label TM4\  
761-782 #domain transmembrane #status predicted #label TM5\  
796-817 #domain transmembrane #status predicted #label TM6\  
826-850 #domain transmembrane #status predicted #label TM7\  
104,233,403,525,  
757 #binding site carbohydrate (Asn) (covalent) #status predicted\  
636,699,961 #binding site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\  
705 #binding site phosphate (Thr) (covalent) (by protein kinase C) #status predicted\  
892 #binding site phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

SUMMARY #length 1218 #molecular\_weight 136638 #checksum 1674

Query Match 12.9%; Score 755; DB 2; Length 1218;  
Best Local Similarity 26.2%; Pred. No. 1,01e-118;  
Matches 189; Conservative 199; Mismatches 279; Indels 54; Gaps 43:

Db 166 IAGVIGSGSSVALQYONLIQINIPQIASIDSIDTLKRYFLRYVPSDTLQARAI 225  
: : : : :  
QY 77 VLAIVGPDSNTNRATYPAALSPFLY-HISYASSETLSVTRQYPSFLRTIPNDKYQVETM 135

Db 226 LDIVKRYNTYVAHTEGNYGESGMFAKELASOEGICIAHSDDKI-YSN-AGEKHPDRL 283  
: : : : :  
QY 136 VILLOKFGWTWISLVSSDDYDGLQVQALNOALVKGICIAFADIMPFSAQVDERMOCL 195

Db 284 LRLRLRLPRARYVCFCEGATVGLMAMRLGVAGEFLILSSDGA-DRDEV-VEGYE 341  
: : : : :  
QY 196 MRHL-AQ-AGATVYVYSSRQLARVFFESVVLNLGK-VWVASSEAMALSRHTITGVGIG 222

Db 342 QEA-VEGIVTKLHS-EVYISFDYFLKRLNTTRNMPFEFQHRQ-CRIGHPLENM 338  
: : : : :  
QY 253 RIGMVGVALOKRAVPGLAFAEAYTA-RADKCAPRCHKSGWCSSNQLQREC-QAFMAH 309

Db 399 NYKNCSGYESLEDNYVDOSKMGFVINAITYAMOGLDHMSHICPGHYGLCKAMPIDGS 458  
: : : : :  
QY 310 TMRKL-KAF-SMSASAY--NA---Y--RAYVAHAGHLQHLG--CASE--LC-SRGRYPPW 355

Db 459 QLEFLMRTSFTVSGEDVWFDENGDTPGRYTEIMNLQYEPG-AFDYINVSWEHGOIST 517  
: : : : :  
QY 356 OLLEQIHKVHFL-LHKDTYAFNDNRPDLSSYNIAMDMWNPKMTFTYLGSSSTSPQOLNI 414

Db 518 DDYIMQ-INSNDVYL-SYSEPPCSKEIKYIRNGEVSCMCITACADNEIVQ-DE-FTCT 573  
: : : : :  
QY 518 DDYIMQ-INSNDVYL-SYSEPPCSKEIKYIRNGEVSCMCITACADNEIVQ-DE-FTCT 573

QY 415 NETKIOMHGKNOHPKSVSCSDCLEGHQRYV-TGFHHCCEFCVPCGAGTFLNKSELYRCQ 473

Db 574 ACDLGMPDPELEGCPEILRLYLE-WGNPESTYQVFAQLGLIVTSFYVFIPLYDTPV 632  
: : : : :  
QY 474 PCGTERRAPBGSTQCFPRVVFALREHTSWVLAANTLILLILLD-TAGLWMDHTDV 532

Db 633 VKSSRELYIILAGIFLIGCFPIIAOPTVASCYLQRLVGLSATMCSALVTKNRI 692  
: : : : :  
QY 533 VRAGRGRLCFMLGSLAASGGS-YGFEGETPRACLLRALPALGTITLSCITVSPDL 592

Db 693 ARLLASKKKICTRKPRRPSAMQVIALYVVO-LT-LEVTLI-TLE-PPMPVKSYGS 748  
: : : : :  
QY 593 IILF-----KFSKVPFTFYHAWQNHGAGLFVMISSAOLLICLTWLVMTPLPAREYR 647

Db 749 IRE-VFLIC-NTSTGVMAVPLNGILLIMSCRY-YAFKTRNPPANENAKYIAFTMYTTC 805  
: : : : :  
QY 648 FPHVLMECTENSLGFTIAFLYNGLLSTS-APACSYLQKDLPEPNEKCVTFSLFNF 706

Db 806 IWLAF-VPIY-FGSNKKIITTSFVSLS-VTVALGCMFSPKYIILAKPERVRSAPFT 862  
: : : : :  
QY 707 VSMIAFFTASVYDQKY-LPANMMAGLSLSGFCGYFLPKCYIILCRPDINSTPHQA 765

Db 863 S 863  
QY 766 S 766

RESULT 15  
ENTRY A46742 #type complete  
TITLE metabotropic glutamate receptor, mGluR6 - rat  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 29-Jan-1999

ACCESSIONS  
REFERENCE A46742  
#authors Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.  
#journal J. Biol. Chem. (1993) 268:11868-11873  
#title Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6 with a high agonist selectivity for L-2-amino-4-phosphonobutylate.

#cross-references M0ID:93280152  
#accession A46742  
#status Preliminary  
#molecule\_type nucleic acid  
#residues 1-871 #label NAK  
#cross-references GB:D13963; NID:9391856; PID:d1003572; PID:9391857  
#experimental\_source retina  
#note sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P133250)

CLASSIFICATION #superfamily metabotropic glutamate receptor 4  
KEYWORDS G protein-coupled receptor; transmembrane protein  
SUMMARY #length 871 #molecular\_weight 95088 #checksum 3942

Query Match 12.5%; Score 729; DB 2; Length 871;  
Best Local Similarity 26.5%; Pred. No. 1.59e-113;  
Matches 215; Conservative 219; Mismatches 308; Indels 70; Gaps 56;

Db 49 RACGAKKKEQGYHRLFAMLYALDRVADPELLPGVRLGRLDLDSGRDYALEQALSFQ 108  
: : : : :  
QY 1 RSC-SFN-SHGHLFQAMRLGVEEINNSTALLPNTIGQLDYDVS-DSANYATLRL-VL 56

Db 109 ALIRGRGDDEASVRCGPVPLRSAPPRVAVVAGASASSIVANVLRFLAIPDISY 168  
: : : : :  
QY 57 SL---PGQ-HHLEIQ--GDL--LHYSPT--VLAIVGPDSNTNRATYPAALSPFLY-HISY 105

Db 169 ASTAPLSDSTRDYDFSRVVPDYSQAQAVDIVRALGNVYSTLASSENGSGEVAEV 228  
: : : : :  
QY 106 AASSETLSVRKQYPSFLRTIPNDKYQVETMVLQKFGWTWISLVSSDDYDGLQVQALE 165

Db 229 QTSREAGYCIASIKIPEPKPGEFHK-VIRLMETPNARCIILFANEDIRRLVLEATR 287  
: : : : :  
QY 166 NQAL-VRGICIAFKDIMPQSAQVGDERMOKLMRHLAQAAGATVYVYSSRQLARVFFESV 224

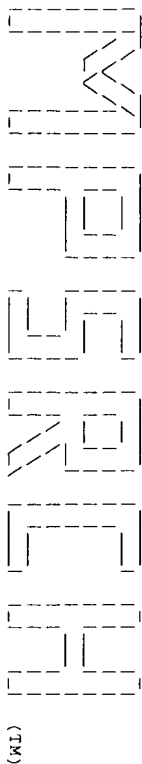












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Mparch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:36:28 2000; MasPar time 93.42 Seconds

Tabular output not generated.

Title: >US-09-361-652-3  
Description: (1-777) from US09361652.pep  
Perfect Score: 5838  
Sequence: 1 RSCSFNENGHYHLFOAMRLGV.....NSTEHFOASIDYTRRCGST 777

Scoring table:  
PAM 150  
Gap 11

Searched: 666290 segs, 103942017 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-pending  
1:Pg 2:060 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B  
10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92  
18:U93 19:U94 20:NEWP 21:NEWU5 22:NEWU8 23:NEWU9

Statistics: Mean 42.646; Variance 177.023; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	5838	100.0	777	23	US-09-361-Sequence 3, Applicatio	0.00e+00
2	5838	100.0	777	1	PCT-US99-1 Sequence 3, Applicatio	0.00e+00
3	4587	78.6	840	2	US-60-172-Sequence 5, Applicatio	0.00e+00
4	4587	78.6	840	23	US-09-361-Sequence 1, Applicatio	0.00e+00
5	4587	78.6	840	1	PCT-US99-1 Sequence 1, Applicatio	0.00e+00
6	4483	76.8	842	1	PCT-US99-1 Sequence 2, Applicatio	0.00e+00
7	4483	76.8	842	23	US-09-361-Sequence 2, Applicatio	0.00e+00
8	1848	31.7	843	18	US-09-361-Sequence 1, Applicatio	1.65e+169
9	1797	30.8	843	18	US-09-361-Sequence 2, Applicatio	2.77e+164
10	1509	25.8	669	18	US-09-361-Sequence 7, Applicatio	7.45e+135
11	1464	25.1	822	2	US-60-172-Sequence 2, Applicatio	2.87e+130
12	1233	21.1	877	2	US-60-172-Sequence 14, Applicati	8.66e+107
13	1182	20.2	1059	16	US-09-134-Sequence 2, Applicatio	1.27e+101
14	1170	20.0	1085	14	US-08-484-Sequence 5, Applicatio	2.08e+100
15	1170	20.0	1085	9	US-08-484-Sequence 2, Applicatio	2.08e+100
16	1170	20.0	1085	9	US-60-172-Sequence 5, Applicatio	2.08e+100
17	1170	20.0	1085	2	US-60-172-Sequence 11, Applicati	2.08e+100
18	1170	20.0	1085	9	US-08-484-Sequence 5, Applicatio	2.08e+100
19	1170	20.0	1085	6	US-08-292-Sequence 5, Applicatio	2.08e+100
20	1163	19.9	1078	2	US-60-172-Sequence 9, Applicatio	1.06e+99
21	1160	19.9	1078	6	US-08-292-Sequence 7, Applicatio	2.14e+99

22	1160	19.9	1078	2	US-60-172-Sequence 6, Applicatio	2.14e+99
23	1160	19.9	1078	1	US-08-484-Sequence 7, Applicati	2.14e+99
24	1160	19.9	1078	9	PCT-US99-1 Sequence 12, Applicatio	2.14e+99
25	1160	19.9	1078	9	US-08-484-Sequence 7, Applicatio	2.14e+99
26	1160	19.9	1078	2	US-60-172-Sequence 7, Applicatio	2.14e+99
27	1160	19.9	1078	2	US-08-434-Sequence 8, Applicatio	2.14e+99
28	1160	19.9	1078	2	US-60-172-Sequence 8, Applicatio	2.14e+99
29	1158	19.8	1079	1	PCT-US98-1 Sequence 59, Applicati	3.41e+99
30	1158	19.8	1079	9	US-08-484-Sequence 8, Applicatio	3.41e+99
31	1158	19.8	1079	9	US-08-484-Sequence 8, Applicatio	3.41e+99
32	1158	19.8	1079	6	US-08-292-Sequence 8, Applicatio	3.41e+99
33	1158	19.8	1079	16	US-09-107-Sequence 59, Applicatio	3.41e+99
34	1158	19.8	1079	9	US-08-484-Sequence 8, Applicatio	3.41e+99
35	1158	19.8	1079	2	US-60-172-Sequence 12, Applicati	3.41e+99
36	1149	19.7	1079	2	US-60-172-Sequence 10, Applicati	2.77e+98
37	1143	19.6	1079	2	US-60-172-Sequence 13, Applicati	1.12e+97
38	1101	18.9	1026	14	US-08-943-Sequence 1, Applicatio	1.97e+93
39	1090	18.7	1001	1	PCT-US99-1 Sequence 8, Applicatio	1.97e+93
40	1074	18.4	1038	1	PCT-US97-0 Sequence 2, Applicatio	1.04e+90
41	1074	18.4	1038	1	PCT-US97-0 Sequence 2, Applicatio	1.04e+90
42	1063	18.2	1088	9	US-08-484-Sequence 6, Applicatio	1.34e+89
43	1063	18.2	1088	9	US-08-484-Sequence 6, Applicatio	1.34e+89
44	1063	18.2	1088	6	US-08-292-Sequence 6, Applicatio	1.34e+89
45	1063	18.2	1088	9	US-08-484-Sequence 6, Applicatio	1.34e+89

## ALIGNMENTS

RESULT ID	1	US-09-361-652-3	STANDARD:	PRT:	777 AA.
XX	xxxxxx				
XX		Sequence 3, Application US/09361652			
DE		Sequence 3, Application US/09361652			
CC		GENERAL INFORMATION:			
CC		APPLICANT: Zuker, Charles S.			
CC		APPLICANT: Adler, Jon Elliot			
CC		APPLICANT: Lindemeyer, Juergen			
CC		APPLICANT: Ryba, Nick			
CC		APPLICANT: Hoorn, Mark			
CC		APPLICANT: The Regents of the University of California			
CC		TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
CC		FILE REFERENCE: 02307E-088610US			
CC		CURRENT APPLICATION NUMBER: US/09/361,652			
CC		CURRENT FILING DATE: 1999-07-27			
CC		EARLIER APPLICATION NUMBER: US 60/094,465			
CC		EARLIER FILING DATE: 1998-07-28			
CC		NUMBER OF SEQ ID NOS: 8			
CC		SOFTWARE: PatentIn Ver. 2.1			
CC		SEQ ID NO 3			
CC		LENGTH: 777			
CC		TYPE: PRT			
CC		ORGANISM: Homo sapiens			
CC		FEATURE:			
CC		OTHER INFORMATION: human G-protein coupled receptor B3 (GPCR-B3)			
CC		SEQUENCE 777 AA: 86285 MW: 3230984 CN:			
SO					
Query Match		100.0%:	Score 5838:	DB 23:	Length 777:
Best Local Similarity		100.0%:	Pred. No. 0.00e+00:		
Matches	777:	Conservative	0:	Mismatches	0:
				Indels	0:
				Gaps	0:
Db	1	RSCSFNENGHYHLFOAMRLGVEETNSALPNTLTGYOLYDVCSDSANVATRVSLSP 60			
OY	1	RSCSFNENGHYHLFOAMRLGVEETNSALPNTLTGTOLYDVCSDSANVATRVSLSP 60			
Db	61	QHHEIIEGLDGLHYSPTVLAVIGPDSNTRATTAALSPFLVHISYAASSTLSEVKRQYPS 120			
OY	61	QHHEIIEGLDGLHYSPTVLAVIGPDSNTRATTAALSPFLVHISYAASSTLSEVKRQYPS 120			
		61 QHHEIIEGLDGLHYSPTVLAVIGPDSNTRATTAALSPFLVHISYAASSTLSEVKRQYPS 120			







```

CC Sequence 5, Application US/60172600
CC GENERAL INFORMATION:
CC APPLICANT: BORAZZI, VIVIER
CC TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
CC TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
CC TITLE OF INVENTION: PROTEIN, AND USES THEREOF
CC FILE REFERENCE: CLO00178
CC CURRENT APPLICATION NUMBER: US/60/172,600
CC CURRENT FILING DATE: 1999-12-20
CC NUMBER OF SEQ ID NOS: 14
CC SOFTWARE: fastseq for Windows Version 4.0
CC SEQ ID NO 5
CC LENGTH: 840
CC TYPE: PRT
CC ORGANISM: UNKNOWN
CC FEATURE:
CC OTHER INFORMATION: SEE GENEBANK REPORT
SQ SEQUENCE 840 AA: 93496 MW: 3932001 CN:

```

Query Match	78.6%	Score 4587	DB 2	Length 840
Best Local Similarity	75.2%	Pred. No. 0.00e+00		
Matches	585	Conservative	99	Mismatches 93
			Indels	1
			Gaps	1
Db	63	RDPSNGHGHLFFQAMRPTVEINNSSALLPNILGVELDYDCESSANVATLRVLA	LOG	122
		1		
Qy	1	RSCSNEHGHLFFQAMRLGVEEINNSTALLPNITLGYOLDYDCSDSANVATLRVLS	PLG	60
Db	123	PHRIEQDLNRHSSKVAEFGPNTDHAVTALLPEFLMPLTVSEASSVLSAKRFP		182
		1		
Qy	61	OHMIELQDLDLHSPTVLAVIGPSTNRMAATLALSPFLVH-ISTASSETLSVKQOY		119
Db	183	SFLRTVPDSDRHOVEVMVOLLOSFCGWWISLIGSYGDYGLQVQALBEEAVRPGI	CAVKD	242
		1		
Qy	120	SFLRTIPNDKYOVEITMVLLOKFGMTWISLIGSSDDYGLQVQALBEOALVRGIC	IFKD	179
Db	243	IYFETARVQDRRMOSSMGLQOATTTVVYFSNNHRLARVFFRSRYVLANLTKG	WVASDQ	302
		1		
Qy	180	IMPEAQVGDEMOCLMRHLAOCATVYVYSSQLARVEFESVLTNLTKGWVASEA		239
Db	303	AISTITSVTGJGIGITGLVAVQOORVPGKKEFEESYRATVTAAPSADEGSC	SNOL	362
		1		
Qy	240	ALSRIITGVPRGIQRGMVLGYAIQKRAVPGKAEEMARADKAPRPPCKGSCSS	NOL	299
Db	363	CRECHFTTRNMPITLGAFSMSAAYRYEAYVAVAHGLHQLGCTSEKCSRG	PYPMOLQ	422
		1		
Qy	300	CRECOAFMAHMPKIKAFKASMSAYNAVAYAAVHGLHQLLGASSELCSGR	YPMQLE	359
Db	423	QIYKYNELLHENTYAFDDNGDTLGYDIIAAMDNGPMTETIIGSASLSPVH	LDINKTKI	482
		1		
Qy	360	QIHKHFELHMDTVAFNNDNRDPLSSYNIIAMDNGPKMTFTVLGSSWSPVQ	LNINETKI	419
Db	483	OMHGNNNOVPYSVCTDCLAGHHRVVVGSHHCCCECPCEAGTFLMNSH	LICQPGTEE	542
		1		
Qy	420	OMHGNNHOVPYSSVSDCLEGHQRVYVGFHHCCECPVCGGTFLNKSELY	ROOPCTEE	479
Db	543	WAPKESTCEPRTEVEFLAMHBPISLVYIIAANTLILLVYAGLFAFHRT	PRVRSAGR	602
		1		
Qy	480	WAPESQICEPRTYVFLARHRTSMVLLAANTLILLLLGLAGLFAHHDT	PPVRSAGR	539
Db	603	LCFLMLGSLVAGSCSEFYSEFGEPTVPACLLRQPLFSLGAFILFSLC	LIRSFOLVIFKFS	652
		1		
Qy	540	LCFLMLGSLVAGSGLVGFGEPTRPACLLRQALFALGFTIFLISCLIV	RSFOLIFKFS	599
Db	653	TKVPFTYTAQONNGAGLFLVYSTVHLICLTLMVMTTRPTREYORFHL	VILCETEY	722
		1		
Qy	600	TKVPFTYTAQONNGAGLFLVYMISSAQAOLICLTLMVMTPLPAREYOR	RFHLVILECTEY	659
Db	723	NSVGLFLAFTNILLISTEVCSTLGEKLEPENYEAACVTFSLINRV	SIATFTMASIY	782
		1		
Qy	660	NSLGLTLFLNGLLISIAFACSTLGGKDLPENYEAACVTSLELNFV	SIATFTTASVY	719
Db	783	OGSYPAVNVLAGLTLTSGGSGYFDEKCYVILCRLPELNNTEHQAS	IODYTRRCGT	840
		1		

Query	720	DKKYLPAANMMGLSSLSGSGSYETLPCKCVILLCRDPLNSTEHFOASIDQTYTRCGST	777
RESULT	4	STANDARD:	PRT: 840 AA.
ID	US-09-361-652-1		
XX	xxxxxx		
XX			
XX			
XX			
XX			
DE	Sequence 1, Application US/09361652		
XX			
CC	Sequence 1, Application US/09361652		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Zuker, Charles S.		
CC	APPLICANT: Adler, Jon Elliot		
CC	APPLICANT: Lindemeier, Juergen		
CC	APPLICANT: Ryba, Nick		
CC	APPLICANT: Hoon, Mark		
CC	APPLICANT: The Regents of the University of California		
CC	TITLE OF INVENTION: Nucleic Acids Encoding a G-protein Coupled Receptor		
CC	TITLE OF INVENTION: Involved in Sensory Transduction		
CC	FILE REFERENCE: 02307E-0886100S		
CC	CURRENT APPLICATION NUMBER: US/09/361,652		
CC	CURRENT FILING DATE: 1999-07-27		
CC	EARLIER APPLICATION NUMBER: US 60/094,465		
CC	EARLIER FILING DATE: 1998-07-28		
CC	NUMBER OF SEQ ID NOS: 8		
CC	SOFTWARE: PatentIn Ver. 2.1		
CC	SEQ ID NO 1		
CC	LENGTH: 840		
CC	TYPE: PRT		
CC	ORGANISM: Rattus sp.		
CC	FEATURE:		
CC	OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)		
CC	SEQUENCE 840 AA: 93496 MW; 3932001 CN;		
Query Match	78.6%;	Score 4587;	DB 23; Length 840;
Best Local Similarity	75.28;	Pctd. No. 0.00e+00;	
Matches	585; Conservative	99; Mismatches	93; Indels 1; Gaps 1;
Db	63	PPDSFGHGHHFFQAMRFVEEINNSALLPNTTIGELYDYDSESANVATLRYVALOG	122
QY	1	RCSFNEHHYHFOANRLVEEINNSALLPNTTIGELYDYDSESANVATLRYVALOG	60
Db	123	PHRIEQDLNRHSSKVAFIGPNDTDAVTTAALLGFTLPLVSYEASSVVLISAKRFP	182
QY	61	OHIEHLOGLLHXSPVLAVIGPDSNRATPAATLSPFLVH-ISAASSETLSVKRQYP	119
Db	183	SLRTVPSRHOVEYVYVOLLQSTGWWISLIGSYGTYGOLGVALLBELVALPRICVAFKD	242
QY	120	SLRTIPNDKYOVETWVLLQKFGWMIWISLVGSSDDYGOLGVALLBNQALVRGICIAFXD	179
Db	243	IYFSAFARVDDPMQSMQHLAQRITVVVVSNSRHLARVFFRSVIVLANLTGYWVASEDN	302
QY	180	IMFSAQVDEDMQCMRLAQAGAVVVVVSRSQCLARVFEESVIVLNLTKGWVVASEAM	239
Db	303	AISTYTSVTGIGQIGTVYGVAVQOQOVPLKEFEESYVRAVTAAPSADESGWSCSTNOL	362
QY	240	ALSRHITVPGIORIGMYGVAIQKRAVYGLKAFEEAVARADKEAPRCPHKGSCMSCNOL	299
Db	363	CCECHFTFRNMPITLGAFSMAAARYVEAVVVAHGLHLLGTSITCSGPRYPMOLLO	422
QY	300	CCECOFTFAHMPKLKAFSSMSRYNARAVIAVAHGLHLLGTSITCSGPRYPMOLLE	359
Db	423	QTYKVNFLLEHTVAFDDNDGTLYGYVDIAMDPMNGSEMTFELLIGSASLSPVHADINKTKI	482
QY	360	QJHKVHFLLKHQTVAFNDNRDPLSSNIIIAMDMNGSKMFTVLGSSTWSPVQNLINETKI	419
Db	483	OMHGKNNQVPSVCTTDLAGCHRRYVYVGSRRCCFESVPCDEAGTFLNKLSELIYCPGCTGE	542
QY	420	OMHGKNNQVPSVCTTDLAGCHRRYVYVGSRRCCFESVPCDEAGTFLNKLSELIYCPGCTGE	479







Query Match 76.8%; Score 4483; DA 1; Length 842;  
Best Local Similarity 74.2%; Pred. No. 0.00e+00;  
Matches 577; Conservative 101; Mismatches 99; Indels 1; Gaps 1;

Db 65 RDSDFNGHYHLFOAMRFTVEEINNSTALLPNTILGYELDYDVCSSESSNVYATLRVPAOOG 124  
1 RSCSFNEHGHYHLFOAMRGLVEEINNSTALLPNTILGYOLYDVCSDSANVYATLRVLSLPG 60

Db 125 TGHLEMRDLRNEHSSKVVALLIGPNTDHAATYTTALLESFIMPLVSYASSVYLSGKRKFP 184  
61 QHHELEGGDLHYSPTVLAVIGPNTINRAATTAALLSPFLVH-ISTYASSETLSVKRQYP 119

Db 185 SFLETPSDKYQVEVIVYRLLOSFGWWSILVSGYDYGQGLQVQALBELATPRGICVAFKD 244  
120 SFLETPNDKYQVEETVMLLQKFGMTWISLVGSSDDYQGLQVQALEQALVRGICIAFKD 179

Db 245 VVPLSAQADPRMQRMLRLARARTYVVFSSNNHLAGVFFRSVYLANLTKWVIASEDW 304  
180 IMPFSAGVGERMOCMLRHHLAQAGATVYVVFSSROLARVFESVYLTNLTKWVWASEAW 239

Db 305 AISTYITNVPGIOGIGTVLVAIQOROVPGIKFEFEESYVOAVMGAPRTCEPSSMGTNOL 364  
240 ALSHITIGVPEIQIRIGVLAIGVAIQKRAVPGIKAEFEAYARADKEAPRCHGSSMCSNOL 299

Db 365 CRECHAFITNMMPBLGAFSMSAAVNYEAYAVAHGLHQLLGCTSGTCARGPVYPMOLQ 424  
300 CREQOAMAHMTPKLKAFMSASAINAYRAVYAVAHGLHQLLGCASELCSRRVYPMOLLE 359

Db 425 QIYVNFELHKKTYAFDDKGPGLCYDIIAMDNGPEKTEFVIGSASISPVHLDINKTKI 484  
360 QIHVHFELHEDYAFNDNRPDLSSYNIIAMDNGPKWTFVIGSSTSPVQULINETKI 419

Db 485 OMHCKNNQVPYSVCTRCLBGNHRLVNGSHHCCFECMPCENGTFLNSELTCOPCGTEE 544  
420 OMHCKNNQVPYSVCSDDLBSHQVYVGFHHCCEVPCGAGTFLNSELTCOPCGTEE 479

Db 545 WAPGSSACFSRTVEFGLWHEPISLVLLAANTLLDLLLIGTAGLFAWRLHTPVYRSAGR 604  
480 WAPGSSQTCFRTVYFALREHTSWLLAANTLLDLLLIGTAGLFAWRLDTPVYRSAGR 539

Db 605 LCFMLGSLVAGSCSLYFEGKPTVPACLLRPLFSLGFAIFLSCLTIRSFOLVYIIFKS 664  
540 LCFMLGSLVAGSCSLYFEGEPTRPACLLRQALFALGFIIFLSCLTVRSQULIIFKS 599

Db 665 TKVPTFYHTAQNHNAGIFVIVSSTVHFLCLTWMATPRTREYORFPHLVLECTEV 724  
600 TKVPTFYHTAQNHNAGIFVIVSSTVHFLCLTWMATPRTREYORFPHLVLECTEV 659

Db 725 NSVGFVAFANHILISTEVCSTLGKELPENYNEAKCVFSLLHFSWTAFTMSIY 784  
660 NSLGFITLAFLYNGLISTISAFACSTLKGDLPENYNEAKCVFSLLFNVSWIAFFTASVY 719

Db 785 QGSYLPANVNLAGLATLSGFGSGYFLPKCYVILCRPELINTEHFOASIQDYTRRCGTT 842  
720 DGKYLPAANMMAGLSLSSGFGGYFLPKCYVILCRPLDNSTEHFOASIQDYTRRCGST 777

RESULT 7  
ID US-09-361-652-2 STANDARD: PRT; 842 AA.

AC xxxxxx  
XX  
DT  
XX Sequence 2, Application US/09361652  
DE  
CC Sequence 2, Application US/09361652  
CC GENERAL INFORMATION:  
CC APPLICANT: Zuker, Charles S.  
CC APPLICANT: Adler, Jon Elliot  
CC APPLICANT: Lindemeier, Juergeen  
CC APPLICANT: Ryba, Nick  
CC APPLICANT: Hoon, Mark

CC APPLICANT: the Regents of the University of California  
CC TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor  
CC TIME OF INVENTION: Involuted in Sensory Transduction  
CC FILE REFERENCE: 02307E-086610US  
CC CURRENT APPLICATION NUMBER: US/09/361,652  
CC CURRENT FILING DATE: 1999-07-27  
CC EARLIER APPLICATION NUMBER: US 60/094,465  
CC EARLIER FILING DATE: 1998-07-28  
CC NUMBER OF SEQ ID NOS: 8  
CC SOFTWARE: Patent'n Ver. 2.1  
CC SEQ ID NO 2  
CC LENGTH: 842  
CC TYPE: PRT  
CC ORGANISM: Mus sp.  
CC FEATURE:  
CC OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)  
CC SEQ ID NO 2

Query Match 76.8%; Score 4483; DA 23; Length 842;  
Best Local Similarity 74.2%; Pred. No. 0.00e+00;  
Matches 577; Conservative 101; Mismatches 99; Indels 1; Gaps 1;

Db 65 RDSDFNGHYHLFOAMRFTVEEINNSTALLPNTILGYELDYDVCSSESSNVYATLRVPAOOG 124  
1 RSCSFNEHGHYHLFOAMRGLVEEINNSTALLPNTILGYOLYDVCSDSANVYATLRVLSLPG 60

Db 125 TGHLEMRDLRNEHSSKVVALLIGPNTDHAATYTTALLESFIMPLVSYASSVYLSGKRKFP 184  
61 QHHELEGGDLHYSPTVLAVIGPNTINRAATTAALLSPFLVH-ISTYASSETLSVKRQYP 119

Db 185 SFLETPSDKYQVEVIVYRLLOSFGWWSILVSGYDYGQGLQVQALBELATPRGICVAFKD 244  
120 SFLETPNDKYQVEETVMLLQKFGMTWISLVGSSDDYQGLQVQALEQALVRGICIAFKD 179

Db 245 VVPLSAQADPRMQRMLRLARARTYVVFSSNNHLAGVFFRSVYLANLTKWVIASEDW 304  
180 IMPFSAGVGERMOCMLRHHLAQAGATVYVVFSSROLARVFESVYLTNLTKWVWASEAW 239

Db 305 AISTYITNVPGIOGIGTVLVAIQOROVPGIKFEFEESYVOAVMGAPRTCEPSSMGTNOL 364  
240 ALSHITIGVPEIQIRIGVLAIGVAIQKRAVPGIKAEFEAYARADKEAPRCHGSSMCSNOL 299

Db 365 CRECHAFITNMMPBLGAFSMSAAVNYEAYAVAHGLHQLLGCTSGTCARGPVYPMOLQ 424  
300 CREQOAMAHMTPKLKAFMSASAINAYRAVYAVAHGLHQLLGCASELCSRRVYPMOLLE 359

Db 425 QIYVNFELHKKTYAFDDKGPGLCYDIIAMDNGPEKTEFVIGSASISPVHLDINKTKI 484  
360 QIHVHFELHEDYAFNDNRPDLSSYNIIAMDNGPKWTFVIGSSTSPVQULINETKI 419

Db 485 OMHCKNNQVPYSVCTRCLBGNHRLVNGSHHCCFECMPCENGTFLNSELTCOPCGTEE 544  
420 OMHCKNNQVPYSVCSDDLBSHQVYVGFHHCCEVPCGAGTFLNSELTCOPCGTEE 479

Db 545 WAPGSSACFSRTVEFGLWHEPISLVLLAANTLLDLLLIGTAGLFAWRLHTPVYRSAGR 604  
480 WAPGSSQTCFRTVYFALREHTSWLLAANTLLDLLLIGTAGLFAWRLDTPVYRSAGR 539

Db 605 LCFMLGSLVAGSCSLYFEGKPTVPACLLRPLFSLGFAIFLSCLTIRSFOLVYIIFKS 664  
540 LCFMLGSLVAGSCSLYFEGEPTRPACLLRQALFALGFIIFLSCLTVRSQULIIFKS 599

Db 665 TKVPTFYHTAQNHNAGIFVIVSSTVHFLCLTWMATPRTREYORFPHLVLECTEV 724  
600 TKVPTFYHTAQNHNAGIFVIVSSTVHFLCLTWMATPRTREYORFPHLVLECTEV 659

Db 725 NSVGFVAFANHILISTEVCSTLGKELPENYNEAKCVFSLLHFSWTAFTMSIY 784  
660 NSLGFITLAFLYNGLISTISAFACSTLKGDLPENYNEAKCVFSLLFNVSWIAFFTASVY 719

Db 785 QGSYLPANVNLAGLATLSGFGSGYFLPKCYVILCRPELINTEHFOASIQDYTRRCGTT 842  
720 DGKYLPAANMMAGLSLSSGFGGYFLPKCYVILCRPLDNSTEHFOASIQDYTRRCGST 777



RESULT	ID	US-09-361-631-1	STANDARD;	PRT;	843 AA.
XX	8				
XX	AC	xxxxxx			
XX	DT				
XX	DE	Sequence 1, Application US/09361631			
CC	CC	Sequence 1, Application US/09361631			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT: Zuker, Charles S.			
CC	CC	APPLICANT: Adler, Jon Elliot			
CC	CC	APPLICANT: Lindemeyer, Juergen			
CC	CC	APPLICANT: The Regents of the University of California			
CC	CC	TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
CC	CC	FILE REFERENCE: 02307E-08872005			
CC	CC	CURRENT APPLICATION NUMBER: US/09/361,631			
CC	CC	CURRENT FILING DATE: 1999-07-27			
CC	CC	EARLIER APPLICATION NUMBER: US 60/095,464			
CC	CC	EARLIER FILING DATE: 1998-07-28			
CC	CC	EARLIER APPLICATION NUMBER: US 60/112,747			
CC	CC	EARLIER FILING DATE: 1998-12-17			
CC	CC	NUMBER OF SEQ ID NOS: 10			
CC	CC	SOFTWARE: PatentIn Ver. 2.0			
CC	CC	SEQ ID NO 1			
CC	CC	LENGTH: 843			
CC	CC	TYPE: PRT			
CC	CC	ORGANISM: Rattus sp.			
CC	CC	FEATURE:			
CC	CC	OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4 amino			
CC	CC	OTHER INFORMATION: acid sequence			
CC	CC	SEQUENCE 843 AA: 95799 MW: 4010925 CN;			

Query Match	31.7%;	Score 1848;	DB 18;	Length 843;
Best Local Similarity	37.5%;	Pred. No. 1.65e-169;		
Matches	293;	Conservative	193;	Mismatches 269;
			Indels	26;
			Gaps	22;

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Db 71 GYNIMQARFVVEEINNNSSLLPGVLKEADVDCYNNTHPHGXYFLA--ODDDLILK 122
Qy 9 GYHLEQARLVEEELNNSTALLPNTLTGQYLDYDCSDSANATLRVLSPGQHIELQG 68
Db 130 DYSOYMPHVAVAGPDNSESATVSNILSHFLIPQITYSATSDLRKDRKHPMSMLRTVPS 189
Qy 69 DLHYSPVYLVAGPDDSTNNRATTAALSPPLY-HISVAASSETLKYRQPSFLRPIPN 127
Db 190 ATTHIEAVVOLAMVHOMWMIYVLVSDDDYGENSHLLSQRLTKSDICIAOEVLPIRES 249
Qy 128 DKYQETVYVLLQKFGKWTWISLVSSDDYGGOLGYALENO-ALYRGICIAFKDIMP--S 184
Db 250 SQVNRSEBQRLDNLILDKLRTSRARVYVESP-ELSYFPEHYLRNNFTGFWIASESW 308
Qy 185 AQV--GDE-R-MQCLMRHLAQAGATVYVVEFSSROLAR-VFESVYVNLNLGKVVASEAW 239
Db 309 AIDVYVHLVLELHRTGTFGLTYQIVSYSPGSSOR--VRDRKGYPPVNTNLRITCNQ 365
Qy 240 ALSRHITGVPGCIQIGVLYAIDQRAAPGAKAEAEAYARDKEA-PAPCRGKSGWCSNQ 298
Db 366 DCDACLN-LTKSFNNILLSGERVYVYVSAYVAVAHALHRLCLCNRRCTKQVYPMOL 424
Qy 299 LCRREGQAMATMKRKLKAFSSMSA-YNNRYRAVYVAHRLHOLLCASELCSRGVYVMOQL 357
Db 425 LREIWHVNFLLGNRLRFDDQGDMPML-LDIIQOMQDISQNPFOSIASYSFTSKRLTYIN 483
Qy 358 LEQIHKVFLELHKDTVAENDNRD-PLSSYNTIADMDWNPCKMTFVLVSGSSTSPQOLNINE 416
Db 484 -NVSYTPNTNTPVPMSCSKSQOPGOMKSVYLLHFCCEFCIDCMQGTLYNRSRDAEFNLSG 542
Qy 417 TKIQMGKNNHOVPPSVCSDDLQEGHQRVYVTFHHCCEFCVPCGAGTFLNKS-ELYRCOPC 475

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Db	543	PGSMSTYNDITCQRRTFLEMEVEPTIVAAIIAAGFESTALIEIF-WRHQTPMVR	601
Oy	476	GTEHAPGECOTCPRPVFVALNEHHSWVLNANTLILLULLGOTAGLFPM-HLDTFVR	534
Db	602	SAGGPMCLMVPULLAFGMVPVYVGPPTVSCCRQAFVVCSTLSCITVRSFOVC	661
Oy	535	SAGGGLCCITMGSLAASGSLYGFEGBPTRACILRQALFALGFIPLSCITVNSFQII	594
Db	662	VEKMARRLPSAYSEPMWRHGPYVVAETAIKVALVVGNNMLATTINFGRTDPDDPIMI	721
Oy	595	IFKSTKVPFTYHAMQNHGAGFLVMTISSAAQLLICLTWLVMTPLP-ARYQKFFPLVM	655
Db	722	LSCHPNYNGLEMTSMDDLISVLGSEFAVNGKLLPNYNEAKITLISMTFSFSSISLC	781
Oy	654	LECETNSLGLFLFLVNGLISISAFACSYGKGLPENYNEAKVTSLSEFNFVSWIAFF	713
Db	782	TFMSHDSVLVITIMDLVTVNLNFAISIG-YFGRCYMLIFEYPERNLSAVFNSMIGQTY	840
Oy	714	TTASVYDGKLYLPANMWAG-LSSLSGGGGYFLPKVCVILICRDPDNLSTEHQASIDQYTR	772
Db	841	R 841	
Oy	773	R 773	

RESULT	9	STANDARD;	PRT;	843 AA
ID	US-09-361-631-2			

AC xxxxxx  
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DT  
XX  
DE Sequence 2, Application US/09361631

CC Sequence 2, Application US/09361631

CC APPLICANT: Adler, Jon Elliot  
CC APPLICANT: Lindemeier, Juergen  
CC APPLICANT: The Regents of the University of California  
CC TITLE OF INVENTION: Nucleic Acids Encoding a G-protein Coupled Receptor  
CC TITLE OF INVENTION: Involved in Sensory Transduction  
CC FILE REFERENCE: 02307E-0887200S  
CC CURRENT APPLICATION NUMBER: US/09/361,631  
CC CURRENT FILING DATE: 1999-07-27  
CC EARLIER APPLICATION NUMBER: US 60/095,464  
CC EARLIER FILING DATE: 1998-07-28  
CC EARLIER APPLICATION NUMBER: US 60/112,747  
CC EARLIER FILING DATE: 1998-12-17  
CC NUMBER OF SEQ ID NOS: 10  
CC SOFTWARE: PatentIn Ver. 2.0  
CC SEQ ID NO 2  
CC LENGTH: 843  
CC TYPE: PRT  
CC ORGANISM: Mus sp.  
CC FEATURE:  
CC OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) B4 amino  
CC OTHER INFORMATION: acid sequence  
CC SEQUENCE 843 AA: 95752 MW: 399656 CN:

Query Match	30.88;	Score 1797;	DB 18;	Length 843;
Best Local Similarity	37.0%;	Pred. No. 2.77e-164;		
Matches	289;	Conservative	191;	Mismatches 275;
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			Gaps	23;

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Db	334	ETFNCLYDSESKNSPDASAFHKAHEGIGAANGTAERPPCTGDENTISVETPYMDETHL	4133
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QY	371	DYVANDNRDPLSSNITIAMNMNGPK-WT-FYVIGS-SINSP-VO-LNINETKIOMHGN	4223
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QY	485	SOTCPRVIVLAREHSHWMLLANLTLTLTLTLTLG-TAGLFAMHLDIPVVSAGRGLCFL	5433
Db	653	LLFSLTLCFSSSLF-EIGEPOMTCRIROPAFGISFVLCISCIJVKTKNRYLWPE-AKI	7093
QY	544	MIGSLIAG-SSSLYIGFEPRPRACLRQALFALGFITFLSCLVRSFOLITIKSESTKV	6023
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QY	662	LGFIAPL-VNGLLISISAFCSYGLGDLPENYNEACVYFSLFLFNVSWIAFFT-ASY	7183
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DE	Sequence 5, Application US/08484719		
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CC	Sequence 5, Application US/08484719		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Edward F. Nemeeth, Edward M.		
CC	APPLICANT: Brown, Steven C. Hebert,		
CC	APPLICANT: Bradford C. Van Wageningen,		
CC	APPLICANT: Manuel F. Balandrin,		
CC	APPLICANT: Forrest H. Fuller, Eric G.		
CC	APPLICANT: Delmar, Scott T. Moe		
CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE		















\*\*\*\*\*  
Molecular Research Unit  
(TM)  
\*\*\*\*\*

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MSEARCH protein - protein database search, using Smith-Waterman algorithm  
Run on: Fri Mar 17 13:35:41 2000; MSEARCH time 13.42 Seconds  
Tabular output not generated.

Title: >US-09-361-652-3  
Description: (1-777) from US09361652.pep  
Perfect Score: 5898  
Sequence: 1 RSCSFNEMGHILFOAMRLGV.....NSTEHFOASIODYTRRCGST 777

Scoring table: PAM 150  
Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 35.945; Variance 174.591; scale 0.206

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	1170	20.0	1085 2	US-08-943-Sequence 5, Applicatio	3.80e-88
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6	1160	19.9	1078 2	US-08-943-Sequence 7, Applicatio	2.82e-87
7	1160	19.9	1078 3	US-08-353-Sequence 7, Applicatio	2.82e-87
8	1160	19.9	1078 1	US-08-485-Sequence 7, Applicatio	2.82e-87
9	1160	19.9	1078 1	US-08-484-Sequence 7, Applicatio	2.82e-87
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23	854	14.6	912 4	PCT-US91-0 Sequence 19, Applicatio	9.20e-61

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25	796	13.6	906 4	PCT-US91-0 Sequence 17, Applicatio	9.03e-56
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37	770	13.2	1212 1	US-08-486-Sequence 12, Applicatio	6.16e-53
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## ALIGNMENTS

Sequence 5, Application US/08484565  
Patent No. 5763569  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
TITLE OF INVENTION: CALCULUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,565  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: Including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993



















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CC	CC	Patent No. 5962314			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT: Edward M. Brown			
CC	CC	APPLICANT: Steven C. Hebert			
CC	CC	APPLICANT: James E. Garrett, Jr.			
CC	CC	TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE			
CC	CC	TITLE OF INVENTION: MOLECULES			
CC	CC	NUMBER OF SEQUENCES: 20			
CC	CC	CORRESPONDENCE ADDRESSES:			
CC	CC	ADDRESSEE: Lyon & Lyon			
CC	CC	STREET: First Interstate World Center			
CC	CC	STREET: Suite 4700			
CC	CC	STREET: 633 West Fifth Street			
CC	CC	CITY: Los Angeles			
CC	CC	STATE: California			
CC	CC	COUNTRY: USA			
CC	CC	ZIP: 90071			
CC	CC	COMPUTER READABLE FORM:			
CC	CC	MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage			
CC	CC	COMPUTER: IBM PC compatible			
CC	CC	OPERATING SYSTEM: PC-DOS/MS-DOS			

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CC SOFTWARE: FASTSEQ
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943, 986
CC FILING DATE: 03-OCT-1997
CC CLASSIFICATION: 530
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/484, 565
CC FILING DATE: 7-June-1995
CC APPLICATION NUMBER: 08/353, 784
CC FILING DATE: 9 December, 1994
CC APPLICATION NUMBER: PCT/US/94/12117
CC FILING DATE: 21 October, 1994
CC APPLICATION NUMBER: U.S. 08/292, 827
CC FILING DATE: 23 August, 1994
CC APPLICATION NUMBER: U.S. 08/141, 248
CC FILING DATE: 22 October, 1993
CC APPLICATION NUMBER: U.S. 08/009, 389
CC FILING DATE: 23 February, 1993
CC APPLICATION NUMBER: U.S. 08/017, 127
CC FILING DATE: 12 February, 1993
CC APPLICATION NUMBER: U.S. 07/934, 161
CC FILING DATE: 21 August, 1992
CC APPLICATION NUMBER: U.S. 07/834, 044
CC FILING DATE: 11 February, 1992
CC APPLICATION NUMBER: U.S. 07/749, 451
CC FILING DATE: 23 August, 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Heber, Sheldon O.
CC REGISTRATION NUMBER: 38, 179
CC REFERENCE/DOCKET NUMBER: 213/006
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (213) 489-1600
CC TELEFAX: (213) 955-0440
CC TELEX: 67-3510
CC INFORMATION FOR SEO ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1078 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;
SQ
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Oy 176 AFKDIM-FSAQVDDEMKQCLMRHLAQAQATVVYVES-RQLARVFESVYVNLNLTKVM 233
Dd 294 LASEMASSLIAMPQYFHVVGATIGFALRAGQDIGFREFLRKVHPKRSVHNQFAKEWE 353
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Oy 234 VASEMA---L-S--R--HingvP-GIQ-RlGMVLgV-A-IQK--R-AVP-GI-KAF-E 274
Dd 354 ETFNCHLOEGAKGLPYDITLRGHEESGDRFSNSSTAIFRPDLCTGDENISSVETPIDYTH 413
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Oy 275 EAVA-R-ADKE-APRPCH--KGSCWSSNDLCRECAQAF-M-A--HTMPRIKA---FS- 318
Dd 414 LRISNYVLAITYSTAHMLADIYTLCPLRGJFTNSSCADIKKVEAMOVYKLKLRLHNETNM 473
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Oy 319 MSSANINRAVYAAHGHHOLGC-AE-EL-----CS-RQRVTPWOLLBDIHNVKHFLLHK 370
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[illegible][illegible]



QY 661 SLGFIILAFI--YNGLLISAFACSYLGKDLPENYNKACVTFSLFNFVSWIAFFTT-AS 717

Db 828 TY-GKFVSAVEVIAIIAA-SFGLLACIFENKIIILFKPSRNTIE 870

QY 718 YVDGKYLPAANMMAGLSLSSGFGGY-FLPKCVIILCRPDLNSTE 761

RESULT 9

ID US-08-484-565-7 STANDARD: PRT: 1078 AA.

XX xxxxxx

Sequence 7, Application US/08484565

CC Sequence 7, Application US/08484565

CC Patent No. 5763569

CC GENERAL INFORMATION:

CC APPLICANT: Edward M. Brown

CC APPLICANT: Steven C. Hebert

CC APPLICANT: James E. Garrett, Jr.

CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

CC NUMBER OF SEQUENCES: 20

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Lyon & Lyon

CC STREET: First Interstate World Center

CC STREET: Suite 4700

CC STREET: 633 West Fifth Street

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90071

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: FASTSEQ

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/484,565

CC FILING DATE: 7 June, 1995

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION DATA: including application

CC PRIOR APPLICATION DATA: described below: 9

CC APPLICATION NUMBER: 08/353,784

CC FILING DATE: 9 December, 1994

CC APPLICATION NUMBER: PCI/US/94/12117

CC FILING DATE: 21 October, 1994

CC APPLICATION NUMBER: U.S. 08/292,827

CC FILING DATE: 23 August, 1994

CC APPLICATION NUMBER: U.S. 08/141,248

CC FILING DATE: 22 October, 1993

CC APPLICATION NUMBER: U.S. 08/009,389

CC FILING DATE: 23 February, 1993

CC APPLICATION NUMBER: U.S. 08/017,127

CC FILING DATE: 12 February, 1993

CC APPLICATION NUMBER: U.S. 07/934,161

CC FILING DATE: 21 August, 1992

CC APPLICATION NUMBER: U.S. 07/834,044

CC FILING DATE: 11 February, 1992

CC APPLICATION NUMBER: U.S. 07/749,451

CC FILING DATE: 23 August, 1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Hebert, Sheldon O.

CC REGISTRATION NUMBER: 38,179

CC REFERENCE/DOCKET NUMBER: 213/006

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (213) 489-1600

CC TELEFAX: (213) 955-0440

CC TELEX: 67-3510

CC INFORMATION FOR SEQ ID NO: 7:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 1078 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 1078 AA; 120573 MW; 6153012 CN;

Query Match 19.9%; Score 1160; DB 1; Length 1078;

Best Local Similarity 31.9%; Pred. No. 2,82e-87;

Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

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Db 118 NKIDSLNIDFPCNCSEHPISTAVVATGSSGVSTAVANLLGLFIPIQVYASSRLLSNK 177

QY 62 HHE-LQ-GDLHYL--PTVLAVIGPDSINRAITLALISPELV-HISYAASSETLSYK 115

Db 178 NQKSFRTIPNDEHQTAMADIIEYFRMNWGTIAADDDYGRGIEKREEREDIC 237

QY 116 RQYPSFLRTIPNDKIVETVWLLQFGWTWISLVSSDDYGLQVQALENOALVIGICI 175

Db 238 DESLISQYSD--EE-IQHVVEVIONSTAKYIVFSSGPDLEPIKE-IVRRNITGIM 293

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Db 294 LASEANASSLLAMPQYFHVVGITIFALKAGQIPQFRFLKKNHPRKSVHNGFAKEPNE 353

QY 234 VSEAWA--L-S--R--HITGP-GIQ-RIGVVLGV-A-IQR--R-AVP-GL-KAF-E 274

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QY 275 EATA-R-AOKE-APRPCH---KGSWCSNQLCREQAF--M-A--HTMKKLA---FS- 318

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QY 425 NHOVPKSVCSDDLBSHOR-VVIGFHHCCFECVPCAGAFILNKSLEYRCOPCGTEWAPD 483

Db 594 NHTSCIAKEIEFLSWTEPFG-IALLFAVLGIFLFAVFGVFIKFRNPITYVATNRELSY 652

QY 484 GSQTCFPRVVFALAREHNSWVLANTLLLLLG-TAGLFAMHLDTPVRSAGRLCF 542

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QY 543 LMGSLAAG--SSSLYGFEGEPTRPACLLRQALFALGFTIFLCLITVRSQLIILIEFKSTK 501

Db 710 IPSEFHRKMGVNLQFLVFLCTFMQIVCIWLYIAPSSVRNODLEDEIIFITCHE-G 768

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Db 769 SL-MALGFILGYTCLLAAICFEFAFKSRKLPENFNEAKFITSMLEFIWISFIPAVAS 827

QY 661 SLGFIILAFI--YNGLLISAFACSYLGKDLPENYNKACVTFSLFNFVSWIAFFTT-AS 717

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RESULT 10

ID US-08-480-751-7 STANDARD: PRT: 1078 AA.

XX xxxxxx







CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
CC TITLE OF INVENTION: MOLECULES  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: First Interstate World Center  
CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90071  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: FASTSEQ  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/484,565  
CC FILING DATE: 7 June, 1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION DATA: including application  
CC PRIOR APPLICATION DATA: described below: 9  
CC APPLICATION NUMBER: 08/353,784  
CC FILING DATE: 9 December, 1994  
CC APPLICATION NUMBER: PCT/US/94/12117  
CC FILING DATE: 21 October, 1994  
CC APPLICATION NUMBER: U.S. 08/292,827  
CC FILING DATE: 23 August, 1994  
CC APPLICATION NUMBER: U.S. 08/141,248  
CC FILING DATE: 22 October, 1993  
CC APPLICATION NUMBER: U.S. 08/009,389  
CC FILING DATE: 23 February, 1993  
CC APPLICATION NUMBER: U.S. 08/017,127  
CC FILING DATE: 12 February, 1993  
CC APPLICATION NUMBER: U.S. 07/934,161  
CC FILING DATE: 21 August, 1992  
CC APPLICATION NUMBER: U.S. 07/834,044  
CC FILING DATE: 11 February, 1992  
CC APPLICATION NUMBER: U.S. 07/749,451  
CC FILING DATE: 23 August, 1991  
CC AFFORNEY/AGENT INFORMATION:  
CC NAME: Heber, Sheldon O.  
CC REGISTRATION NUMBER: 38,179  
CC REFERENCE/DOCKET NUMBER: 213/006  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (213) 955-0440  
CC TELEFAX: (213) 489-1600  
CC TELEX: 67-3510  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1079 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: Protein  
CC SEQUENCE 1079 AA: 120867 MW: 6054255 CN:  
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Query Match 19.88; Score 1158; DB 1; Length 1079;  
Best Local Similarity 31.48; Pred. Mismatches 261; Indels 78; Gaps 55;  
Matches 262; Conservative 233;  
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RESULT 12  
ID US-08-480-751-8 STANDARD; PRT; 1079 AA.  
XX xxxxxx  
AC  
XX  
DT  
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DE Sequence 8, Application US/08480751  
XX  
CC Sequence 8, Application US/08480751  
CC Patent No. 5858684  
CC GENERAL INFORMATION:  
CC APPLICANT: Edward F. Nemeth  
CC APPLICANT: Edward M. Brown  
CC APPLICANT: Steven C. Hebert  
CC APPLICANT: Forrest H. Fuller  
CC APPLICANT: James E. Garrett, Jr.  
CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Lyon & Lyon  
CC STREET: First Interstate World Center  
CC STREET: Suite 4700  
CC STREET: 633 West Fifth Street  
CC CITY: Los Angeles  
CC STATE: California



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CC CC COUNTRY: USA
CC CC ZIP: 90071
CC CC COMPUTER READABLE FORM:
CC CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
CC CC COMPUTER: IBM PC compatible
CC CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC CC SOFTWARE: FASTSEO
CC CC CURRENT APPLICATION DATA:
CC CC APPLICATION NUMBER: US/08/480,751
CC CC FILING DATE: 7 June, 1995
CC CC CLASSIFICATION: 435
CC CC PRIOR APPLICATION DATA:
CC CC PRIOR APPLICATION DATA: including application
CC CC PRIOR APPLICATION DATA: described below: 9
CC CC APPLICATION NUMBER: 08/353,784
CC CC FILING DATE: 9 December, 1994
CC CC APPLICATION NUMBER: PCT/US/94/12117
CC CC FILING DATE: 21 October, 1994
CC CC APPLICATION NUMBER: U.S. 08/292,827
CC CC FILING DATE: 23 August, 1994
CC CC APPLICATION NUMBER: U.S. 08/141,248
CC CC FILING DATE: 22 October, 1993
CC CC APPLICATION NUMBER: U.S. 08/009,389
CC CC FILING DATE: 23 February, 1993
CC CC APPLICATION NUMBER: U.S. 08/017,127
CC CC FILING DATE: 12 February, 1993
CC CC APPLICATION NUMBER: U.S. 07/934,161
CC CC FILING DATE: 21 August, 1992
CC CC APPLICATION NUMBER: U.S. 07/834,044
CC CC FILING DATE: 11 February, 1992
CC CC APPLICATION NUMBER: U.S. 07/749,451
CC CC FILING DATE: 23 August, 1991
CC CC ATTORNEY/AGENT INFORMATION:
CC CC NAME: Heber, Sheldon O.
CC CC REGISTRATION NUMBER: 38,179
CC CC REFERENCE/DOCKET NUMBER: 213/004
CC CC TELECOMMUNICATION INFORMATION:
CC CC TELEPHONE: (213) 489-1600
CC CC TELEFAX: (213) 955-0440
CC CC TELEX: 67-3310
CC CC INFORMATION FOR SEQ ID NO: 8:
CC CC SEQUENCE CHARACTERISTICS:
CC CC LENGTH: 1079 amino acids
CC CC TYPE: amino acid
CC CC TOPOLOGY: linear
CC CC MOLECULE TYPE: protein
CC CC SEQUENCE 1079 AA: 120867 MW: 6054255 CN:
Dh Query Match 19.8%; Score 1158; DB 2; Length 1079;
Dh Best Local Similarity 31.4%; Pred. No. 4,21e-87;
Dh Matches 267; Conservative 233; Mismatches 261; Indels 78; Gaps 55.
Dh 60 CIRYNFGEFRLQAMIFAIEEINSSPILPMNLGYRIFDTCNTVSKALA--TLISFAVQ 117
Dh 3 C-SENEHGHYHLFOAMRLGVEEININSTALLPITLTGYOLYDCSDSANVYATLRLVSLPGQ 61
Dh 118 NKIDSLNDEFCNCGSEHSPRTIAYVAGAGSGVSTAVANLGLFTIIPQVYSAASSRLLSNK 177
Dh 62 HHLE-LQ-GDILHYS--PIVLAIGIPSTIRAAVITTAALLSPFLV-HIISAASETISVK 115
Dh 178 NOYKSLFTIPINDEHOATAMADIIEYEFWMVNGTIAADDYGRGIRKEFREAEERDICI 237
Dh 116 RQYPEFLTINIDKQYVETVLLILQKFEWTLISLVSSDDYGGQGLGVALENQALVRICII 175
Dh 238 DFESELTISQSD--EETIQ-VVEYIQNSTAKVIYVFSGGDLEPLIKE-IYRNRITGRIV 293
Dh 176 AFKIDMP-FSAQVGDERMOCILMRHLAQAGATVVVVFSS-ROLARVFESVYLTMLTKWV 233
Dh 294 LASEMASSSLIAMPEYHHVVGITGELKAGQIPGFREFLOKVHPRKSVHNGFAKFEWE 353
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[illegible]



Cc		CLASSIFICATION:	514	
Cc	Prior Application Data:			
Cc	Prior Application Data:	including application		
Cc	Prior Application Data:	described below:	8	
Cc	Application Number:	PCT/US/94/12117		
Cc	Filing Date:	21 October, 1994		
Cc	Application Number:	U.S. 08/292,827		
Cc	Filing Date:	23 August, 1994		
Cc	Application Number:	U.S. 08/141,248		
Cc	Filing Date:	22 October, 1993		
Cc	Application Number:	U.S. 08/009,389		
Cc	Filing Date:	23 February, 1993		
Cc	Application Number:	U.S. 08/017,127		
Cc	Filing Date:	12 February, 1993		
Cc	Application Number:	U.S. 07/934,161		
Cc	Filing Date:	21 August, 1992		
Cc	Application Number:	U.S. 07/834,044		
Cc	Filing Date:	11 February, 1992		
Cc	Application Number:	U.S. 07/749,451		
Cc	Filing Date:	23 August, 1991		
Cc	Attorney/Agent Information:			
Cc	Name:	Heber, Sheldon O.		
Cc	Registration Number:	38,179		
Cc	Reference/Docket Number:	209/069		
Cc	TELECOMMUNICATION INFORMATION:			
Cc	Telephone:	(213) 489-1600		
Cc	Telefax:	(213) 955-0440		
Cc	Telex:	67-3510		
Cc	Information for Seq. ID No:	8:		
Cc	Sequence Characteristics:			
Cc	Length:	1079 amino acids		
Cc	Type:	amino acid		
Cc	Molecule Type:	protein		
SQ	SEQUENCE	1079 AA; 120867 MW; 6054255 CN;		
Db	Query Match	19.8%; Score 1158; DB 3; Length 1079;		
Db	Best Local Similarity	31.4%; Pred. No. 4,21e-87;		
Oy	Matches	262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;		
Db	60 CIRYRFGFRLQAMIFAEIEINSSPLLPMWTGYRFPTCMTVSKALEA--TLSPVAO 117			
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21      XX
22      Sequence 8, Application US/08943986
23
24      Sequence 8, Application US/08943986
25      Patent No. 5962314
26      GENERAL INFORMATION:
27      CC APPLICANT: Edward M. Brown
28      CC APPLICANT: Steven C. Hebert
29      CC APPLICANT: James E. Garrett, Jr.
30      CC TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
31      CC TITLE OF INVENTION: MOLECULES
32      CC NUMBER OF SEQUENCES: 20
33      CC CORRESPONDENCE ADDRESS:
34      CC ADDRESSEE: Lyon & Lyon
35      CC STREET: First Interstate World Center
36      CC STREET: Suite 4700
37      CC STREET: 633 West Fifth Street
38      CC CITY: Los Angeles
39      CC STATE: California
40      CC COUNTRY: USA
41      CC ZIP: 90071
42      CC COMPUTER READABLE FORM:
43      CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
44      CC COMPUTER: IBM PC compatible
45      CC OPERATING SYSTEM: PC-DOS/MS-DOS
46      CC SOFTWARE: FASTSO
47      CC CURRENT APPLICATION DATA:
48      CC APPLICATION NUMBER: US/08/943,986
49      CC FILING DATE: 03-OCT-1997
50      CC CLASSIFICATION: 530
51      CC PRIOR APPLICATION DATA:
52      CC APPLICATION NUMBER: 08/484,565
53      CC FILING DATE: 7-June-1995
54      CC APPLICATION NUMBER: 08/353,784
55      CC FILING DATE: 9 December, 1994
56      CC APPLICATION NUMBER: PCT/US/94/12117
57      CC FILING DATE: 21 October, 1994
58      CC APPLICATION NUMBER: U.S. 08/292,827
59      CC FILING DATE: 23 August, 1994
60      CC APPLICATION NUMBER: U.S. 08/141,248
61      CC FILING DATE: 22 October, 1993
62      CC APPLICATION NUMBER: U.S. 08/009,389
63      CC FILING DATE: 23 February 1993

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CC	APPLICATION NUMBER: U.S. 08/017,127	
CC	FILING DATE: 12 February, 1993	
CC	APPLICATION NUMBER: U.S. 07/934,161	
CC	FILING DATE: 21 August, 1992	
CC	APPLICATION NUMBER: U.S. 07/834,044	
CC	FILING DATE: 11 February, 1992	
CC	APPLICATION NUMBER: U.S. 07/749,451	
CC	FILING DATE: 23 August, 1991	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Heber, Sheldon O.	
CC	REGISTRATION NUMBER: 38,179	
CC	REFERENCE/DOCKET NUMBER: 213/006	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (213) 489-1600	
CC	TELEFAX: (213) 955-0440	
CC	TELEX: 67-3510	
CC	INFORMATION FOR SEQ ID NO: 8:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 1079 amino acids	
CC	TYPE: amino acid	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: protein	
CC	SEQUENCE 1079 AA; 120867 MW; 6054255 CN;	
CC	Query Match 19.8%; Score 1158; DB 2; Length 1079;	
CC	Best Local Similarity 31.4%; Pred. No. 4,21e-87;	
CC	Matches 262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;	
Db	60 CIRYNEGFRLQAMIFAEIEINSSPLLPMKLGRIYFDTCNTVSKALEA--TLSEVAQ 117	
OY	3 C-SFNEHGHLFQAMRLGVEEINSTALLPRLITGLGYLDVCSDSANYATRLVLSLPGQ 61	
Db	118 NKIDSLNIDECNCSERLPTITAVVGATGSGSVSTAVANLGLFTIIPQVSTASSRLLSNK 177	
OY	62 HHIE-LO-GDILHYS--PVLAVIAGPSTINRAATITALLSPFLY-HISYASSETLSVK 115	
Db	178 NQYSFLITINDEHQATAMADIIEYFPMNMGVITIAADDYDGRGIEKFEAREERDICI 237	
OY	116 RQYSFLITINDRKYQVETWMLLQKFEWTISLVGSSDDYGGQAGVALENQALVKGICI 175	
Db	238 DFEELISQYSD--EELIQ--VEVYIONSTAKVIVVFSSGPDLEPLIKE-IVRRNITRIW 293	
OY	176 AFKDIMP-FSAQYDGERMQCLMRHLQAGATVYVVSF-RQLAVFPESVYLTNLTKW 233	
Db	294 LASEMASSSLIAMPETHYVVGITGEGELKAGQIDGFEPELIQKYHPRKSVHNGFAKEFWE 353	
OY	234 VASEMA--L-SR---HITGVP-GIQ-RIGMYLGV-A-IOK--R-APV-GL-KAF-E 274	
Db	354 ETPNCHLOEAGKGPLVDPTVFRSHHEGGRNLNLSSTARPLCTGDENTSVETP-VYDYE 412	
OY	275 EAYIA-R-AD--KEA-P-----RPHCKGS-W--CASN-Q-LCRECOAMATMPKLAIFS 318	
Db	413 HLRISTYNYLAVYSIAHALADITYCLPGRGLFTNNGSCADIKVEMOYLKHLRLNFTNN 472	
OY	319 -MSSAYNYAVRAYVAHGLHQLLGC-AS-EL-----CS-RRRVYPMQDLBDIHVHLLH 369	
Db	473 MGEQVTEDECCDLVGNSTIIMHLSPEDGSIYFEKVEGYNYNYAKKGERLFTNEBKILMSG 532	
OY	370 K-DTVAFNDNDPDLSTSYNIIMDMWNGPK-WT-FTVLGS-STWSP-VQ-LTINETKIOHWG 423	
Db	533 FSRVPEFNCGRDOAGTRKGIIBSEFPCCBCEYBCPGEYSGETDASACDKCDDPWSN 592	
OY	424 KNHQPKSVCSDDCLEGQR-VVYGFHNHCECEVPCGAGTILNSELRYRCPGCTEEMAP 482	
Db	593 EHNHTSICAKIEFLAFTPEPG-IATLTPAVLGIFLTAFLVFLFKFNTPTVYKATNELS 651	
OY	483 EGSQICEFRITYFLALREHTSVWLLAANTLLILLILG-TAGLFAMHNDTPVYRSAGRLC 541	
Db	652 YLLFLSLCCESSSLF-EIGEPDWTCHRLROPARGISFVLCSILVKTNRVLVFE--A 708	
OY	542 FLMSGSLAAG--SGSLYGFGEETPRACLLRQALFALGTFITLSCGLYRSFQILIIIFNST 600	
Db	709 KIPISFHHKMGWGLNIQTLFLVCTFMQLICIMLYTAPBSSYRNHHEDEIIITTCHEG 768	

[illegible]











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 WATSON  
 (TM)  
 \*\*\*\*\*

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MSearch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Mar 17 13:26:21 2000; Maspar time 39.48 Seconds

Tabular output not generated. 466.217 Million cell updates/sec

Title: >US-09-361-652-3  
 Description: (1-777) from US09361652.pep  
 Perfect score: 5838  
 Sequence: 1 RSCSFNHCYHLFQAMRLGV.....NSTEHFQASIDYTRRCGST 777

Scoring table: PAM 150  
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-geneseq36  
 1:geneseqp

Statistics: Mean 38.193; Variance 172.438; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1170	20.0	1085	1	M89563	Bovine parathyroid cal 4.34e-94
2	1170	20.0	1085	1	M54844	Bovine parathyroid cal 4.34e-94
3	1170	20.0	1085	1	M38272	Bovine parathyroid cal 4.34e-94
4	1160	19.9	1078	1	M54846	Human parathyroid calc 3.73e-93
5	1160	19.9	1078	1	M89565	Human parathyroid calc 3.73e-93
6	1160	19.9	1078	1	M11889	Parathyroid calcium re 3.73e-93
7	1160	19.9	1078	1	M38274	Human parathyroid cell 3.73e-93
8	1158	19.8	1079	1	M94928	Rat kidney extracellular 5.73e-93
9	1158	19.8	1079	1	M34847	Rat kidney calcium rec 5.73e-93
10	1158	19.8	1079	1	M89565	Rat parathyroid calcin 5.73e-93
11	1158	19.8	1079	1	M38275	Rat kidney cell calcin 5.73e-93
12	1101	18.9	1026	1	M32059	Dogfish shark kidney c 1.20e-87
13	1064	18.2	1088	1	M38273	Human parathyroid cell 3.37e-84
14	1063	18.2	1088	1	M54845	Human parathyroid calc 4.17e-84
15	1063	18.2	1088	1	M89564	Human parathyroid calc 4.17e-84
16	1063	18.2	1088	1	M11888	Parathyroid calcium re 4.17e-84
17	992	17.0	1219	1	M25763	Amino acid sequence of 1.09e-77
18	951	15.3	1058	1	M25762	Amino acid sequence of 1.09e-77
19	915	15.7	779	1	M94921	Rat pheromone receptor 2.35e-70
20	845	14.5	912	1	M82558	Human mglur4. 5.73e-64
21	845	14.5	912	1	R72092	Human mglur4. 7.09e-64
22	801	13.7	1056	1	M25764	Amino acid sequence of 8.14e-60
23	796	13.6	906	1	R25081	GLU-G-R subtype 1b. 2.35e-59

24	796	13.6	1199	1	R25080	GLU-G-R subtype 1a. 2.35e-59
25	790	13.5	906	1	R64250	Human mglurB. 8.40e-59
26	786	13.5	1056	1	M25765	Amino acid sequence of 1.96e-58
27	787	13.5	1194	1	R42199	mglur1. 1.39e-58
28	781	13.4	872	1	R95052	Human metabotropic glu 5.66e-58
29	771	13.2	850	1	M94901	Mouse pheromone recept 4.71e-57
30	769	13.2	1180	1	R64253	Human mglurB. 7.20e-57
31	770	13.2	1212	1	R64250	Human mglurB. 5.83e-57
32	763	13.1	877	1	R64255	Human mglurB. 2.57e-56
33	761	13.0	872	1	R89580	Metabotropic glutamate 3.92e-56
34	757	13.0	908	1	M41568	Human metabotropic glu 9.14e-56
35	756	12.9	908	1	M49928	Human metabotropic glu 1.13e-55
36	731	12.5	866	1	M94920	Rat pheromone receptor 2.24e-53
37	731	12.5	877	1	M01099	Metabotropic glutamate 2.24e-53
38	718	12.3	877	1	M94903	Mouse pheromone recept 3.49e-52
39	714	12.2	548	1	M94917	Rat pheromone receptor 8.11e-52
40	714	12.2	667	1	M94919	Rat pheromone receptor 1.53e-51
41	711	12.2	877	1	R82657	Human mglur3. 8.11e-52
42	713	12.2	768	1	R64252	Human mglur3. 1.00e-51
43	703	12.0	768	1	M94918	Rat pheromone receptor 8.27e-51
44	676	11.6	605	1	M94925	Rat pheromone receptor 2.45e-48
45	675	11.6	867	1	R72093	Human mglur4 clone cmr 3.02e-48

## ALIGNMENTS

RESULT 1  
 ID M89563 standard; Protein: 1085 AA.  
 AC M89563;  
 DT 19-MAR-1999 (first entry)  
 DE Bovine parathyroid calcium receptor BOPCAR 1.  
 KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;  
 KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;  
 KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;  
 KW neonatal distress; neurodegenerative disease; Alzheimer's disease;  
 KW Huntington's disease; Parkinson's disease; dementia; muscle tension;  
 KW depression; anxiety.  
 OS Bos sp.  
 PN US658664-A.  
 PD 12-JAN-1999.  
 PF 07-JUN-1995; 480751.  
 PR 23-AUG-1991; US-480751.  
 PR 11-FEB-1992; US-749451.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; WO-012117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGM) BRIGHAM & WOMEN'S HOSPITAL.  
 PI (NPSF-) NPS PHARM INC.  
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,  
 PI Hebert SC, Nemeth EF, Van Wagenen BC;  
 DR WPI: 99-119871/10.  
 DR N-PSDB: V82483.  
 PT Screening for calcium receptor active compounds - by recombinant  
 PT expression of nucleic acid encoding calcium receptor and determining  
 PT the effect of compounds on calcium receptor activity  
 PS Claim 1: Fig 47: 176pp: English.  
 CC A method has been developed of screening for a compound able to affect  
 CC one or more activities of a calcium receptor (CR) comprises: (A)  
 CC contacting a recombinant cell with a test compound, where the  
 CC recombinant cell comprises a recombinant nucleic acid expressing the  
 CC provided that the cell does not have functional CR expression from  
 CC endogenous nucleic acid; (3) determining the ability of the test  
 CC compound to affect one or more activities of the calcium receptor; and  
 CC (C) comparing the ability with the ability of the test compound to  
 CC affect the one or more CR activities in a cell not comprising the  
 CC recombinant nucleic acid. The present sequence represents bovine  
 CC parathyroid CR, designated a BOPCAR 1. The nucleic acid sequence of  
 CC BOPCAR 1 can be used as part of the recombinant nucleic acid in the



method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 1085 AA:

Query Match	20.08;	Score 1170;	DB 1;	Length 1085;
Best Local Similarity	31.98;	Pred. No. 4.34e-94;		
Matches 263; Conservative	227;	Mismatches 256;	Indels 78;	Gaps 56

D	b	61	CINRYRFRRLQAMTFIAEELINSSPALLPMNTIGYRFDTCNTVSALBA--TLSPVAQ	118
Q	y	3	C-SFNEHGYHJFQARLGEVEEINNSTALLPITITGQYLDVCSQSNVAVYTLRLSLPG	61
D	b	119	NKIDSLNDEPCNCEHJLPTIAVVGATSGISITAVANLGLFIYPOVYASSRLLSNK	178
Q	y	62	HIIE-LO-GDLLHS---PYLVANIYGPSTIRAKTATALLSPFLY-HISTAASSETLSK	115
D	b	179	NOFSLELTPINDEHOATAMADIIIEFRMNWGTIAADDPGRDIEKFEFEAEERDICI	238
Q	y	116	ROYPSLELTPINDKQVETWMLLOKFGMTWISLVGSSDDYQGLGYOALENOALVRGCI	175
D	b	239	DESE-L-ISQYSDERKIQOQVVEYQNSYAKIYVYESSPDLEPIKE-IYRRNTGRLWL	295
Q	y	176	AFKDIIMPYSAOYGDERMCKLRHLAQAATVAVVFSS-RQIARFEFSVALTNLTGQVW	234
D	b	296	ASEMASSSLTAMPEYFHVVGITGFGLKAOQIGREFLOKVPYRKSYNHNGFAKEWEE	355
Q	y	235	ASEMA---L-SR-----HITGP-GIQ-RIGMWGV-A-IOK---R-AYP-GL-KAF-EE	275
D	b	336	TFNCHLOGANGPLVPDTFLNGHEBEGARLSNPTAFRPLCTGSENISVETPYMDYTHL	415
Q	y	276	AYA-R-AD-KEA-P-----RPHCKG-SWCCSNODC-RE-C-OAFNAHTMPKLKAFS-M	319
D	b	416	RISYVAVYAVYSIAHALDIDITCIPGRGLFTNGSCADIKKYEAQVUKHLRLHNTSNMG	475
Q	y	320	SSAIVAYAVYAVAHGLHOLLGC-AS-EL-----CS-RGRVYPMOLLEOHKXVFLIAK-	370
D	b	476	EQYTFDECDGDIAGNYSIINMHLSPEDGSIYKEVGYVYVYAKKGERLFIINDEXILMSGFS	535
Q	y	371	DYVANDNRDPLSSYNIITAMDMNGK-WT-FTVLGS-STWSP-VQ-LININETKIOMHGKN	425
D	b	536	REVPYNSNSRCLAGTRKGIIEGEPTCCFEVCEPDGEYSDETASACDKCPDDFMSEN	595
Q	y	426	HOVPYSVSSDCLSEGHOR-VVTGHHCCFECPVCGAGFIMKSELRYKQCPGTEWMAPEG	484
D	b	596	HTSCIAKIEFLSWTEPRG-IATLFLVAFGLTFAFYGVIKFRNPYIKATNRELSTYL	654
Q	y	485	SOTCPRRVYVFLALREHNSWVLLAANTLILLLLLLG-TAGLEFAMHLDIPVRSAGRGCEL	543
D	b	655	LLFSLLCCFSSSLF-FIGEPDQWTCRLQOPAFGISFVLCISCIIVKTNRLVAFE-AKI	711
Q	y	544	MIGSLAAG-SGSLTGFGEFEPTRPACLLRQALFALGFTITFLSCVLVRSFOLIIFFKESTKY	602
D	b	712	PTSFPRKMWGINTLOFLIVFLCTFMQIYCAIWMLTAPSSVRNHLEDELIIFITCHE-GS	770
Q	y	603	PT-FYHAWQNHGAGLFPWISSAAQOLLCLTWLAVVMTPLPAREORPPLHVMLECIETNS	661
D	b	771	L-MALGFLIGYTCILAAICFFFAFSKRLIPENFENAEKFIITSMILFIYWISFIPAVAT	829
Q	y	662	LGFLIAFL-YNGLISIAFACSVYLGKRLPENYNKACVIFESLLFNVSMTIAFFT-ASY	718
D	b	830	Y-GKFSVAEVIYALIAA-SFGLACIFPNKYIILFKPSRNTIE	871
Q	y	719	YDKYLPANMMAGLSSLSGFCGV-FLPCKYVILLCBPDINSTE	761

ID W54844 standard; Protein; 1085 AA.

AC W54844;

DT 01-SEP-1998 (first entry)

Bovine parathyroid calcium receptor 1 protein 5kb fragment.

Calcium ion concentration; parathyroid hormone; homeostasis;

kidney; calcium receptor; detection.

US BOS sp.  
DN ITC57635

PN 053 / 03303-A.  
PD 09 - TTN-10098

ED 03-0001-1995: 484565  
PE 07-TTN-1995:

07-JTN-1995: US-484565

23-AUG-1991: TS-749451

11-FEB-1992: US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-U12117.

PR 08-DEC-1994; US-353784.

PA (BGHM ) BRIGHAM &amp; WOMEN

PA (NPSP-) NPS PHARM INC.

PI Brown EM, Garrett JE, Hebert SC,

WPI; 98-347412/30.

DR N-PSDB; VZ69962.

calcium receptor poly:peptide(s) - useful for drug screening of

anti-body proc  
De Clais E, Fie

es  
cradling; fig 47; 1/4pp; English.  
The book is a collection of 1000 and a half

protein. The tissue

proteins are classified into which class receptor and receptors from human parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulate  $\text{Ca}^{2+}$  homeostasis in blood and extracellular fluid, and kidney function alters through changes in  $\text{Ca}^{2+}$  levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays.

Query Match	20.0%	Score 1170	DB 1	Length 1085
Best Local Similarity	31.9%	Pred. No. 4,34e-94		
Matches	265	Conservative	227	Mismatches 256; Indels 78; Gaps 56;
Db	61	CIRYNEGFRLQAMFAIEEINSSPALLPMNTGYIFDTCNTVSKALAA--TLSEFAO 118		
Qy	3	C-SFENHGYHFFQAMRGVEEINNSTALLNITITGYOLYDVCSSANAVYATLTVLSLPGO 61		
Db	119	NKIDSLINDEFNCNSEHPISTIYAVAGTSGISITAVANLGLFPIPOVSAASSRLLSNK 178		
Qy	62	HHIE-LQ-GDLLHS---PLYANIGDSTIRATTAALLSPFLY-HISYASSSETLSYK 115		
Db	179	NOFKFLLTINDEHQATMAADITETFRMKNVGTIAADDYIGRPGIKFEEAEERDICI 238		
Qy	116	ROYPEFLTINDKYOVETWYLLQKKGWMTSLVSGSDDYGGOLQVADNLVGRICI 175		
Db	239	DFSE-L-ISQXDEEKIQOVVEIONSTAKIYVSSGPDLEPIKE-IYRRNITGRIML 295		
Qy	176	AFKDIIMPSSAQVGBRGMCLMRHLAQAGAIYVVFSS-ROLARFEFSVLTMLTGVMV 234		
Db	236	ASEMAASSLLAMPDEYHHVVGITIGFGLKAGQIDGFEPEFLQKYHPKRSVINGAKPEW 335		
Qy	235	ASEMAA--L-SR---HITGVP-GID-RIGMWGV-A-IQK--R-AVY-GI-KAF-EE 275		
Db	356	TENCLOGAGKPLVPDTFLGHEEGGARLINSPTARPLCTGEBNTSVEETPYMTLH 415		
Qy	276	AYA-R-AD-KEA-P-----RPGIKG-SWSSNLC-RE-C-QAFNAHMPKIKAFS-M 319		
Db	416	RISYNYIYAVYSIAHALODIYITCIPGSGLFTNGSCADIKKYEAOMVYKHLRLHNTFSNMG 475		
Qy	320	SSAYNAVAVYVAHGHQHLGIC-AS-EL-----CS-RGVYVWMOLEQCHKXKFFLHK- 370		



Db	61	CIRKYNCFRMLQAMTRAFIEINSSPALLPMITIGYIFDTCNTVSKALDA--TLSPVAQ	118
Qy	3	C-SFENHCYHLFQAMRGLVEIDINSTLPLITGLGYLDYDCSSANAVYTLRLSPQ	61
Db	119	NKIDSLNDEFCNCSSEHPTIAYVAGTSGISTAVANLGLFYIPQVSAASSRLSNK	178
Qy	62	EHIE-LQ-GDLLHS---PTLVANIGDSTIRACTTALLSPFLV-HISAASETLSVK	115
Db	179	NOFKSELTPTINDEHQATAMADIIEYRKMNVGTIAACDDYGRPGIEKFEAEERDICI	228
Qy	116	KQPSFELRTIENDYQVETWLLLOKFGMTISLVSGSSDDYGQGLGVALNOALVRICICI	175
Db	239	DFSE-L-TSQSDSEKIQQVVEVQNSIAKIVYESSGPDLPIKX-IYRRNTGSIWL	295
Qy	176	AFKIDMPFSAOQDERMOCRLRHIAQAGATVYVFTSS-RQIARVFESVYLTNIGVWV	234
Db	296	ASEAWASSLLIAMEDEYFVVGITGFGLKAGQIDPGREFLOKVHPRKSVNGFAKKEWE	355
Qy	235	ASEAWA--L-SR---HITGVP-GIQ-RIGMWLVG-Y-IQK--R-AVP-GL-KAF-EE	275
Db	336	TFNCHLDGAGAGPLVDITFLGHGEGARLSNSTARPLCTGGENISSETPMDYTHL	415
Qy	276	AYA-R-AD-KEA-P---RPCHKG-SWSSNDLC-RE-C-QAFNAHTMPKIKLAS-M	319
Db	416	RISYVYIAVYSIAHALODITYCIPSGSLFNGSCADIKKEAWQVKLRLHLEFSSNG	475
Qy	320	SSAYNAAYAVYAAVAGHLQLLGC-AS-EL-----CS-RGRNYPMQLEQIHKNVFLHK-	370
Db	476	EQVTFDECGDLAGNYSIINHLSPEQDSIVFKEVGYNYVYAKKGERLFINDEKILMSGFS	535
Qy	371	DTVAFNDRRDLSSNIITIAMWMPNK-WT-FTVIGS-STWSP-VQ-LININETKIQWGNK	425
Db	536	REVPESNRQCLAGTRKGIIEGPTCOFCEVECPDEGYSEPTASACDQCPDDFMEN	595
Qy	426	HOVPSVSSSCIEBHQK-VITGHHRCSECVPCGAGCTFYSKSLIKYQCGCIBEMAPDG	484
Db	596	HITCIAKEIEFLSWTEPPG-IALLFLAVLGITLAFVLYGFIKERNTPIYKATNRELSTYL	654
Qy	485	QOTCPRTVIVFLALREHISWVLLAANTLLILLILG-TAGLFAWHLDPVVRASAGRLCFL	543
Db	655	LLFSLLCGFSSSLF-FIGEPODMTCRLROPAPFGISFLVLCISLVTKNRVLAYE-AKI	711
Qy	544	MCGSLAAG-SSSYLGFEPEPRPACLLRLQALFALGTFITFSLCLVRSFOLITIKSTKV	602
Db	712	PTSEFRKMKGLNLOFLVFLCTFQVQIYCAIMLTAPSSYRNHELEDEIIIFITCHE-GS	770
Qy	603	PT-FYHAWVQHHGAGFLFVMSAQQILITLWLVMPFLPARREVQRPHLYMLECETNS	661
Db	771	L-MAIGLIGTCLLAAICFFPAKRSKRLPENPEAKFTIFSMLIFITWISFLPAVAST	829
Qy	662	LGFILAFI--YNGLLSISAFCSYLGDLDPENYNEACVFTSLEFNVSMAIAPFTT-ASV	718
Db	830	Y-GKFSVAEVIATILAA-SFGLICIFENKRYIILIFKPSRNTIE	871
Qy	719	YDGKYLPAANMMAGISLSSSGFgy-FLPKCYV-LTCDPLNSTE	761
RESULT	4		
ID	W54846	standard; Protein; 1078 AA.	
AC	W54846:		
DT	01-SEP-1998	(first entry)	
DE	Human parathyroid calcium receptor 4.0 protein 4kb fragment.		
KM	Calcium ion concentration, parathyroid hormone, homeostasis;		
OS	Kidney; Calcium receptor; detection.		
CS	Homo sapiens.		
UN	U55763569-A.		
PD	09-JUN-1998.		
PF	07-JUN-1995: 484565.		

PR 07-JUN-1995; US-4834505.  
PR 23-AUG-1991; US-749451.  
11-FEB-1992; US-834044.  
PR 21-AUG-1992; US-934161.  
PR 12-FEB-1993; US-0117127.



PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; WO-012117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPSB-) NPS PHARM INC.  
 PI Brown EM, Garrett JE, Hebert SC;  
 DR WPI: 98-347412/30.  
 DR N-PDB: V26964.  
 PT Calcium receptor poly:peptide(s) - useful for drug screening or  
 PT antibody production  
 PS Claim 7; Fig 49; 174pp; English.  
 CC The tissue from which the human parathyroid calcium receptor and  
 CC receptors from bovine parathyroid and rat kidney are derived, respond to  
 CC changes, and control changes, in calcium ion concentration,  
 CC e.g. parathyroid hormone regulates Ca<sup>2+</sup> homeostasis in blood and  
 CC extracellular fluid, and kidney function alters through changes in Ca<sup>2+</sup>  
 CC levels in juxtaglomerular and proximal tubule cells in the kidney. The  
 CC purified receptors (produced recombinantly) can be used to screen for  
 CC compounds that modulate calcium receptor activity, especially those that  
 CC can be used to treat diseases associated with the receptors in these  
 CC tissues. They can also be used to raise antibodies for use in detection  
 CC assays.  
 SQ Sequence 1078 AA;

Query Match 19.9%; Score 1160; DB 1; Length 1078;  
 Best Local Similarity 31.9%; Pred. No. 3,73e-93;

Matches 263; Conservative 232; Mismatches 250; Indels 80; Gaps 57;

DB 60 CTRNRCGRWLOAMFALBEINSSPALPNTLGRIPDTCTVSKALEA--TISFVAQ 117  
 QY 3 C-SFNHGHLFQAMRLGVEINNSTALLPNTILGQLYDVCDSANVATLVLSLPGQ 61  
 DB 118 NKIDSLNIDFQCSCSHIPSTIIVAGTSGSTAVANILGLTYIOYVASSRLLSNK 177  
 QY 62 HHE-LQ-GDLHYS---FTVLAVIGPDSNTRATTAALISPLYV-HISPAASETLVSK 115  
 DB 178 NOFKSELTIPNDEHQAAMADIEFRNMGVSTIADDYGRPGIEKFEAEEDICT 237  
 QY 116 RQPSFLRTIPNDKYQVEMVLLQKFGMTWISLVGSSDYGGLGVALENQALVAGICT 175  
 DB 238 DSELSISQSD-E-E-IQHVVEVIONSTAKVIVFSSGDEPLEIKE-IVRNITGKIW 293  
 QY 176 AFDIDMP-FSAQGDERMOCIMRHLAQAGATVYVFS--RQLARVEFESVTLNLGKW 233  
 DB 294 LASEMASSSLAMPYFHVVGSTIGFALKAGIIPFRERLKVHRKSHNFAEFWE 353  
 QY 234 VASEAQA--L-S--R--HITGP-6IQ-RIGVLCV-A-IQR--R-AVP-GL-KAF-E 274  
 DB 354 EFTNCHLQAGAKGPLVDFTFLNGHESGDRFSSSTAFLRPLCTGDNISSEVETPIDYTH 413  
 QY 275 EAVA-R-AJKE-APRCH--KSGWSSNQLCREQAF--M-A--HTMPLKA----FS- 318  
 DB 414 LRISVAVYVIAIAHALDIYCLDPRGLFTNGSCADIKKVAQVYLKHLRLNFTNNK 473  
 QY 319 MSSAVNAVAVAVAHGLHQLLCC-AS-EL-----DS-RGRVYPMQLDEQIHRYVFLHK 370  
 DB 474 GEGVTEDEGDLVGNYSIINMHLSPEDGSTVEKVEGYVYNAKGRRLTNEKILMSG 533  
 QY 371 -DIVAANDRNDPLSSITNITAMDNNGK-WT-FTVLDS-STWSP--VO-LNINERKIOWHG 424  
 DB 534 SREVPSNCRDLACTRKGIIIGEPTCECEYCEPDGSESDTDSACNCKDDPMUNE 593  
 QY 425 NQGVPSVSSSCLBEHQH-VYGFHHCECEYCPGAGITFLNSELXKROPCTEMAPE 483  
 DB 594 NHTSCIATKIEFLSWTEPRG-IALLFAVLGIFLFAVLGVTFKFRNTPIVAKTNBELSY 652  
 QY 484 GSGTCPRVVFALREHLSWVLLANTLILLILG-TAGLFAMHLDTPVRSAGRCLG 542  
 DB 653 LLLFSLICESSSLF-FIGRPDMTCRLQRPAGISFVLCISCIYKTNVLLVFE--AK 709  
 QY 543 LMGSLAAG-SGLVGFEGEPTRPACLLRLQALFALGFTIFLSCLTVRSFOLLIIIFKSTK 601

DB 710 IPTSFRRKWMGNILOFLVFLCTFMQIVICVIMLYTAPSSYRNOLEDEIFITCHE-G 768  
 QY 602 VPT-FYHANVQNHAGLFLFMISAAQLLCLTWLVWTPDLPAREQRPFLHMLCTEN 660  
 DB 769 SL-MALGFLIGYTCILAAICFFAFKSRRLPENNEAKETFSMTLFIWISFPAYAS 827  
 QY 661 SGFLIAFL--YNGLSTISAFKCSYLGKLPENYNAKVFSLFLFVSWIAFFT--AS 717  
 DB 828 TY-GKVSAYEVIALIAA-SPLLACIFENKRYIILFKSRNTIE 870  
 QY 718 VIDGKTLPANMMAGLSLSSGFGI-FUPKCYVILCRDLNSTE 761

# RESULT

ID W89565 standard; Protein; 1078 AA.

AC W89565; 19-MAR-1999 (first entry)

DE Human parathyroid calcium receptor phupcar 4.0.

KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;

KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;

KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;

KW neonatal distress; neurodegenerative disease; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; dementia; muscle tension;

KW depression; anxiety.

OS Homo sapiens.

PN US585684-A.

PD 12-JAN-1999.

PF 07-JUN-1995; 480751.

PR 07-JUN-1995; US-480751.

PR 23-AUG-1991; US-749451.

PR 11-FEB-1992; US-834044.

PR 21-AUG-1992; US-934161.

PR 12-FEB-1993; US-017127.

PR 23-FEB-1993; US-009389.

PR 22-OCT-1993; US-141248.

PR 19-AUG-1994; US-292827.

PR 21-OCT-1994; WO-012117.

PR 08-DEC-1994; US-353784.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA (NPSB-) NPS PHARM INC.

PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,

PI Hebert SC, Nemeth EF, Van Wagenen BC;

DR WPI: 99-119871/10.

DR N-PDB: V82485.

PT Screening for calcium receptor-active compounds - by recombinant

PT expression of nucleic acid encoding calcium receptor and determining

PT the effect of compounds on calcium receptor activity

PS Claim 1; Fig 49; 176pp; English.

CC A method has been developed of screening for a compound able to affect

CC one or more activities of a calcium receptor (CR) comprises: (A)

CC contacting a recombinant cell with a test compound, where the

CC recombinant cell comprises a recombinant nucleic acid expressing the CR,

CC provided that the cell does not have functional CR expression from

CC endogenous nucleic acid; (B) determining the ability of the test

CC compound to affect one or more activities of the calcium receptor; and

CC (C) comparing the ability with the ability of the test compound to

CC affect the one or more CR activities in a cell not comprising the

CC recombinant nucleic acid. The present sequence represents human

CC parathyroid CR, designated a phupcar 4.0. The nucleic acid sequence of

CC phupcar 4.0 can be used as part of the recombinant nucleic acid in the

CC method described above. The compounds identified can be used to treat

CC diseases or disorders characterized by abnormal calcium homeostasis, e.g.

CC hyperparathyroidism, osteoporosis and other bone and mineral-related

CC disorders. They can also be used for the treatment of diseases and

CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures,

CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in

CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative

CC diseases such as Alzheimer's disease, Huntington's disease and

CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.

Query Match 19.9%; Score 1160; DB 1; Length 1078;







Qy	319	MSSAVNAVRAYVAAGHGLHQLGCG-AS-EL-----CS-RGVVYTWQGLDTHKVFLLHK	370
Dd	474	GEQYTFDECGDLVGNYSITINNHLSPEDGSIYFKVGYINYVAKRGERLFINEEKILMSG	533
Qy	371	-DTVAFNDRPDLSSYNIADMDWNGPK-WT-FVLVGS-STWSP-VQ-LNINETKIQWHGK	424
Dd	534	SREVPFNSCSDDCLAGTNRKGIIEBEPNCCFCFCVCGPDGEYSDEEDNABAKNCKPDPDFMSNE	593
Qy	425	HNQVPRKSYCSDSCDEBGRH-VVTGHHCCFCBCVCGAGTFPLNKSLEYRCOPCGTEENAPE	483
Dd	594	NHTSCIAKEIEFLSWTEPEFG-IATLFEAVLGIPTFAVLGVFIFFRNTPIYKATNRELST	652
Qy	484	GSQCFFPTVYFALREHSTWVLAAANTLLLLLLLG-TAGLFAHNDLPVRSAGRLCF	542
Dd	653	LLLSFLCCFSSSLF-FTGEPODWTCLROPASGISFVLCISCLIVKTRNVLVEE--AK	709
Qy	543	LMGLSLAAG-SGSLVGEFGFPTPRACLLRQALFALGFIIEFVLSCLTVRSFQIIIFKFKSTK	601
Dd	710	IPTSHRKMWGLNQLFLVFLCTFMQIYICVIMLYTAPRPSSTRNQLDEDEIFITCHE-G	768
Qy	602	VPT-PYAHMVONHGAGLELVMTSSAAQLICLTLMVLVWTPLEARYQRPPLHVMLECEYN	660
Dd	769	SL-MALGFLIYCYTCLLAAICFFFAFKSRKLEPENENEAKEFTFSMLIFFIWISEPIYAS	827
Qy	661	SLGFLIATL--YNGLLSTISARACSYLKGDLPENNENAKCYFTSLIFNFVSMIAFTT-AS	717
Dd	828	TY-GREVASAEVIAIILAA-SFGLLACIFENKIYIILKPSRNTIE	870
Qy	718	YVDGKYLPRANMMAGLSLSSGFGGY-FLPKCYVILCRPDLNSTE	761
RESULT	7		
ID	W38274	standard; Protein; 1078 AA.	
AC	W38274;		
DE	08-MAY-1998	(first entry)	
KW	Human parathyroid cell calcium receptor 4.0; Hupcar 4.0;		
KN	calcium homeostasis; hyperparathyroidism; osteoporosis.		
OS	Homo sapiens.		
PN	US5688938-A.		
PD	18-JUN-1997.		
PF	07-JUN-1995:	485588.	
PR	07-JUN-1995:	US-485588.	
PR	23-AUG-1991:	US-749451.	
PR	11-FEB-1992:	US-834044.	
PR	21-AUG-1992:	US-934161.	
PR	12-FEB-1993:	US-017127.	
PR	23-FEB-1993:	US-009389.	
PR	22-OCT-1993:	US-141248.	
PR	19-AUG-1994:	US-292827.	
PR	21-OCT-1994:	WO-012117.	
PR	08-DEC-1994:	US-353784.	
PA	(BGMH ) BRIGHAM & WOMENS HOSPITAL.		
PA	(BNSP-) NPS PHARM INC.		
PI	Brown EM, Fuller FH, Garrett JE, Hebert SC;		
DR	WPI: 98-008040/01.		
DR	N-PSDB: T95859.		
PT	DNA encoding calcium receptor polypeptide(s) - useful for		
PT	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis		
PS	Claim 20: Columns 125-134; 174pp; English.		
CC	The present sequence is human parathyroid cell calcium		
CC	receptor 4.0 (hupcar 4.0).		
CC	The specification includes details of molecules that can modulate		
CC	one or more inorganic ion receptor activities, and antibodies and		
CC	antibody fragments targetted to inorganic ion receptor proteins. The		
CC	proteins, nucleic acids and antibodies may be used to treat		
CC	disorders by modulating one or more inorganic ion receptor		
CC	activities, preferably disorders of calcium homeostasis, e.g.		
CC	hyperparathyroidism and osteoporosis.		
CC	Sequence 1078 AA;		
CC	50		
Query Match	19.9%;	Score 1160;	DB 1; Length 1078;

[illegible]







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QY 275 EAYV-R-AD-KEA-P-----RPHKGS-W---CSSN-Q-LCRECOAFMAHMPKLFKAFS 318
DB 413 HLRISYNYVLAIVYSIAHALODIYTCLPGRGFTNGSCADIKKEVAMOVYKHLRHLFTNN 472
QY 319 -MSSAVNAYRAYVAVAHGJHLLGC-AS-EL-----CS-RGRVYPMQJLEQIHVHFLH 369
DB 473 MGEQVTFDECGDLVGNYSIIMNHLSPEDGSIYKEVGYNYAKGERLFINDEKILMSG 532
QY 370 K-DIVAENDNDPLSYNIIMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQMHG 423
DB 533 FSRVFPSCNRDQACGRKRIIGSEPTCCCEVCECPDGEISGETDASADCKCPDDFWSN 592
QY 424 KNHVPKSVCSDDLEGHQR-VVTFGHHCCFECVPCGAGTFLNKSELYRCQPCGTCEWAP 482
DB 593 ENHSTIAKEIEFLAMTEPFG-IALTFLAVLGIPTLAVLGIKFRNTPIYKATNELS 651
QY 483 EGSQTCFPTVFLALREHITSVLLAANTLLLLLG-TAGLFAMHLDTPVRSAGGRIC 541
DB 652 YLLFSLCCFSSSLF-FIGEPDWTCLRQAPAGISFVLICISILVKNRVLLVFE--A 708
QY 542 FLMLGSLAAG-SSSLYGFGEPTRPACILRQALFALGFTIFLSCLTVRSFQJLIIFKST 600
DB 709 KIPSFIRKMGWGLQFLVFLCFTFMQILICITWLTAPSSYRNHLEDEIITITCHEG 768
QY 601 KVPF-FYHAMVQNHGAGLFVMISSAQLICLTWLVWTPLPAREYORFPHLVMECTET 659
DB 769 SLMLAGSLIGTCLLAACEFFAFKSRKLPENNEAKFIPEFSLIFETWISFIPAYAT 828
QY 660 NSLGILALFNLGLSISAFACSTLGDLPENNEACVITSLFNVSWIAFETT-ASV 718
DB 829 Y-GKFSVAEYIALIA-SEGLACIFENKVIYILFPRNTIEVRSSTAHA 880
QY 719 YDKYFLPAANMAGLSSISGFGYV-FLPKCYVILCRDLNSTEHPQASIDYV 771

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RESULT 10
ID W89566 standard: Protein: 1079 AA.
AC W89566;
DE 19-MAR-1999 (first entry)
DE Rat parathyroid calcium receptor prakcar 3A.
KW Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;
KW calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;
KW spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;
KW neonatal distress; neurodegenerative disease; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; dementia; muscle tension;
KW depression; anxiety.
OS Rattus sp.
PN US5858684-A.
PD 12-JAN-1999.
PE 07-JUN-1995; 480751.
PR 07-JUN-1995; US-480751.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-011127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGM) BRIGHAM & WOMENS HOSPITAL.
PA (NPS) NPS PHARM INC.
PI Balandrin ME, Brown EM, Del Mar EG, Garrett JE,
PI Hebert SC, Nemeth EF, Van Wagenen BC;
DR WPI: 99-119871/10.
DR N-PSDB: W82486.
PT Screening for calcium receptor-active compounds - by recombinant
PT expression of nucleic acid encoding calcium receptor and determining
PT the effect of compounds on calcium receptor activity
PS Claim 1: Fig 50: 176pp; English.
CC A method has been developed of screening for a compound able to affect
CC one or more activities of a calcium receptor (CR) comprises: (A)

```

contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the CR, provided that the cell does not have functional CR expression from endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence represents rat parathyroid CR, designated a prakcar 3A. The nucleic acid sequence of prakcar 3A can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety.

Sequence 1079 AA;

Query Match 19.8%; Score 1158; DS 1; Length 1079;

Best Local Similarity 31.4%; P-adj. No. 5.73e-93;

Matches 262; Conservative 233; Mismatches 261; Indels 78; Gaps 55;

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DB 60 CINYRGRFMLOAMTFAIEEINSSPSLPMNTLGRIFDTONVSKALEA--TISFVAO 117
QY 3 C-SFNEGHVFLPMALGVEINSSALLPNTLIGVQLDVCSDANVATILRVSLPQ 61
DB 118 NKIDSLNDFEPCSHISTAVNGATGSGVSTAVANLGLFYDQVYASSRLSK 177
QY 62 HHIE-LQ-GDLHYS--FTVLAVIGPDSITNRAATLALISFLV-HISYASSELISYK 115
DB 178 NOKSFRLTPNDENHATAMADIEFEYFEMWVGTIAADYDGPGRKEKEBEEDICI 237
QY 116 RQPSFLRITPNDKYVEVWVLLQKFTWVLSGSSDYGQVLAENQALVRGIC 175
DB 238 DFSELISQYSD--EEDIQ-VVEVIONSTAKYIVFSSGDDLEPIKE-IVRNITGRIM 293
QY 176 AFDQIMP-ESAQYDGBRMQCLMRHLAQAATVYVSS-RQLARVEFEEVJLNLGKW 233
DB 294 LASEANASSLIMPTFYHVGCTIGFGLKAGIOPGFREFLOKHPKRVHNGFAKEP 353
QY 234 VASEANA--L-SR---HITGP-GIQ-RIMVGLV-A-IOK--R-AVP-GL-KAF-E 274
DB 354 EFTNCHLGAKGKPLVDVFRSHGEGNRLNSSFAPRPLCTGDNINSVETP-YMDYE 412
QY 275 EAYV-R-AD-KEA-P-----RPHKGS-W---CSSN-Q-LCRECOAFMAHMPKLFKAFS 318
DB 413 HLRISYNYVLAIVYSIAHALODIYTCLPGRGFTNGSCADIKKEVAMOVYKHLRHLFTNN 472
QY 319 -MSSAVNAYRAYVAVAHGJHLLGC-AS-EL-----CS-RGRVYPMQJLEQIHVHFLH 369
DB 473 MGEQVTFDECGDLVGNYSIIMNHLSPEDGSIYKEVGYNYAKGERLFINDEKILMSG 532
QY 370 K-DIVAENDNDPLSYNIIMDMNGPK-WT-FTVLGS-STWSP-VQ-LNINETKIQMHG 423
DB 533 FSRVFPSCNRDQACGRKRIIGSEPTCCCEVCECPDGEISGETDASADCKCPDDFWSN 592
QY 424 KNHVPKSVCSDDLEGHQR-VVTFGHHCCFECVPCGAGTFLNKSELYRCQPCGTCEWAP 482
DB 593 ENHSTIAKEIEFLAMTEPFG-IALTFLAVLGIPTLAVLGIKFRNTPIYKATNELS 651
QY 483 EGSQTCFPTVFLALREHITSVLLAANTLLLLLG-TAGLFAMHLDTPVRSAGGRIC 541
DB 652 YLLFSLCCFSSSLF-FIGEPDWTCLRQAPAGISFVLICISILVKNRVLLVFE--A 708
QY 542 FLMLGSLAAG-SSSLYGFGEPTRPACILRQALFALGFTIFLSCLTVRSFQJLIIFKST 600
DB 709 KIPSFIRKMGWGLQFLVFLCFTFMQILICITWLTAPSSYRNHLEDEIITITCHEG 768
QY 601 KVPF-FYHAMVQNHGAGLFVMISSAQLICLTWLVWTPLPAREYORFPHLVMECTET 659

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[illegible]

RESULT	11
ID	W38275 standard; Protein; 1079 AA

DT 08-MAY-1998 (first entry)  
 DE Rat kidney cell calcium receptor 3A (RakCar 3A) .  
 KW Rat kidney cell calcium receptor 3A; RakCar 3A;  
 KM calcium homeostasis; hyperparathyroidism; osteoporosis.  
 OS *Rattus* sp.  
 PN US5688938-A .  
 PD 18-NOV-1997 .  
 PF 07-JUN-1995; 485588.  
 PR 07-JUN-1995; US-485588.  
 PR 23-AUG-1991; US-749451.  
 PR 11-FEB-1992; US-834044.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; WO-012117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGHM ) BRIGHAM & WOMEN'S HOSPITAL.  
 PA (NPSP-) NPS PHARM INC.  
 PI Brown EM, Fuller FH, Garrett JE, Hebert SC.  
 DR WPI: 98-008040/01.  
 DR N-PSDS: T95860.  
 PT DNA encoding calcium receptor polypeptide(s) - useful for  
 PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis  
 PS Claim 20: Columns 133-142; 174pp; English.  
 CC The present sequence is rat kidney cell calcium  
 CC receptor 3A (RakCar 3A).  
 CC The specification includes details of molecules that can modulate  
 CC one or more inorganic ion receptor activities, and antibodies and  
 CC antibody fragments targeted to inorganic ion receptor proteins. The  
 CC proteins, nucleic acids and antibodies may be used to treat  
 CC disorders by modulating one or more inorganic ion receptor  
 CC activities, preferably disorders of calcium homeostasis, e.g.  
 CC hyperparathyroidism and osteoporosis.  
 CC Sequence 1079 AA:

Query Match	19.8%;	Score 1158;	DB 1;	Length 1079;
Best Local Similarity	31.4%;	Pred. NO. 5.73e-93;		
Matches	262;	Conservative	233;	Mismatches 261; Indels 78; Gaps 55

Db	60	CIRNFGFGFRLQALMAIEEINSPPLLPMITGYLEPDCNVSXALEE--GLTSVAQ	117
Qy	3	C-SNEHGCHLFOAMRIGVEEINNSTALLPRITLGYOLDYDCSDSANAVYATLRSLPQ	61
Db	118	NKIDSLNDEFCNCSSEHPTSTIANVGATGSGVSTAVANLGLFTIPDYSTASSRLLSNK	177
Qy	62	HHIE-IG-GDLHNS---PTVLAVIGDSTIRATRTALLSPFLV-HISYAASETLSVK	115
Db	178	NOYKSLFTIPNDEHQATAMADIEYFRMMVVGITIAADDGVRGICKEFREAEERDICI	237
Qy	116	ROYSEFLRTIPNDKXQYETWMLLQKRGWIMSLVSGSSDDYGGUAGVALENQALVRICL	175
Db	238	DFSELISQYSDE--EETIQ--VVEYIONSTAKVIVFSSGPDLELIKE-IVRNITGRIM	293
Qy	176	AFKXIDIM-FSQYQVDEHMOCLMRHLAOGAIVVVFSS--ROLARVFESVLTLTLTXYW	233
Db	294	LASEPMASSSLIAMPYFHVYVGGIIGGLKAGQICRGREFLQIHNPRKSYHNGAKFEWE	353
Qy	234	VASEPAMA---L-SR---HITGV-P-GIO-RGIMVLGV-A-IQK--R-APV-GI-KAF-E	274

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Db 354 ETPNHOEGAKGGLPVDTPFRHSBEGGNLNSITAFRELCIGDEINSVEP-YMDE 412
Qy 275 EAYIA-R-AD--KEA-P-----RPHCKPS-W-----CSSY-Q-LCEBCEQAFMHTPKLKAFS 318
Db 413 HLRISTVNYLAVYSIAHALCDIYTCLEGRGLFENGSCADIKYEAOMOVNLHLHLINTFN 472
Qy 319 -MSSAYNNYRAVYVAAGHLOLLCG-AS-EL-----CS-RGRVYPMOLLQITKAVHLLH 369
Db 473 MGEQVTEDECDDLVGNSIIMHLLSPEDGSIVREKVGVYVYAKKGRIELEINEEKILMSG 532
Qy 370 K-DIVAEFNDNDPLSYNTIIAMDNNGK-R-WT-FIVLGS-STWSP-VQ-LVINETKIQWNG 423
Db 533 FSREVPSSNGSRDCOAGTRKGIIEGPTCCFECVECPDGYECSSETDASACDKPDPFWSN 592
Qy 424 KNHQVPKVCSDDCLEGHOR-VVTFGHHCCEGVCPCAGTFILNKSLEYRCQPGTEEMAP 482
Db 593 ENHNSCIAKELEELFAMWEPBPS-LALLFVAVLGIFLTFVGLVFLKPRNTPIYATNRELS 651
Qy 483 EGSOCTCPRIYVFALEBHTSWVLPLANTLLELLLELG-TAGLEAMWHLDTVPVMSAGRLC 541
Db 652 YLLLFSLIACCSSSLP-FIGEPOMTCRLROPAGFISFVCIICILYKTRIVLVEE--A 708
Qy 542 FLMLGSLAAG-SGSLYGFPGGPTRPALLQALFALCCTFTFLSCLYKRSQLLIIRKFT 600
Db 709 KIPTSFRHKMWGLNLOFLVFLCTPFMOIJCIIIMLYTAPSSYRNHLEDELIIFITCHEG 768
Qy 601 KVPIT-FYHAWQNHGAGLEFVWISSAQLICTFPLVYVTEPLPAREVQRPHLWMLBCTET 659
Db 769 SLMLAGSLIGTCLLAATCEFFAKRSKKLDEPNEAKFIFPSMLIFPIVYISLIPAYST 828
Qy 660 NSLGFILAFILNGSLISAPACSYLGDEDPENYNEACVTFSLLEFVNSIAFTTT-ASY 718
Db 829 Y-KGFVSVEVEVIALIA-SFGLACIFENKVIILIFKPSNTITEEVNSYAAHA 880
Qy 719 YDGRITPLPAAWMAGLSSISSGFGR-F-LPCYVILLCFPLDNLSTEHQOASIQDYTT 771

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## RESULT 12

ID	standard; Protein; 1026 AA
W32059	
W32060	

AC	W32059;
DT	27-MAR-1998 (first entry)

Dogfish shark kidney calcium receptor related protein (SKCAR-RP).

KM polycation-sensing receptor; aquaculture; fish farming;  
KM Calcium receptor related protein; CaR-RP; cog:ish shark; SKCaR-RP;

salinity tolerance.

OS	Location/Qualifiers
EH	Key
OS	<i>Squalus acanthias</i> .

FT	Region	351.39
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highly divergent from mammalian PVCR"

Region	870
FT	

/note= "region in C-terminal domain that is highly divergent from mammalian PVCR"

PN W09735977-A1.

PD 02-OCT-1997.  
PE 27-MAR-1997: IT05031.

PR 27-MAR-1996; US-622738.

PA (BCHM) BRIGHAM & WOMENS HOSPITAL.  
PI Brown E. Harris HW. Hebert S:

DR WPT; 97-489640/45.

DR N-PSDB; T89290.  
PT New isolated Aquatic polycation-sensing receptor - used to

develop products for increasing or decreasing the salinity tolerance

PT of fish for use in aquaculture  
claim 9. Fig 5A-B: 5700: English  
PS

CC This protein comprises dogfish shark kidney calcium receptor

CC related protein (SKCAR-RP), an aquatic polyvalent cation-sensing  
CC receptor (PVCPR). Its amino acid sequence was deduced from a kidney

CC cDNA clone (see T89290). It shows 74% homology to rat kidney

PCVR and bovine parathyroid PVCR and possesses general features that are homologous to PVCR proteins including a large

extracellular domain, 7 transmembrane domains and a cytoplasmic

CC C-terminal domain. Also claimed are: an isolated pVCR present in



CC the plasma membranes of aquatic species, especially on the apical  
 CC membrane of epithelial cells of elasmobranch fish, particularly  
 CC from cells found in the collecting duct or late distal tubule in  
 CC the kidney, intestine, gill, rectal gland, gonad or brain: an  
 CC antibody that specifically binds to a pVCR, and a method of  
 CC screening for aquatic pVCR agonists and antagonists. Modulation of  
 CC the expression of the aquatic pVCR activates or inhibits aquatic  
 CC pVCR mediated ion transport and endocrine changes that permit fish  
 CC to adapt to fresh or salt water. The method facilitates the  
 CC aquaculture of marine fish and can provide for the development of  
 CC marine fish that are easily adaptable to fresh water aquaculture.  
 SQ Sequence 1026 AA;

Query Match 18.9%; Score 1101; DB 1; Length 1026;  
 Best Local Similarity 31.2%; Pred. No. 1,20e-87;  
 Matches 256; Conservative 231; Mismatches 253; Indels 81; Gaps 54;

DB 64 CIRYNRGRFWLQAMFALEINNSMTLPNLTIGRIPTQNTYSKALBA--TLSEVAQ 121  
 QY 3 C-SFNEHGYHLFOAMRLGVEEINNSTALLPNTLGQYLDVCSDSANVATLRLVSLPQ 61  
 DB 122 NKIDSLNDFEFCNSDHPSTIANVGATGSGISTAVANLGLTFIPQVSAASSRLLSNK 161  
 QY 62 HHE-LQ-GDLHYS--PTVLAVIGPDSNRATTAALSPFLV-HISYAASETLSVK 115  
 DB 182 NEKAFLEITPNDQOATAAEIIEHFMVMWVGTIADDDYGRPGDKFEFAVRKDCI 241  
 QY 116 ROYPSFLRTIPNDKYOVETVLLQKRGWMTISLVSSDDYDGLQVALLNQLVKGIC 175  
 DB 242 DSEF-M-ISQYVQKOLEFIADYIQNSANVIVFSSGPDLEPLI-QEIVRNITRIML 298  
 QY 176 AFEDIPFSQVQDERQCMRLHQAQATVYVFS--ROLARVFEFSVLTMLTGKVV 234  
 DB 299 ASRAMASSSLIAPEFHVVGITIGFALRAGRIGEFKFIKEVHPAPRMGSLRSSGR 358  
 QY 235 ASRAMA--L-SR---HITGVP-GIQ-RIGWLVGA-IOK--RAV-P--GL-KA--- 272  
 DB 359 LQDLHREDLTQKNSKVPSHGPAQDGSKAGNSRRTALRHPTGENTISVETPLYD 418  
 QY 273 FEFAVARAD---KEA--P-R-PC-H-KSGMCS-SNQ--LCRDE--QAFAMHMPKAKF 317  
 DB 419 THLRISTNVYVAYSTAHADIDHSCKPGTGIFANGSCADIKYEAQOVINHLHLEFTN 478  
 QY 318 S-MSSAYNAAYAVAHAGHQLGCG--ASEL-----CS-RGRVYPMQLLEQIHKVFLL 368  
 DB 479 SMGEQVDFDQGLGKGYITINMQLSADESVLFHEVGNNAVAKPSDRINNEKKILMS 538  
 QY 369 HK-DYAFANDNRPLSYNIIAMDMPK-WT-FYVLGS-STWS-PVO-LINETKIQWH 422  
 DB 539 GFSSVVPFNSCDVCPGTRKGIIEGPTCCFCMACABGEFSDENDASACTCPDNFWS 598  
 QY 423 GKHWQPKSVCSGDCLEGHQR-VYTFHNCFCFECVPCGATFLNKSLSLYGCGGTSEMA 481  
 DB 599 NEHHTSCIAKEIYLSWTEFG--IALTIPAVLGLITSEVLGVFIFKRNTPYKAINREL 657  
 QY 482 PEGSQTCFPTVYVLAIRETSMVLLAANTLLILLIG--TAGIFAMHLDTPVRSAGRL 540  
 DB 658 SYLLSILCOFSSSLI-FIGEPRDMTCRLKOPAFGSFVLCSILCIKYNRVLAVE-- 714  
 QY 541 CFMLDSLSLAAG-SGLTFEGEPTPRACLRQALFAGTIFLISCLTVRSFOLILIFKS 599  
 DB 715 AKIPTSLHRKWLNLQFLVLCIIVQITCIIMLTAPSSRYNHELDEVFITICDE 774  
 QY 600 TKVPT-FYHAWQNHGAGLFVMSAQLILCLTWLVWMPFLPAREQRPHVMECTE 658  
 DB 775 -GSL-MALGFLITCLLAICFPFAKSKRLPENNEAKFITPSMIFITWISPIPAY 832  
 QY 659 TNSLIGLIFL--YNGILSISAFACSYLGRDLPENNEACVTSFLFNVSIAFEFTT- 715  
 DB 833 VSTY-GKFSYAVEVIAILAS-SFGLGCIIFENCCYILFKP 871  
 QY 716 ASYVDGKYLPAANMAGLSLSSGFGY-FLPCYVILCRP 755

RESULT 13  
 ID W38273 standard; Protein: 1088 AA.

AC W38273;  
 DT 08-MAY-1998 (first entry)  
 DE Human parathyroid cell calcium receptor 5.2 (HupCar 5.2).  
 KW Human parathyroid cell calcium receptor 5.2; HupCar 5.2;  
 KW calcium homeostasis; hyperparathyroidism; osteoporosis.  
 OS Homo sapiens.  
 PN US5688938-A.  
 PD 18-NOV-1997.  
 PE 07-JUN-1995; 485588.  
 PR 23-AUG-1991; US-749451.  
 PR 11-FEB-1992; US-834044.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; WO-012117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGM ) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPSF-) NPS PHARM INC.  
 PI Brown EM, Fuller FH, Garrett JE, Hebert SC;  
 DR WPI; 98-008040/01.  
 DR N-PSDB; T95858.  
 PT DNA encoding calcium receptor polypeptide(s) - useful for  
 PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis  
 PS Claim 20; Columns 117-126; 174pp; English.  
 CS The present sequence is human parathyroid cell calcium  
 CC receptor 5.2 (HupCar 5.2).  
 CC The specification includes details of molecules that can modulate  
 CC one or more inorganic ion receptor activities, and antibodies and  
 CC antibody fragments targeted to inorganic ion receptor proteins. The  
 CC proteins, nucleic acids and antibodies may be used to treat  
 CC disorders by modulating one or more inorganic ion receptor  
 CC activities, preferably disorders of calcium homeostasis, e.g.  
 CC hyperparathyroidism and osteoporosis.  
 SQ Sequence 1088 AA;

Query Match 18.2%; Score 1064; DB 1; Length 1088;  
 Best Local Similarity 31.6%; Pred. No. 3.37e-84;  
 Matches 264; Conservative 231; Mismatches 250; Indels 90; Gaps 59;

DB 60 CIRYNRGRFWLQAMFALEINNSPALPNTLIGRIPTQNTYSKALBA--TLSEVAQ 117  
 QY 3 C-SFNEHGYHLFOAMRLGVEEINNSTALLPNTLGQYLDVCSDSANVATLRLVSLPQ 61  
 DB 118 NKIDSLNDFEFCNSDHPSTIANVGATGSGYSTAVANLGLTFIPQVSAASSRLLSNK 177  
 QY 62 HHE-LQ-GDLHYS--PTVLAVIGPDSNRATTAALSPFLV-HISYAASETLSVK 115  
 DB 178 NQKSFLEITPNDHQATMAADIEEFVFNWVGTIADDDYGRPGIEKFEFAERDICI 237  
 QY 116 ROYPSFLRTIPNDKYOVETVLLQKRGWMTISLVSSDDYDGLQVALLNQLVKGIC 175  
 DB 238 DPELSLSQSDS--EE-IGHVEVIONSTAKYIVFSSPDLEPLIKE-IVRNITGKTW 293  
 QY 176 AFEDIMP-FSAQGDGRMQLMRHLQAQATVYVFS--ROLARVFEFSVLTMLTGKWW 233  
 DB 294 LASEAASSSLTAMPQYFVAVGTIGFALKAGQIDPREFLKKVHRKRVHNGFAKEFE 353  
 QY 234 VASEAMA--L-S--R--HITGVP-GIQ-RIGWLVGA-IOK--RAV-GL-KAF-E 274  
 DB 354 EFNCHLQGGANGPLVDVFLRGHESGDRFNSSTAFRPLCTGDNISVETPYIDYTH 413  
 QY 275 EAVA-R-ADKE-APRCH--KSGMCSNQLCRECAF--M-A--HTMPKLA---FS- 318  
 DB 414 LRISYVYLAIVYSIAHADIDITCLPBGRLFTNGSCADIKYEAQOVINHLHLEFTN 473  
 QY 319 MSSAYNAAYAVAHAGHQLGCG--AS-EL-----CS-RGRVYPMQLLEQIHKVFLLK 370



[illegible]

ID	RESULT	14
WS4845	standard; Protein; 1088 AA.	
AC	WS4845.	
DT	01-SEP-1998 (first entry)	
DE	Human parathyroid calcium receptor 5.2 protein 5kb fragment.	
KW	Calcium ion concentration; parathyroid hormone; homeostasis; kidney;	
KW	calcium receptor; detection.	
OS	Homo sapiens.	
PN	US5763569-A.	
PD	09-JUN-1998	
PF	07-JUN-1995	484565
PR	23-AUG-1995	US-484565.
PR	11-FEB-1992	US-749451.
PR	21-AUG-1992	US-834044.
PR	12-FEB-1993	US-017127.
PR	23-FEB-1993	US-009389.
PR	22-OCT-1993	US-141248.
PR	19-AUG-1994	US-292827.
PR	21-OCT-1994	WO-012117.
PR	08-DEC-1994	US-353784.
PA	(BGHM ) BRIGHAM & WOMENS HOSPITAL.	
PA	(NPSP-) NPS PHARM INC.	
PI	Brown EM, Garrett JE, Hebert SC;	
DR	WPI: 98-347412/30.	
DR	N-PSDB: V26963	
PT	Calcium receptor poly.peptide(s) - useful for drug screening or	
PT	antibody production	
PS	Claim 6; Fig 48; 14pp; English.	
CC	The tissue from which the human parathyroid calcium receptor and	
CC	receptors from bovine parathyroid and rat kidney are derived, respond to	
CC	changes, and control changes, in calcium ion concentration,	
CC	e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and	
CC	extracellular fluid, and kidney function alters through changes in Ca2+	
CC	levels in juxta glomerular and proximal tubule cells in the kidney. The	
CC	purified receptors (produced, recombinantly) can be used to screen for	
CC	compounds that modulate calcium receptor activity, especially those that	
CC	can be used to treat diseases associated with the receptors in these	
CC	tissues. They can also be used to raise antibodies for use in detection	
CC	assays.	
SO	Sequence	1088 AA;
Query Match	18.2%;	Score 1063; DB 1; Length 1088;
Best Local Similarity	31.6%;	Pred. No. 4, 17e-84;

	Matches	264;	Conservative	231;	Mismatches	250;	Indels	90;	Gaps	59
Db	60	CIRYNFGRFMQLQAMIFAEIEINSSPALLPNLLGRIYFDICNTVSKALEA--TLSEVAQ	117	I : :	:	:	:	:	:	:
Oy	3	S-FNENHGHLFOAMRLGVEEIINSTALLPNIITGYOGLDYDCSDSANYYATLAVLSIPQ	61	:	:	:	:	:	:	:
Dd	118	NKIDSLNDFENCNSEEHPTITAVYGATGSVSTAVANLLCFPIPOVSASSRILSNK	177	:	:	:	:	:	:	:
Oy	62	BHIE-IQ-GDLHFYS--FTVLAVIGPSITNRATLTALLSPFLV-HISYAASEETLSVK	115	:	:	:	:	:	:	:
Dd	178	NOFKSELRTIPDEHQATAMADIIEFPWMNVGIADDDVGDRGIEKFREAREEDICI	237	:	:	:	:	:	:	:
Oy	116	ROYPEFLTIPNDKIQTVELLYLKLFQEWMTISLVSGSSDITGGOLGVQLENAQALVRGICI	175	:	:	:	:	:	:	:
Dd	238	DFSELISOYSDE--EE-IDHVEVENIONSTAKVIWFSFGSDPLELIKE-IVRRNITGIW	293	:	:	:	:	:	:	:
Oy	176	AFKDIMP-FSAQVGBERNQCIMRHQAQALVVVFFS-RQLAVVFESVLTMLTKXW	233	:	:	:	:	:	:	:
Dd	294	LASEMASSSLIAMQIYHVVTGTIGPALKAQIQIPEREELKKVHPKRKSVHNGFAKEFE	353	:	:	:	:	:	:	:
Oy	234	VASEMA--L-S'-R'-HITGP-GIO-RGMVLGV-A-IOK--R-AVP-GL-KAF-E	274	:	:	:	:	:	:	:
Dd	354	EFEFNCHDEGAAGRPVDPTFRGEHEGSDRSNSTARPLCTGDENISSVEPYDIYTH	413	:	:	:	:	:	:	:
Oy	275	EAYIA-R-ADKE-APPFGH---KGSMCSSLNQCRECOAF-X-A-HTPPKA---FS-	318	:	:	:	:	:	:	:
Dd	414	LRISNYVLAVYSIALAQDIYTCLPGKRGLETNSCADIKKVEAMQVLEKLRLHNTNM	473	:	:	:	:	:	:	:
Oy	319	MSAAVNATRAYAAVANHGHJOLLC-AS-EL-----CS-RGNVYPMOLEQIHKYHFLHK	370	:	:	:	:	:	:	:
Dd	474	GEQVTFDECGLVGNYSIIINHLSBEDGISIVEKEYGVINYAKKERLFIENEKILMSGF	533	:	:	:	:	:	:	:
Oy	371	-DIVAFNNRNPRLSSSYNIAMDWNGPK-WT-FVLGS-STWSP-VQ-LINETRKiOWHG-	423	:	:	:	:	:	:	:
Dd	534	SREPLTFVLSLVGFNFSCSRDCAGTRKGIIBEERPCCEFCVCPDGEGVEDENASCN	593	:	:	:	:	:	:	:
Oy	424	-KNH-----QPKVSYCSSDCLEGHOR-VVITGFHHCCFECVCAGATFLNKSELYRCQ	473	:	:	:	:	:	:	:
Dd	594	KCPDDFWSENHTSCIAKEIEFLSKTEPFPG-IALTFLAVLGIPTAVLGVIKFRNTPI	652	:	:	:	:	:	:	:
Oy	474	PGCTEMAPESGQTCFPPTVFLALREHTSVLLAANTLILLLLLG-TAGFAHHLDTPV	532	:	:	:	:	:	:	:
Dd	653	VKANRELSTYLLSLSCFFSSSLF-FIGEPODWTCRLROPASISFYLCISGLFVXTNR	711	:	:	:	:	:	:	:
Oy	533	VRSAGRCICFMLGSIAGA-SGSLYGEFGEPTZRACILLRQALFALGFTIFELCTVRSFQ	591	:	:	:	:	:	:	:
Dd	712	VLVVE--AKIPTSHRKWNGLNLOFLVEICTMQIYCIWLYTAPSSYENOEDE	769	:	:	:	:	:	:	:
Oy	592	LIIRKSTKVPT-FYHAMVONHGAGLEVSSAAOLLICITLWVTPLPARYORPH	650	:	:	:	:	:	:	:
Dd	770	IIFIRCHE-GSF-MALGLIGYCCLAICEFFFKSRKXLENENAKFIIFSMLIFPIV	827	:	:	:	:	:	:	:
Oy	651	LMECTETENSGLTAL--YNGLLISAACGYLGRDPENNNEAKCYVLSLEPFVS	708	:	:	:	:	:	:	:
Dd	828	WISFIPAVASTY-GKFSAVEVIALLA-SFGLLACIFENKIYITLKPSNITE	880	:	:	:	:	:	:	:
Oy	709	WIAFFT-ASYVDGKYLPAAMMAGLSLSGSGFGY-FLPCYVILCRPDLNSTE	761	:	:	:	:	:	:	:
RESULT	15									
ID	W89564	standard; Protein; 1088 AA.								
AC	W89564;									
DT	19-MAR-1999	(first entry)								
DE	Human parathyroid calcium receptor pRUBCAR 5.2.									
KM	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;									
KM	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;									
KM	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;									
KM	neonatal distress; neurodegenerative disease; Alzheimer's disease;									
KM	Huntington's disease; Parkinson's disease; dementia; muscle tension;									
OS	Homo sapiens.									
PN	US385864.A.									
PD	12-JAN-1999.									

[illegible]



PR 07-JUN-1995; 480751.  
 PR 07-JUN-1995; US-480751.  
 PR 23-AUG-1991; US-749451.  
 PR 11-FEB-1992; US-834044.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; MO-012117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGM ) BRIGHAM & WOMEN'S HOSPITAL.  
 PA (NPSP-) NPS PHARM INC.  
 PI Baladrin MF, Brown EM, Del Mar EG, Garrett JE,  
 PI Hebert SC, Nemeth EF, Van Wagenen BC;  
 DR WPI: 99-119871/10.  
 DR N-PSDB: 982484.  
 PT Screening for calcium receptor-active compounds - by recombinant  
 PT expression of nucleic acid encoding calcium receptor and determining  
 PT the effect of compounds on calcium receptor activity  
 PS Claim 1; Fig 48; 176pp; English.  
 CC A method has been developed of screening for a compound able to affect  
 CC one or more activities of a calcium receptor (CR) comprises: (A)  
 CC contacting a recombinant cell with a test compound, where the  
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,  
 CC provided that the cell does not have functional CR expression from  
 CC endogenous nucleic acid; (B) determining the ability of the test  
 CC compound to affect one or more activities of the calcium receptor; and  
 CC (C) comparing the ability with the ability of the test compound to  
 CC affect the one or more CR activities in a cell not comprising the  
 CC recombinant nucleic acid. The present sequence represents human  
 CC parathyroid CR, designated a pParCar 5.2. The nucleic acid sequence of  
 CC pParCar 5.2 can be used as part of the recombinant nucleic acid in the  
 CC method described above. The compounds identified can be used to treat  
 CC diseases or disorders characterized by abnormal calcium homeostasis, e.g.  
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
 CC disorders. They can also be used for the treatment of diseases and  
 CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures,  
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
 CC diseases such as Alzheimer's disease, Huntington's disease and  
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
 CC Sequence 1088 AA;

Query Match 18.2%; Score 1063; DB 1; Length 1088;  
 Best Local Similarity 31.6%; Pred. No. 4,17e-84;  
 Matches 264; Conservative 231; Mismatches 250; Indels 90; Gaps 59;

DB 60 CIRNFRGFRWLQAMIFAIIEINSSPALLPNTLIGRIFDTCNTVSKALEA--TISEYAAQ 117  
 QY 3 C-SFNEHGYHFLFOAMRLGVEEINSTALLPNTLIGYOLYDCSDSANYATLRLVSLPQ 61  
 DB 118 NKIDSLNDEFCNCEHPISTAVAGATGSGSVSTAVNLGLFIPIQVSYASSSRLLSNK 177  
 QY 62 HHIE-LQ-GDLHHS--PTVLAVIGPDSTNRAATTAALISFLIV-HISTAASSETLSVK 115  
 DB 178 NQFSFLTIPNDEHOATAMADIIIEFRMNWGTIAADDDYGRPGIEKFEFEAEERDICI 237  
 QY 116 ROYPSFLTIINDKQVETWVLQKPGMTWISLVGSSDDYQGLGVQALENALVIGICI 175  
 DB 238 DPFELISOYDE--EE-IQHVVEVIONSTAKYIVVSSGPDLEPLIKE-IYARNITGKIW 293  
 QY 176 AFKDIMP-FSAQVGDERMQCLMRHLAQAATVYVSS-ROLARVEFESVLTNLTKYW 233  
 DB 294 LASEMASSSLIAMPOYFHVVGITGFALKAQIIGFREFLKVPKSYHNGFAKEFWE 353  
 QY 234 VASEMA--L-S--R--HITGVP-GIQ-RIGMVLGV-A-IQK--R-AVP-GL-KAF-E 274  
 DB 354 ETEFNHLOEGAGPLPVTFTLGHESGDRFGNSSTARPLCTGDENISVETPYIDYTH 413  
 QY 275 EAYA-R-ADKE-APRPH---KSGMSSNQJCREQAF--M-A--HYMPKLKA---FS- 318  
 DB 414 LRISYNYLAVYSIAHALQDIYTCPLPGRGLTNGSCADIKKVEAMQVLKHLNHLNFTNM 473

QY 319 MSSAYNNAVRAVYAAVAGHLOHLCG-AS-EL-----CS-RGRVYPWOLLEQIHKVFLLHK 370  
 DB 474 GEQYTPDECCGLVGNYSIIIMWHLSPEDGSIVFEKVEGYNNYAKGDELFINERKILMSGF 553  
 QY 371 -DTAFENDNRPLSSYINILAMDWNGPK-WT-FTVLGS-STWSP-VQ-LTINERKIQWHG- 423  
 DB 534 SREPLTFVLVLYQVFPNSCRDCLAGTRKGIIEGEPCFECEVCPGEGESDETDASACN 593  
 QY 424 -KNH-----QYPKVCSDDCEGHQR-VYGFHHCCECEVCPGAGTILNSELARQC 473  
 DB 594 KCPDEMSNENHSCIAKEIEFLSWTEPEG-IAVTFVAGITLAFVIGFIKFRNTPI 652  
 QY 474 PCGTEENAPESQCFPRIVFALREHNTSWVLLAANTLLILLLG-TAGLFAMHLDTPV 532  
 DB 653 VKATNRELSTVLLSLGCCSSSIF-FIGRPQDWTCLRQPARGISVLCISGILVYKTR 711  
 QY 533 VRSAGRLCFMLGSLIAG--SGSLYGFGEPTRPACILROLALFALGFTIFLSCTVNSFO 591  
 DB 712 VLVYFE--AKIPTSFHRKMWGLNQLFLVFLCTFMQIVICVIMLYTAPSPSYRNOLEDE 769  
 QY 592 LIITFKSTKVT-FTYAWQNHGAGLFVMISSAOLLICLWLVYVTPPLPAREYQRFPH 650  
 DB 770 IITTCHE-GSL-MALGFLIGYTCLLAICFFFAKSRKLPENENAKFTFSMLIFFIY 827  
 QY 651 LYMLECTETSLGFIILAFI--YNGILSISAFACSYLGKDPENYNEAKCYTFSILFNFS 708  
 DB 828 MISFIPYASY-GKFSAYEVAIILAA-SFGLACIFFNKIYIILKPSRNTIE 880  
 QY 709 WIAFFT-ASYVDKYLPLANMAGLSSSGFGGY-FLPKCYVILCRPDLNSTE 761

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2000, 09:04:09 : Search time 2691.14 Seconds  
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Perfect score: 2771

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Scoring table: IDENTITY\_NUC

Searched: 4886541 seqs, -2018352991 residues

Database : Pending\_Patents\_NA.\*

Word size : 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2771	100.0	2771	2	Sequence 5, Appl
3	2166.8	78.2	2579	1	Sequence 6, Appl
4	2166.8	78.2	2579	2	Sequence 7, Appl
5	1566.6	56.5	2333	1	Sequence 8, Appl
6	1566.6	56.5	2333	2	Sequence 9, Appl
7	447.6	16.2	2993	51	Sequence 10, Appl
8	436	15.7	2532	51	Sequence 11, Appl
9	395	14.3	1147	54	Sequence 12, Appl
10	392.8	14.2	2010	51	Sequence 13, Appl
11	350.8	12.7	2466	87	Sequence 14, Appl
12	269.2	9.7	571	93	Sequence 15, Appl
13	252	9.1	558	85	Sequence 16, Appl
14	252	9.1	558	86	Sequence 17, Appl
15	252	9.1	558	86	Sequence 18, Appl
16	244.8	8.8	459	92	Sequence 19, Appl
17	220.6	8.0	412	92	Sequence 20, Appl
18	204.8	7.4	376	92	Sequence 21, Appl
19	204.8	7.4	382	92	Sequence 22, Appl



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## ALIGNMENTS

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: Sequence 4, Application PC/US9917099
: GENERAL INFORMATION:
: APPLICANT: Zuker, Charles S.
: APPLICANT: Adler, Jon Elliot
: APPLICANT: Lindemeier, Juergen
: APPLICANT: Ryba, Nick
: APPLICANT: Hoon, Mark
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
: TITLE OF INVENTION: Involved in Sensory Transduction
: FILE REFERENCE: 02307E-088610PC
: CURRENT APPLICATION NUMBER: PCT/US99/17099
: CURRENT FILING DATE: 1999-07-27
: EARLIER APPLICATION NUMBER: US 60/094,465
: EARLIER FILING DATE: 1998-07-28
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 2771
: TYPE: DNA
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
PCT-US99-17099-4

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RESULT 2
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; Sequence 4, Application US/09361652
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliott
; APPLICANT: Lindemeier, Juergen
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 02307E-0886100S
; CURRENT APPLICATION NUMBER: US/09/361,652
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/094,465
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor B3 (GPCR-B3)
US-09-361-652-4

Query Match 100.0%; Score 2771; DB 92; Length 2771;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	30.1	cttgagagaaataaacaactccctcgccctgtgcttcccaactcaacctcgagggtatctagcgt	360
Db	30.1	cttgagagaaataaacaactccctcgccctgtgcttcccaactcaacctcgagggtatctagcgt	360
QY	36.1	acgaagctgtgtctcaagaaactctgtcccaatgtgtatgtccacacctgtgaaggtgtctgtcccgcaag	420
Db	36.1	acgaagctgtgtctcaagaaactctgtcccaatgtgtatgtccacacctgtgaaggtgtctgtcccgcaag	420
QY	42.1	ggccccgcacatatgagataacagaaagacctctgcacaacacactccctccaaaggtgtgtgcct	480
Db	42.1	ggccccgcacatatgagataacagaaagacctctgcacaacacactccctccaaaggtgtgtgcct	480
QY	48.1	tcaatccggtctgtgaataaacaactgtgacacacgctctcaactacgctctgctctgtctgtgctcttcc	540
Db	48.1	tcaatccggtctgtgaataaacaactgtgacacacgctctcaactacgctctgctctgtctgtgctcttcc	540
QY	54.1	tgaatccccctgtgtacagtaatgaagacaagacgctgtgtactcaagtgtgcaagcgcaagttcc	600
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Db	60.1	cgctcttccctctgtacacggtcccccagtgaaacggagacaaggtgtgaaggtacatgtgtacgctgtgc	660
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Db	96.1	gggacatctccacgttaataataacacagctgtgaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1020
QY	102.1	gt	1080
Db	102.1	gt	1080
QY	108.1	gggtgtgtgaagaagctgtctcccaagcgtctgtgcacggaggggtctctgtgtgtgtgtgtgtgtgtgt	1140
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[illegible]



Db	2261	tcgtctgcagcttacccttcggtgtaaggaactgcgcagaagaactatataatgaagccaaatgtgtca	2340
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Db	2341	cccttaagcctctcctcctaacttcgtatccctgatactgcctctctcctaacaatggtccaaacattt	2400
Qy	2401	accagggcagcttaacctccctgcgtgcgttcaatgtgtcttcggcaaggctctgaaccaactgaagcggcg	2460
Db	2401	accagggcagcttaacctccctgcgtgcgttcaatgtgtcttcggcaaggctctgaaccaactgaagcggcg	2460
Qy	2461	gcttcagaggtgttactctctccccaaggtgcattgtgatcttcctgcgcgcttcagaactccaaca	2520
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Qy	2521	atacagaacaccttccaaagccttcacccacagagctacacagagcgctgcgcgcaacttacctat	2580
Db	2521	atacagaacaccttccaaagccttcacccacagagctacacagagcgctgcgcgcaacttacctat	2580
Qy	2581	ccactcgtgaagaaggtgcagacgaggggaaggaagcctctctcttcgtctgaaggtgcgggtccc	2640
Db	2581	ccactcgtgaagaaggtgcagacgaggggaaggaagcctctctctcttcgtctgaaggtgcgggtccc	2640
Qy	2641	agtcggggccgggaagcttgtaggtgtcttcgggggaagcttcgggcacaagcttaccatgataagc	2700
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Qy	2701	acgcggaagaatccagctgcataataagaacgggaagtgtgaataaaaaaaataaaaaaaataaa	2760
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Qy	2761	aaaaaaaaaa 2771	
Db	2761	aaaaaaaaaa 2771	
RESULT 3			
PCT-US99-17099-5			
: Sequence 5, Application PC/TUS9917099			
: GENERAL INFORMATION:			
: APPLICANT: Zuker, Charles S.			
: APPLICANT: Adler, Jon Elliot			
: APPLICANT: Lindemeier, Uergeren			
: APPLICANT: Ryda, Nick			
: APPLICANT: Hoon, Mark			
: APPLICANT: The Regents of the University of California			
: TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
: TITLE OF INVENTION: Involved in Sensory Transduction			
: FILE REFERENCE: 02307E-088610PC			
: CURRENT APPLICATION NUMBER: PCT/US99/17099			
: CURRENT FILING DATE: 1999-07-27			
: EARLIER APPLICATION NUMBER: US 60/094,465			
: EARLIER FILING DATE: 1998-07-28			
: NUMBER OF SEQ ID NOS: 8			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 5			
: LENGTH: 2579			
: TYPE: DNA			
: ORGANISM: Mus sp.			
: FEATURES:			
: OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)			
PCT-US99-17099-5			

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Query Match      78.2%   Score 2166.8; DB 1; Length 2579;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 2316; Conservative 0; Mismatches 223; Indels 6; Gaps 1.

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QY      103 actgctggccttcacagcttgccaaagacagagtcctctcaagcttcaagcttcttcggag 162

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[illegible]



OY	1243	ccacgagctccacacagctctctcggagtgtaattctgaagtcctgttccagagagccagact	1302
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OY	1303	accctctgacagctctcttcacagacatcacacaaggtgaaattctcttaacatgaatactg	1362
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OY	1423	atggacacgaaatgagaccccttggagatcatctgacctcgtccacatcgctccatgtaactcg	1482
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OY	1903	gcagactctataagactctctcggggagacccaagtgcccgctgctgtgctgcgcgcacgccc	1962
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OY	2023	tcaatcatcttcaaaagtctttctacacaaggtgcccacatctcacacgttaccgtgggcccanaacc	2082
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OY	2203	ttctcaggtgacaagaggtcaactctgtagagcttccctgttgcttcaaccacaacatctc	2262
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OY	2263	tcacctcatcagacacttctgtgagcttaccctgttgtaagaaatgcacagaaactata	2322
Db	2223	tcacctcatcagacacttctgttctgtgagcttaccctgttgtaagaaatgcacagaaactata	2282

QY	2323	atgaagccaatggtacacttaagcctgctctcaactgtctacocgtgagtcgcctct	2382
Db	2283	acgaagccaatggtacacttaagcctgctctccacactgtacccgtgagtcgcctct	2342
QY	2383	tcaccatgycgaagatlttaacagagcgagctactgtcgtcgtgtcaatggtcgtcgaagcg	2442
Db	2343	tcaccatgtccagatlttaccagcgagctactacccgcygtcaatggtcgtcgaagcg	2402
QY	2443	tgaacacactgtagggcggtttagcggttactctctcccaagtgctatggtattctt	2502
Db	2403	tggcacactgtagggcggtttagcggttactctctccctaaatgctacgtgattctct	2462
QY	2503	gcgcgtccagaactcaacaatacagaacacttttagcgctccatccacagatcaacgaagcg	2562
Db	2463	gcgcgtccagaactcaacaacagaaacacttttagcgctccatccacagatcaacgaagcg	2522
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RESULT      4
US-09-361-652-5
; Sequence 5, Application US/09361652
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeyer, Juergen
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02307E-088610US
; CURRENT APPLICATION NUMBER: US/09/361,652
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/094,465
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2579
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse G-protein coupled receptor B3 (GPCR-B3)
US-09-361-652-5

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Query Match	78.2%	Score 2166.8	DB 92	Length 2579
Best Local Similarity	91.0%	Prod. No. 0		
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			Gaps	1
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QY	103	actgctggagcttcacagctgcgcacaagagacagagatctccttcacagcttcacagcttccttcctgggg	162	
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QY	163	actctccctcttgcaagctctgtctccctccatcagtgatcagctctgcaagctgagacacaagac	222	
Db	123	actctctcccttgcaagctctgtctccctccatcagtgatcagctctgcaagctgagagacacagac	182	
QY	223	ctctcgtgtacaagatgtgtacaagagcccgacagcttcacaagcgacatggtctacacactcttc	282	
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QY	283	aagcacaatcggtgtacactgtttgagagagataaanaactctctggccctgtctcccaacata	342	
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QY	343	ccccgvggtatagagctctatagacgtctggtcccaagaattcgccaatctggtatagccacctga	402
Db	303	ccccggvggtatagaaactctatatacgtctgcccagaagattcttccaattgtctatagccacctga	362
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Qy	163	tttaggtgtgvcacctgtgcgaaccccggaacctttcccaaacctgaagtcaactcaacatctgccc	1682
Db	1563	tcagatgtcatctccctcttgcgaagcctgaggacaattctccacaacagcttagacttcaaaccttgc	1622
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Qy	1843	tgaagatgaacgctgagggtgctgaagccttgccttcccaatgtctggtccctctgttgcgcggaaagt	1902
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Qy	2203	ttctccgaattgcacagaggtctaaactctgtatgagcttctctgttgccttcaaccaacaactctc	2262
Db	2163	ttcttgaattgcacagaaggtctaaactctgtatgagcttctctgttgccttcaaccaacaactctc	2222
Qy	2263	tcccttccatcatgaacaccttgcgtctgcagctaacctctgggtgaaggaaactgtgcagaagaaacta	2322
Db	2223	tcccttccatcatgaacaccttgtgtctgcagctaacctctgggtgaaggaaactgtgcagaagaaacta	2282
Qy	2323	attgaagacaaatgtgttcaaccttcaagcctgctccctcaactctgtatccctgtgactgcgtctct	2382
Db	2283	acgaagaacaaatgtgttcaaccttcaagcctgctccctcaactctgtatccctgtgactgcgtctct	2342
Qy	2383	tcaccaatgcacgaattattacacagcgagcttactcgtcgtctgtaattgtctgcgggaagc	2442
Db	2343	tcaccaatgcacgaattattacacagcgagcttactcgtcgtctgtaattgtctgcgggaagc	2402
Qy	2443	tgaacacacatgaagcggtgtcttgcagcgttactccttccccaagctgctatgtgacttctct	2502
Db	2403	tgcacacactctgaatggtgcggcttcaagcggctatttctcccttaaaagctcaagtgtattcctct	2462
Qy	2503	ggcgttccagaactcaacaatacagaacacacttcaagccttcaatccagaactcaacagagc	2562



Db	2463	gcgcctccagaactacacacacagaaacactttcagcctccatccaggaactacacgagc	2522
QY	2563	gctgcggcgaactaactatcattccactcg	2586
Db	2523	gctgcggcgaactaactatcagcgcctcg	2546

## RESULT 5

```

PCT-US99-17099-6
Sequence 6, Application PC/7US9917099
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Lindemeyer, Juergen
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
TITLE OF INVENTION: Involved in Sensory Transduction
FILE REFERENCE: 02307E-088610PC
CURRENT APPLICATION NUMBER: PCT/US99/17099
CURRENT FILING DATE: 1999-07-27
EARLIER APPLICATION NUMBER: US 60/094,465
EARLIER FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 2333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human G-protein coupled receptor (GPCR-B3)
PCT-US99-17099-6

```

Query Match	56.5%	Score 1566.6	DB 1	Length 2333
Best Local Similarity	80.0%	Pred. No. 0		
Matches 1869; Conservative	0	Mismatches 464	Indels 4	Gaps 2

[illegible][illegible]



QY	1863	ctgagcttcctcaatcagctcgggtctccctcgtagcgccgaagtgtgaagctctctatagctcttc	1922
Db	1617	ctgagctctcttaagctcgggctctccctcgtagcgagcagtagtgcagcctctatagctcttt	1676
QY	1923	gggggaagcccaagcgtagcccgagtgctgtgctgcgtcaacccctctttctctcgggttcc	1982
Db	1677	ggggaaacccaaagagcctcgctgcgtctgctcaagccagccctcttgcccttgattcaac	1756
QY	1983	atctctctctctcgtccgtaacatccgctctctctcaacagctgcatactctcaagtctct	2042
Db	1737	atctctcgtctcgtcgcgcagagtgctgcgtctcaatctcaactatcatctctcaagtttcc	1796
QY	2043	accaaggtgcccaatctcaatccgttaacctgagcccaaaccaatggtgcaggtctatcgtc	2102
Db	1797	accaaggttaacctatctcaactccacgcgcgtggtctcaaacacagctgtcgtcgtttgtg	1856
QY	2103	atgtcagcctcccaaggtgcatttgcctcatctgtctcaactatgcttgtaatgtgagcccca	2162
Db	1857	atgatacagctccaagggcccgccgctgctctatctctcaactctgctggtgtgtgtagcccca	1916
QY	2163	cgaaaccacagaggaatcacccagcgctctccccaactgtgattctcgtagtcagacaagctc	2222
Db	1917	ctgctgcttagaggaatcacccagcgctctccccaactgtgattctgtagtgcacagaagcc	1976
QY	2223	aacctgttaagctctcctggtgtgctcttcaaccacaacatctctctctcaatgaatccttc	2282
Db	1977	aacctccctgagctctcaatacagcgctctctctcaacaatgagctctctctcaatgattcctt	2036
QY	2283	gtctgcagctcaacctgggttaagaggaactgcagagaaataatgaagccaaatggtctaac	2342
Db	2037	gtctgcagctcaacctgggttaagaggaactgcagagaaataatgaagccaaatggtctaac	2096
QY	2343	ttaagcctgctctcctcaactcctatgctctccttgatctgcctcttcaacatgtgcagcaattac	2402
Db	2097	ttaagcctgctctcctcaactcctgctctgctctgctgatctgcctcttcaacagcgcaagctctac	2156
QY	2403	cagggcagcagctacgtcgtctggtgcgaatgtgctgcagagggcgtcaacaactgtagcgcgcc	2462
Db	2157	gaaggcaagtaacctgctcgtgcgcgaacatgattgtgtgctgttagagagctgtgacgagcgcc	2216
QY	2463	ttaagcgttactctcccccagaatgctatgtatctctgctgcgcaggaactaacaat	2522
Db	2217	ttaagcgttactctctcgtcttaagtgtctaaagtgtgtgctgtgctgtgctgtgctgtgctgtg	2276
QY	2523	acagaagaacttcaagcctccatccacaggaactaacagagagcgctgtgagcaactctga	2579
Db	2277	acagaagaacttcaagcctccatccatcaaggaactaacagagagcgctgtgagcaactctga	2333
RESULT 6			
US-09-361-652-6			
Sequence 6, Application US/09361652			
GENERAL INFORMATION:			
APPLICANT: Zuker, Charles S.			
APPLICANT: Adler, Jon Elliot			
APPLICANT: Lindemeier, Juergen			
APPLICANT: Ryba, Nick			
APPLICANT: Hoon, Mark			
TITLE OF INVENTION: The Regents of the University of California			
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor			
FILE REFERENCE: 02307E-08861005			
CURRENT APPLICATION NUMBER: US/09/361,652			
CURRENT FILING DATE: 1999-07-27			
EARLIER APPLICATION NUMBER: US 60/094,465			
EARLIER FILING DATE: 1998-07-28			
NUMBER OF SEQ. ID NOS: 8			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 6			
LENGTH: 2333			
TYPE: DNA			
ORGANISM: Homo sapiens			

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; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR-B3)
US-09-351-652-6

Query Match: 56.5%; Score 1566.6; DB 92; Length 2333;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 1669; Conservative 0; Mismatches 464; Indels 4; Gaps 2;

QY 243 agggccgaaggttcaacgcccattgctacacccctctccaaagcattcggttcaactgt 302
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 aggtcttgaggttcaatgagcatgctacacccctccaaagcattcggttgggtt 60
QY 303 gaggagataaacaactctctcgccctgtcttcccaacacacccctgggtatagctgtac 362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6- gaggagataaacaactccacgcccctctgtgtcccaacacacccctgggtatagctgtat 120
QY 363 gaggctgtctgaatctgtcccaattgtatgtacacccctggaggtgtcttgccttcgaagg 422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 gctgtgtgtcttcgcaactccgccaatgtgtatgtaccagccctgaaggtgtcttccctgcgaagg 180
QY 423 ccccgccacataagagatacagaagaagacctctgcgaacacacctccccaaggtctgtcccttc 482
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 caacacacataagagcttcccaaggaagaccttctccactatctccccaaggtgtctgtcaggt 240
QY 483 atcgggctgtgaataaacctcgacacagctctcaactacccctgtcctctgtgtgttcttctgt 542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 atctggccctgtgaacacacacacacacgctgtcttccacacacacacgcccctcttgagcccttctgt 300
QY 543 atgcccctctgtcagcttatgaggaagaagcagcgtgtgtactcagctgcgaagcgaagctcccg 602
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 gtg----catattagctatgtggccgacgacgagacagctccagcgtgaaagcggcagatcccc 357
QY 603 tcttctctctgtacccgttcccccagtgacacggacacacagctgtgaggtatgtgtcagactgtgtg 662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 tcttctctgtgtacacatcccccaatgacaaagtacaaagctgtgagacatgtgtgtgtgtgtgt 417
QY 663 caggaaatttggtgtgtgtgtgtatctcgtctcaattgtgcacatacgtgtatgtacggcagctgt 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 cagaaagcttcgggtgtgaccttgatctctctctgtgtctggcagcagatgtgaactatgtgagagctta 477
QY 723 ggtgtgtcagagcagctctgagagacgtgtgcccctgtcccccggcactgtgtgtcgtccctcaagag 782
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 ggggtgtcagagcactgtgaaacaacagggcccctgtgtcaggggtcactgtgatgtcttcaagagac 537
QY 783 atcgtgtccttctctgtcccccgtgtgggtgtgaccccgagatgtcagagacatgtatgcagcatctg 842
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 atcagtgcccttctctgtcccagatgtgggtgtgagatgtgacagtgactgtctatgcgcaactgt 597
QY 843 ggtcagggcagagacacacacgctgtgtgtgttcttcttcaacggcacactgtgcagagtgttc 902
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 gcccaaggccgggggcacacacgctgtgtgttcttcttccacggcagatgtgtgcagaggtgtgttc 657
QY 903 ttcaaggtccgtgtgtgtcgtcccaacacctgtgacaaagatgtgtgtgtcgtccctcagaagaactgtg 962
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 ttggtgtcgtgtgtgtgtgtgacacacctgtgcagagtggtgtgtgtcgtccctcagaagaactgtg 717
QY 963 gccatctccacgttaccatcacacagcgtgtgacgtggatccaaagcatgtggagcgtgtcgtgt 1022
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 gccctctccaggtacacatcacctgtgggtgtgcccgggattccacggcactgtgatatgtgtgtgggc 777
QY 1023 gtgggctccgtccagagacagagcagatccctctgtgtgtgaagggctgttgaggagtcttatgtcagg 1082
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 778 gtgggacacccagaaabaaggctgtctccctgtgacctgtgaagggcgttttgagaagacctatgtccccgg 837
QY 1083 gctgttaacagatgtgtcccccagcgtcttgccccggagaggtctctgtgttcagacactacaacacgtg 1142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 838 gcaagcacaaggagcccccttaggccttgtaaac-aagggtctctgtgtcagagagaatcatcagctc 896
QY 1143 tgcgggtgtgtccacacgttcaagcactgtatacatgtcccaacgctttggaagccttcttcaag 1202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 897 tgcagaagaatgtcccaagcttctatgtgcacacacagatgtgtcccaagccttcaagccttcttcatgt 956

```



[illegible]

Accession	Gene	Protein	Length (aa)	Accession	Gene	Protein	Length (aa)
D82037	gcccgcagcctactcgtggttaagagactctggccagagaaactaaagaagcccaatggttcacc		20936	D82037	gcccgcagcctactcgtggttaagagactctggccagagaaactaaagaagcccaatggttcacc		20936
QY2343	ttcagcgtcgtcctcctcaactctgtatctcccttgatccgcctcttcaacatgagcagaactttac		24022	QY2343	ttcagcgtcgtcctcctcctcaactctgtatctcccttgatccgcctcttcaacatgagcagaactttac		24022
D82097	ttcgcgtcgtcctctcaactctcgtctccctggtatccgctcttcaacacagcgccagcgtctac		2156	D82097	ttcgcgtcgtcctctcaactctcgtctccctggtatccgctcttcaacacagcgccagcgtctac		2156
QY2403	cagcgacgactactcgtcgtcgtgctcaatgtgtcgtcgagcgaggtaccacagctagcgtgcgc		2462	QY2403	cagcgacgactactcgtcgtcgtgctcaatgtgtcgtcgagcgaggtaccacagctagcgtgcgc		2462
D82157	gaagcagaagtaacctgcgtcgtcgccacaatgagtgctgctgagcagcctgagcagcggc		2216	D82157	gaagcagaagtaacctgcgtcgtcgccacaatgagtgctgctgagcagcctgagcagcggc		2216
QY2463	ttcagcggttactctccctccccaagtgctatgtatctcttgcgcgtcgagaactcaaat		2522	QY2463	ttcagcggttactctccctccccaagtgctatgtatctcttgcgcgtcgagaactcaaat		2522
D82217	ttcgtgtggtatcttctctgcctaagtgctacgtatccctctgcgcgcagactcaaacgc		2276	D82217	ttcgtgtggtatcttctctgcctaagtgctacgtatccctctgcgcgcagactcaaacgc		2276
QY2523	acagaaacactttcagcgtcctcatccagagactacacagagcgtctgcgcgaactactga		2579	QY2523	acagaaacactttcagcgtcctcatccagagactacacagagcgtctgcgcgaactactga		2579
D82277	acagagagacttccagcgtcctcatcttcggagctacacagagcgtctggtctccacctga		2333	D82277	acagagagacttccagcgtcctcatcttcggagctacacagagcgtctggtctccacctga		2333

## RESULT 7

```

1  Sequence 3 Application US/09361631
2  -----
3  GENERAL INFORMATION:
4  APPLICANT: Zuker, Charles S.
5  APPLICANT: Adler, Jon Elliot
6  APPLICANT: Lindemeyer, Juegen
7  APPLICANT: The Regents of the University of California
8  TITLE OF INVENTION: Nucleic Acids Encoding a G-protein Coupled Receptor
9  TITLE OF INVENTION: Involved in Sensory Transduction
10 FILE REFERENCE: 02307E-08872005
11 CURRENT APPLICATION NUMBER: US/09/361,631
12 CURRENT FILING DATE: 1999-07-27
13 EARLIER APPLICATION NUMBER: US 60/095,464
14 EARLIER FILING DATE: 1998-07-28
15 EARLIER APPLICATION NUMBER: US 60/112,747
16 EARLIER FILING DATE: 1998-12-17
17 NUMBER OF SEQ ID NOS: 10
18 SOFTWARE: PatentIn Ver. 2.0
19 SEQ ID NO 3
20 -----
21 LENGTH: 2993
22 TYPE: DNA
23 ORGANISM: Rattus sp.
24 FEATURE:
25 OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4
26 US-09-361-631-3

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query match	16.28;	Score 447.6;	DB 51;	Length 2993;
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Best Local Similarity 51.68; Pred. No. 1e-104;  
 Watched 1066; Consumptions 0; Visited 1144; Total 43; Cost 6

Matches 1266; Conservative 0; Mismatches 1144; Indels 42; Gaps 9;

QY	142	cagagcttcagagctctccggggagactctctcttcagagtcgtctccctccatgagagact	201
Db	95	ctgactctccacactcggccggaggaacacccctcgggtgagccctcttaacccctcagcaag	154
QY	202	gtctcgacaggtgagaca---acagacctctggtgacaagttgtgacagagcccgatcctca	258
Db	155	tgaagagcatctccacactccctcagctcaggtgcccaggtgcatgagttcacatga	214
QY	259	acggcccatggtataccactctctccaaagcattgggtttcaactggttgaggagataaacaact	318
Db	215	agggtgttgggctataaacaactcatgaaagccctcgtttctcgttcggagggatacaacaact	274
QY	319	cctctgcgcctcgtcttccccaacatcaccccttgggtgatgacgttgcacgaacgttgcctagaat	378
Db	275	gtagctccctcgtctaccccggtgtgtgtcgtgcatacgatgtgagatctcgtttacactct	334
QY	379	ctgagccatgtgtatgacacacctgagaggtgtcttgcctcgcacaagggcccccgccaatatgaga	438
Db	335	ccaacaataatccacaccttgggctctactctctctgccaacagacg---acgacatctctccca	391











Dh	1751	cgctgcgcacattcgtcatctctcttggaagacatttccaaagccgacattggtgcgtccgcgg	1811
Qy	1855	ggggtaagctctgtcttcctccaaatgcgtggttccctgtgtgcggaaattgcagcttctata	1914
Dh	1811	ggcgccccaatgtgtcttcctatgtgtgtgcgcctgcgtcttcggatgvtgcccg	1870
Qy	1915	gctctctcggggagcccaacgggtgcccgggtgctctggtgtgaagccctctttctccg	1974
Dh	1871	tgatgtagggcccccccaacggtcttctctgttctctgcgcgaagcctttctcaacgltt	1930
Qy	1975	gatttgcaatcttcctctctctgtcgttcaaatccgcctctccaaattgtaataatctca	2034
Dh	1931	gctctctccgtctgcctctctctgtatcaagggtgcgtcctctccagattgtgtgcttca	1990
Qy	2035	agttttctacaaagtgtccacattcttaacgttaactgtggcccaaaacaaatgtgtcaagt	2094
Dh	1991	agatgtagcaagcgtcttgcacaaagctctacggtttctctgtgtgtatccaagccctacg	2050
Qy	2095	tattctgcatctgtcagctcccaaggtccatttg---ctaatcgtcttcaaatggtctgtaa	2151
Dh	2051	tctctgtgcctctatcaacgcccgttcaaaagtgcgtctctgtgtggcggaacatgtgcgca	2110
Qy	2152	tgtagaccccacagccacacaaagggaatacaagcgtctcccccatctggtagatccaggt	2211
Dh	2111	ccaccatacaaccocatgtgcgcgaacccggaacccgatgaccccaataatcactctctct	2170
Qy	2212	gcacagaagctcaactctgttaggtcttcgttltgtcttcaaccacacatactctctctca	2271
Dh	2171	ggcaaccttaactaacggaacgggtctactcttcaaacacagcatgtgaattgtcgtctgc	2230
Qy	2272	tcaatccttcgtctctgacgttaacctgtgtgaaggaaactgccagaataataatgaagcca	2331
Dh	2231	tgctgtgggtttcaagttctgcgtacgtgtgggaagaagaaactgccacatacaagaagcca	2290
Qy	2332	aattgtcaccttcaagcctctctctcaactctgtatccctggatcccggtatgcctcttccacac	2391
Dh	2291	agttcacaccccctcaagaatgaactcttctcttcaaccctcccaactccctctgcgaattca	2350
Qy	2392	ccaaatcttaccagggagacgtactactctgcgtgtacatgtgtgtgcgaaggtcgtgaacac	2451
Dh	2351	tgctgtccaaagatlggtggtctgttcaacatcatgtatctctctgttaactgtgccaaact	2410
Qy	2452	tgaagcgagcgtctcaagcgttactctccctcccaagtgtactgtatctctgtccgtccag	2511
Dh	2411	ttctgcgcacatcgctgtggtgtactcttgcgcccaaatgtacatgatctcttctctaccgg	2470
Qy	2512	aaccacaataacagaacacttccagcgtctccatccacaggaactaacagagggc	2563
Dh	2471	agcgcaactctagcttatttaataagatgattcagggtcaacagatgag	2522
RESULT 9			
US-09-471-275-7046			
Sequence 7046, Application US/09471275			
GENERAL INFORMATION:			
APPLICANT: Hysq, Inc.			
TITLE OF INVENTION: Novel Configs Obtained			
TITLE OF INVENTION: From Various Libraries			
FILE REFERENCE: 782			
CURRENT APPLICATION NUMBER: US/09/471,275			
CURRENT FILING DATE: 1999-12-23			
EARLIER APPLICATION NUMBER: US 09/235,076			
EARLIER FILING DATE: 1999-01-20			
EARLIER APPLICATION NUMBER: US 09/234,611			
EARLIER FILING DATE: 1999-01-22			
EARLIER APPLICATION NUMBER: US 09/240,371			
EARLIER FILING DATE: 1999-01-29			
EARLIER APPLICATION NUMBER: US 09/277,227			
EARLIER FILING DATE: 1999-03-25			
EARLIER APPLICATION NUMBER: US 09/271,490			
EARLIER FILING DATE: 1999-03-18			
EARLIER APPLICATION NUMBER: US 09/293,972			
EARLIER FILING DATE: 1999-04-15			

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: EARLIER APPLICATION NUMBER: US 09/274,861
: EARLIER FILING DATE: 1999-03-23
: EARLIER APPLICATION NUMBER: US 60/125,453
: EARLIER FILING DATE: 1999-03-19
: EARLIER APPLICATION NUMBER: US 60/126,605
: EARLIER FILING DATE: 1999-03-26
: EARLIER APPLICATION NUMBER: US 09/306,350
: EARLIER FILING DATE: 1999-05-07
: EARLIER APPLICATION NUMBER: US 09/399,720
: EARLIER FILING DATE: 1999-09-21
: EARLIER APPLICATION NUMBER: US 09/404,284
: EARLIER FILING DATE: 1999-09-21
: EARLIER APPLICATION NUMBER:
: EARLIER FILING DATE: 1999-12-16
: NUMBER OF SEQ ID NOS: 10451
: SOFTWARE: pt.ct.genes Version 1.0
: SEQ ID NO 7046
: LENGTH: 1147
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: (6)...(965)
: OTHER INFORMATION: similar to g14337086 in the genepept database release 114
: OTHER INFORMATION: Run with FASTXY 3.3c00, default parameters
US-09-471-275-7046

Query Match          14.3%: Score 395; DB 54; Length 1147;
Best Local Similarity 75.2%; Pred. No. 2.5e-91;
Matches 506; Conservative 0; Mismatches 165; Indels 2; Gaps 1;

QY 977 cataccagcgctgacgtggaatccaaagcatatggagacgtgtcgtgtgtgtccatcaga 1035
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 cattagtaacgtgctgggtggaattccgcgcatatggatgtgtgtgtgtgtgtccatcaga 64

QY 1037 gagaacagtcctcgtggc--tgaagagatttgagagctcttaatgtcagggtc--aacagct 1094
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 gaaggcgtcttcctcgtcctgtatgtcgtttgaaagaagcctatgccgggcagacaagaag 124

QY 1095 gctccagcgcttcccgagggggtcctcgtgtgacgaactaaacagcttggccggagttgc 1154
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 gccctcagccttgcacaagggctcctcgtgtgacgaacatcagctctgcagaagaatgc 184

QY 1155 cacacgttcaacgactcgttaacatgccacgccttggagccttccatagatgcgcgctac 1214
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 caaacttcaatgagacacacagcatgcccacaagctcaaaagcctctccatggtctcgtctac 244

QY 1215 aagatgtatagaagcgtgtacgctgtggtgcgccagcgctccacaagctccttgatgtact 1274
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 aagcatatcggggtgtgtatgctgtgcgtcccaatgcgtccacaagctcctcgtgtgccc 304

QY 1275 tctagatcgttccaaagcccaatgttaacctgtgcagctcttcaagacagatctcaag 1334
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 tctgagactgttccaaaggcgagatctaacctctggcagcttlttgagacagatcccaag 364

QY 1335 gtgatttctctcaatggcaatcactgtgcgaatttgatagaacaagggaacactcaggt 1394
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 365 gtgatttctctcaacaagaagaactgtgtggctttaatgacaacaagatatccctcagat 424

QY 1395 tactacagacatcacgcgctggagactggaaatggagccctgaatgagacctttagatcatgtgc 1454
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 agcatatacataatgtcgtggaacttggaataggcccaaggagagccttcaacggtctcgt 484

QY 1455 tctgtcctcaatgcttccagttcatc--tgacataataataagaacaaaatccaatggcaggg 1514
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 485 tctccacatatgtctccacgttcagcttaaacatataatgataccaaaatccaatgtgcagga 544

QY 1515 aagaacacatcgggtcgtgtgctgaagtgtgacacagcagatgttgcgaaggccacccag 1574
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 545 aaggaacacacgggtcgtgtgctgaagtgtgacacagcagatgttgcgaaggccacccagga 604

QY 1575 gtgtgtgtgtgtgtcccaacacgtcgtgatttgagttgtgtgtgtgtgtgtgtgtgtgtgtgt 1634

```







Db 1532 tctctatgcatcttatacaccagcttaccacaaatgctatctgtgttaattgtgcatatgctgcgcac 1591  
OY 2155 ggaaccccccagccccccacaggaatataccagcgtctcccccattgtgtgtttctcagtgca 2214  
Db 1592 ggcctcagctccacccccctcagctcagaccagatgaccccaagatacacaattgtctctgta 1651  
OY 2215 cagaagctactctgttaagctctcgttgcgttaccacacaacattctccctcatca 2274  
Db 1652 acccaactaaccgaacacagcctcgtgttcaaacacagccttgagacctgtgtctcagtgtg 1711  
OY 2275 gtacctgtctgcagctacatcgtgtgtaaggaatgcgcagagaataataatgaagccaaat 2334  
Db 1712 tgggttcatgcttcgcctacatagcgcaagagctgcaccacatacagaagcgcaagt 1771  
OY 2335 gtgttaaccttaagcctgtctctccaaactctgtatccttgatctgcctcttccacatggcca 2394  
Db 1772 tcatcaacctcagcatgacctcttatacaccatccgtctccctcgcacacctcatgt 1831  
OY 2395 gcaattacacagggcagctacatcgtcctgcgtcaaatgtgtgcagggccttgaccacactga 2454  
Db 1892 ctgcctaaagcgggtgtcgtgttcaaccatcgttgaaacctctgtgtacgtgtgtcaacctcc 1891  
OY 2455 gcggcgcgttcaagcgttactctctccccaagtgtatgtgattctctgcgcgttccagaac 2514  
Db 1892 tgcgcctacagcctggtcactctgcgcaccaagtgtcatatgctctcttcttcaaccggagc 1951  
OY 2515 tcaaaataacagaacacttccagcctccatccagaactacacagcgagcgctgcgcgc 2570  
Db 1952 gcaacacgcgcgcctacttcaacagcatgataccagggctaacaccatgagagagagac 2007

RESULT 11  
US-60-172-600-1  
: Sequence 1, Application US/60172600  
: GENERAL INFORMATION:  
: APPLICANT: Bonazzi, Vivien  
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
: TITLE OF INVENTION: RECEPTOR, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
: TITLE OF INVENTION: PROTEIN, AND USES THEREOF  
: FILE REFERENCE: CLO000178  
: CURRENT APPLICATION NUMBER: US/60/172,600  
: CURRENT FILING DATE: 1999-12-20  
: NUMBER OF SEQ ID NOS: 14  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 2466  
: TYPE: DNA  
: ORGANISM: HUMAN  
: US-60-172-600-1

Query Match 12.7%, Score 350.8; DB 87; Length 2466;  
Best Local Similarity 48.0%; Pred. NO. 9.6e-80;  
Matches 1154; Conservative 0; Mismatches 1217; Indels 33; Gaps 4;

OY 159 gggagactccctcctgtcagcgtctgttctccctccatgctgtgactgtctcaggtgtagaac 218  
Db 7 ggggactacgtgtcgggggctgttccctcctgcggagggccgagagagctgtgctcgcgc 66  
OY 219 agacctcgtgtgacaagctgtgacagggcccgacacgttcaacggcagctatcacacctc 278  
Db 67 agccggaacagggccagcagccctgtgtgacacaggttctctcaaacggcctgtgtctcgg 126  
OY 279 ttcaacgcaatgcgttcaactgttgaagagataaacaaactcctgcggcctcttcccaac 338  
Db 127 gcaactgcacatgaaatgctgcgttgagagatcaacaaagctgatatgtgtgcgcggg 186  
OY 339 atcacccgggtgtatgactgtgacagcgtgtctcagaatctgcgcaatg---tgtatgcg 395  
Db 187 ctgcgcctcgtggtcactcttctgatacagtgctcggaaacctgtgtgcatgaagccgc 246  
OY 396 accctgaggtgtcttgcctcgtcaagggcccgccacatagagatacagaagaacctctgcg 455

Db 247 agccctcatgttctcgtccgaagcgcagcgcgcgcagcaatcgcgcgcctactgcactgaatacag 305  
OY 456 aaccactctctcaagggtgtgtgtccttcatgtggcctcacaacactgtaccagacgtgtcaact 515  
Db 307 cagtaaccagccccctgtgtctgtctgtcatctggcccccaactgtatgaagctgcacatgtgc 366  
OY 516 acccgtgcctgtgcgggggtccctctctgatggccctgtgtcaagctatgaggaacagcagctg 575  
Db 367 accggcaaggtctctcatgcttctctctcatgtgccaggttcagctcagtgctcagatagag 426  
OY 575 gtactcagtgccaaagcgcgaattccgcgtcttctcctgtacacgcctcccaatgtacggcaac 635  
Db 427 ctgtcagagcgcgcggaggaactctccctctctcttccgcacacggcgcccaagcagacgtgtg 486  
OY 636 caggtgtgagcgcacagtgacatcctcagaggttttggtgtgtgtgtatctgcctcatc 695  
Db 487 cagctgtacggccgc 546  
OY 696 ggcagctacagctgaattgaagggcagactgtgtgtgcagsgcgcgcgcgcgcgcgcgcgcgcgc 755  
Db 547 ggcagcgcagcagaggtacagc 606  
OY 756 cggggcatctcgtcgcgccttcaagagacatcgctgcctt-----ctctgcgcgcgcgcgcgc 809  
Db 607 cgggcacatctgcatcgcgcagcagggcctgtgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 666  
OY 810 gaaccagagagcgcagagcatatgacagcatcgtgtcagcgcgcgcgcgcgcgcgcgcgcgcgc 869  
Db 667 ctggggaagggctgcagagatctctcgcacagctgaacagagacgcgtgcaggtgtgtgtgtgt 725  
OY 870 gtctctctaaacgcgcgcacactgtgcctagaggtgtctctcaagctgcgcgcgcgcgcgcgcgcgc 929  
Db 727 ctgttgcctcctgcgtgcagcgcgcgcgcgcgcgcgcctcttcaactacacatagacagcagctg 786  
OY 930 actgtgcaagctgtgtgtgtcgcctcctcagaaactgtggcacaatccacgtatatacaccagcgtg 989  
Db 787 tgcgcacaaggtgtgtgtgtgtgc 846  
OY 990 actgtgacccaagagcaatcgtgagacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1049  
Db 847 cccgcgcacatggccagatgtgacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 906  
OY 1050 gggcgtgaagaggttgaagatcttattgtcagcgcctgaacagcgcctcccaagcagctgtgc 1109  
Db 907 gagtctcccccagtaagctgaagacgcacctgtgcctgtgcacacgcgcgcgccttctgtcctct 956  
OY 1110 ccggaagggctcctgtgtgacgacataccagcctgtgtgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1169  
Db 967 gccctggcgagagggagcagcaggtctgtgagagagacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1026  
OY 1170 cgtaacatgtcccaagcctgtgagccttctcacaatgtgtccgcctcacaagatgtatgaggtc 1229  
Db 1027 tgtgactgtcatcacagcttcaaaacgtgtgagcgcaaggtcaaaatccacaacacagcttctct 1086  
OY 1230 gttgtacgctgtgtgcacagcgtctccacagcgtctctgtgagtgatcttctgagatctgttctc 1289  
Db 1097 gtctacgacgtgtgtatagcgt 1146  
OY 1290 agagc-----ccagctacccctcgc 1334  
Db 1147 tcaagctgtcccccgcgcagcagcccgctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1205  
OY 1335 gtgaatttcttctacatagaaatactgtgtgcatctgtgtgcaacgcgcgcgcgcgcgcgcgcgcgc 1394  
Db 1207 ctgaactctccacgtgtggc 1256  
OY 1395 tacaagacatcacatgcctgtgacgtgacatgtgacatgtgacatgtgacatgtgacatgtgacatgtgac 1454  
Db 1267 gagtacgaacctggaagctgt 1326  
OY 1455 tctgcctactgttctccagcttcatctgtgacataaataagacaaaatccacatcagctgtgcaggg 1514



[illegible]

```

RESULT 12
US-60-178-308-1069
: Sequence 1069, Application US/60178308
: GENERAL INFORMATION:
: APPLICANT: Bonazzi, Vivien
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USES THEREOF
: FILE REFERENCE: CLO00204
: CURRENT APPLICATION NUMBER: US/60/178,308
: CURRENT FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 3344
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1069
: LENGTH: 571
: TYPE: DNA
: ORGANISM: HUMAN
: US-60-178-308-1069

```

Query Match	9.7%;	Score 269.2;	DB 93;	Length 571;
Best Local Similarity	81.1%;	Pred. NO. 5.9e-59;		
Matches 313;	Conservative	0;	Mismatches 73;	Indels 0;
				Gaps 0;

QY	1647	gagcttcaacatctgcgcagcctcttggaataacagaagaattggacaccccaagaagagagcaactt	1706
Db	186	gacctctcaacagatgycacagccctctgtggaaagaagaattggacaccccgaaaggagaagcaagacc	245
QY	1707	tgctctcccaagcagcagctgtgaagtgtctctgtggtcttgagcatgaaccccatctctctgtgctaa	1766
Db	246	tgctctcccgagcaactgtgtgtgttttggctcttggcgtggagcacacacctctctgggtgtgtgtg	305
QY	1767	gcagactcaacagctatctgcctgcctgcctgcctgtgttggaagcctgcctgcctgttctgtgcgat	1826
Db	306	gcagactcaacagctgcctgcctgcctgcctgcctgtgttggaagcctgcctgcctgttctgtgcgat	365
QY	1827	tttcaacacacctgtgaatggaatgacagctgggggttaagctcttgcttccatctatgctgtgttc	1886
Db	366	ctaaagacacccctctgtgtggaggtctaaagaaaggagggccggccgtgctcttctctatgcttgagcc	425
QY	1887	ctggctggccggaagtctgaactctctataactctctctctctggagaaccccaagctgcaccgcgtgc	1946
Db	426	ctggcgagcaaggtatgttgacagccctctatgctctctcttctggggaaaccccaagcgcgtgtgc	485
QY	1947	ttgctgtgcgtacgcccctctttctctcgtgggttggtccatctctctctcgtcgtctgaacaatc	2006
Db	486	ttgtctacgcaagggccctcttggcctctgtgtttcaacacatctctcgtctcgtcgtgacagtt	545
QY	2007	cgctccttcgaactgtgctacatcctt	2032
Db	546	cgctccttcgaactgaatcaccatcctt	571

```

RESULT 13
US-60-160-202-36
; Sequence 36, Application US/60160202
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
; FILE REFERENCE: C1000114
; CURRENT APPLICATION NUMBER: US/60/160,202
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 4392
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 558
; TYPE: DNA
; ORGANISM: HUMAN
; US-60-160-202-36

```



```
Query Match          9.1%; Score 252; DB 86; Length 558;
Best Local Similarity 76.5%; Pred. No. 1.6e-54;
Matches 309; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 544 tgcctctgtcaagctatgaagcaagcagctgtgtactcaatgtccaagcgaagtccct 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 tccatagatagatagctatgcgcagcagcagacgtcagcgttaagcgaagatccct 214

QY 604 ctctctctgtaccgtctcccaagtgaccgcagccagctggaggtgtatgtgtcagctgtgc 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 ctctccgcgcacacatcccaatgacagtgagtgagacattgtctcgtctgc 274

QY 664 agagtttggtgtggtgtgtgtctgcgtctcaattgccaagctacagtgatcagcgagctgg 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 agaatctcggtgtgacctgtgactctctgtgtgtgcagcaatgtgaagatacgggagctag 334

QY 724 gtgtgcagcgctgtgagagctgtgcgttgcctccggcgacatctgccttccaagaca 783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 gggtgcagcgacgtgagagacacagcactgttcaggggagatctgattgtcttcaagaca 394

QY 784 tctgtcctctctctgtcccggtgtgtgtacccgagagatgcagagcatatcagcacttg 843
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 tcatgccctctctgcgcaggtgtgcsatgagagatgcagtgctcatctgcacacttg 454

QY 844 ctcaagcgcaagcacacccgtgtgtgtgtctctctcaaccgcagcactgtgcagagtgctct 903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 ccaagcgcgggcgccacacgtgtgtgtgttcttccagccggcagattgccaaggtgtctt 514

QY 904 tcaggtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 tcgagtcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 558

RESULT 14
US-60-169-841-23
; Sequence 23, Application US/60169841
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
; FILE REFERENCE: CL000163
; CURRENT APPLICATION NUMBER: US/60/169,841
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 2910
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
US-60-169-841-23

Query Match          9.1%; Score 252; DB 86; Length 558;
Best Local Similarity 76.5%; Pred. No. 1.6e-54;
Matches 309; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 544 tgcctctgtcaagctatgaagcaagcagctgtgtactcaatgtccaagcgaagtccct 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 tccatagatagatagctatgcgcagcagcagacgtcagcgttaagcgaagatccct 214

QY 604 ctctctctgtaccgtctcccaagtgaccgcagccagctggaggtgtatgtgtcagctgtgc 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 ctctccgcgcacacatcccaatgacagtgagtgagacattgtctcgtctgc 274

QY 664 agagtttggtgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 agaatctcggtgtgacctgtgactctctgtgtgtgtgcagcaatgtgaagatacgggagctag 334

QY 724 gtgtgcagcgctgtgagagctgtgcgttgcctccggcgacatctgccttccaagaca 783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 gggtgcagcgacgtgagagacacagcactgttccaggggagatctgattgtcttcaagaca 394
```

```
QY 784 tctgtcctctctctgtcccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 843
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 tcatgccctctctgtcccaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 454

QY 844 ctcaagcgcaagcacacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 ccaagcgcgggcgccacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 514

QY 904 tcaggtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 tcgagtcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 558

RESULT 15
US-60-169-842-23
; Sequence 23, Application US/60169842
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
; FILE REFERENCE: CL000162
; CURRENT APPLICATION NUMBER: US/60/169,842
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 5232
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
US-60-169-842-23

Query Match          9.1%; Score 252; DB 86; Length 558;
Best Local Similarity 76.5%; Pred. No. 1.6e-54;
Matches 309; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 544 tgcctctgtcaagctatgaagcaagcagctgtgtactcaatgtccaagcgaagtccct 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 tccatagatagatagctatgcgcagcagcagacgtcagcgttaagcgaagatccct 214

QY 604 ctctctctgtaccgtctcccaagtgaccgcagccagctggaggtgtatgtgtcagctgtgc 663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 ctctccgcgcacacatcccaatgacagtgagtgagacattgtctcgtctgc 274

QY 664 agagtttggtgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 723
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 agaatctcggtgtgacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 334

QY 724 gtgtgcagcgctgtgagagctgtgcgttgcctccggcgacatctgccttccaagaca 783
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 gggtgcagcgacgtgagagacacagcactgttcaagggatctgattgtcttcaagaca 394

QY 784 tctgtcctctctctgtcccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 843
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 tcatgccctctctgtcccaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 454

QY 904 tcaggtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 tcgagtcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 558
```

Search completed: March 22, 2000, 09:52:34  
Job time: 2905 sec







GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 17:45:41 ; Search time 97.56 Seconds  
(without alignments)  
3400.480 Million cell updates/sec

Title: US-09-361-652-4

Perfect score: 2771

Sequence: 1 attcacatcagagctgtgct.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY\_NNC

Searched: 214294 seqs, 59861208 residues

Database : Issued\_Patents\_NA:\*

Word size : 0

Number of hits that pass the threshold : 428588

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/5C\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/5D\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/5E\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/PTUS9\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	181.6	6.6	3809	1	US-08-485-588-3	Sequence 3, Appl1
2	181.6	6.6	3809	2	US-08-484-565-3	Sequence 3, Appl1
3	181.6	6.6	3809	3	US-08-480-751-3	Sequence 3, Appl1
4	181.6	6.6	3809	4	US-08-943-986-3	Sequence 3, Appl1
5	181.6	6.6	3809	5	US-08-353-784-3	Sequence 3, Appl1
6	176.4	6.4	5275	1	US-08-485-588-1	Sequence 1, Appl1
7	176.4	6.4	5275	2	US-08-480-751-1	Sequence 1, Appl1
8	176.4	6.4	5275	3	US-08-480-751-1	Sequence 1, Appl1
9	176.4	6.4	5275	4	US-08-943-986-1	Sequence 1, Appl1
10	176.4	6.4	5275	5	US-08-353-784-1	Sequence 1, Appl1
11	170.2	6.1	5006	1	US-08-485-588-2	Sequence 2, Appl1
12	170.2	6.1	5006	2	US-08-484-565-2	Sequence 2, Appl1
13	170.2	6.1	5006	3	US-08-480-751-2	Sequence 2, Appl1
14	170.2	6.1	5006	4	US-08-943-986-2	Sequence 2, Appl1
15	170.2	6.1	5006	5	US-08-353-784-2	Sequence 2, Appl1
16	160.6	5.8	4131	1	US-08-485-588-4	Sequence 4, Appl1
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19	160.6	5.8	4131	4	US-08-943-986-4	Sequence 4, Appl1
20	160.6	5.8	4131	5	US-08-353-784-4	Sequence 4, Appl1
21	138.2	5.0	3384	4	US-08-687-289A-1	Sequence 1, Appl1
22	137	4.9	4000	4	US-08-687-289A-2	Sequence 1, Appl1
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24	73.2	2.6	3919	1	US-08-072-574-5	Sequence 5, Appl1
25	73.2	2.6	3919	2	US-08-486-270-5	Sequence 5, Appl1
26	73.2	2.6	3919	5	US-08-367-264-5	Sequence 5, Appl1
27	67.8	2.4	4085	1	US-08-072-574-7	Sequence 7, Appl1
28	67.8	2.4	4181	1	US-08-072-574-9	Sequence 9, Appl1
29	67.8	2.4	3282	1	US-08-072-574-11	Sequence 11, Appl1
30	67.8	2.4	4085	2	US-08-486-270-9	Sequence 9, Appl1
31	67.8	2.4	4181	2	US-08-486-270-9	Sequence 9, Appl1
32	67.8	2.4	3282	2	US-08-486-270-11	Sequence 11, Appl1

33	67.8	2.4	4085	5	US-08-367-264-7	Sequence 7, Appl1
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36	67.4	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl1
37	60.4	2.2	4095	6	PCT-US91-09422-18	Sequence 18, Appl1
38	60.4	2.2	2426	6	PCT-US91-09422-20	Sequence 20, Appl1
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43	56.6	2.0	4300	2	US-08-463-642-1	Sequence 1, Appl1
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45	56.6	2.0	4300	3	US-08-465-157-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-485-588-3  
; Sequence 3, Application US/08485588  
; Patent No. 5688938  
; GENERAL INFORMATION:  
; APPLICANT: Edward M. Brown  
; APPLICANT: Steven C. Hebert  
; APPLICANT: Forrest H. Fuller  
; APPLICANT: James E. Garrett, Jr.  
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: First Interstate World Center  
; STREET: Suite 4700  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FASTSEQ  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,588  
; FILING DATE: 7 June, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; APPLICATION DATA: described below: 9  
; APPLICATION NUMBER: 08/353,784  
; FILING DATE: 9 December, 1994  
; APPLICATION NUMBER: PCT/US/94/12117  
; FILING DATE: 21 October, 1994  
; APPLICATION NUMBER: U.S. 08/292,827  
; FILING DATE: 23 August, 1994  
; APPLICATION NUMBER: U.S. 08/141,248  
; FILING DATE: 22 October, 1993  
; APPLICATION NUMBER: U.S. 08/009,389  
; FILING DATE: 23 February, 1993  
; APPLICATION NUMBER: U.S. 08/017,127  
; FILING DATE: 12 February, 1993  
; APPLICATION NUMBER: U.S. 07/934,161  
; FILING DATE: 21 August, 1992  
; APPLICATION NUMBER: U.S. 07/834,044  
; FILING DATE: 11 February, 1992  
; APPLICATION NUMBER: U.S. 07/749,451  
; FILING DATE: 23 August, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hebert, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 213/005



```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SRO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-485-588-3

Query Match      6.6%; Score 181.6; DB 1; Length 3809;
Best Local Similarity 49.6%; Pred. No. 3.6e-38;
Matches 522; Conservative 0; Mismatches 524; Indels 6; Gaps 2;

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RESULT 2
US-08-484-565-3
Sequence 3, Application US/08484565
Patent No. 5763569
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PASTISO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
```



```

1 NAME: Heber, Sheldon O.
2 REGISTRATION NUMBER: 38,179
3 REFERENCE/DOCKET NUMBER: 213/006
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (213) 469-1600
6 TELEFAX: (213) 955-0440
7 TELEXT: 67-3510
8 INFORMATION FOR SEQ ID NO: 3:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 3809 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: single
13 TOPOLOGY: linear
14 MOLECULE TYPE: cDNA to mRNA
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 375..3606
18 OTHER INFORMATION:
19 OS-08-484-565-3

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Query Match	6.6%	Score 181.6	DB 2	Length 3809
Best Local Similarity	49.6%	Pred. No. 3.6e-38		
Matches 522	Conservative 0	Mismatches 524	Indels 6	Gaps 2

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3  
US-08-480-751-3  
Sequence 3, Application US/08480751  
Patent No. 5858684  
GENERAL INFORMATION:  
APPLICANT: Edward F. Nemeth  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: Forrest H. Fuller  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPIER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,751  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/357,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCI/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992



```

APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-480-751-3

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Query Match          6.68; Score 181.6; DB 3; Length 3809;
Best Local Similarity 49.68; Pred. No. 3,6e-38;
Matches 522; Conservative 0; Mismatches 524; Indels 6; Gaps 2;

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DB 2590 GTGATCTGGCTCTACACCGGGCCCCCTCAAGCTACCGCAACGAGAGCTGAGATGAG 2649
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DB 2650 ATCATCTTCATCAAGTCCAGGGGGGCTCCCTCATGGCTTCCCTGATCGGGCTAC 2709
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DB 2710 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2769
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DB 2770 AACTTCATGAGGACGATGATCAGCTTGTGATGATGATGATGATGATGATGATGATG 2829
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2830 TCCCTTCATTCAGGCTATWGCACACCTATGCAAGTTGTCTGTGCTGAGAGGTGATT 2889
QY 2436 gcaaggtgtgacacactgtagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2495
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DB 2890 GCCATCTGGAAGCAGCTTTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2949
QY 2496 attctgcgttccagaactcaacaatacaga 2527
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DB 2950 ATTCTTCAAGCATCCCGCAACACCATCGA 2981

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RESULT 4
US-08-943-986-3
Sequence 3, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127

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APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-353-784-3

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Query Match      6.68; Score 181.6; DB 5; Length 3809;
Best Local Similarity 49.68; Pred. No. 3.6e-38;
Matches 522; Conservative 0; Mismatches 524; Indels 6; Gaps 2;

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QY 1479 ctgacataataagaacaaatccagtgccaggggaagaacaatcaggtgctgtgtca 1538
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DB 1933 CTCTTCATCAACGAGGAGAAATCTGTGAGTGGTCTCCAGGAGAGTCCCTTCCTC 1992
QY 1539 gtgtgaccagagctgtgtgctgagggagac---cacaggtgtgtgtgtgtccacac 1595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1993 AACTGACGCCAGACTGCTTGCGAGGACGACGAAAGGATCATTTAGAGGGGAGCCACC 2052
QY 1596 tgctgtcttgatgtgtgctgcccgcgaagcttggaaccttccacaatgagtgagctcac 1655
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DB 2053 TGTGCTTTGATGTGTGAGTGTGCTGATGGGGAGTATGATGATGAGACGATGCCACT 2112
QY 1656 atctgcagcctgtgtgaacagaagaatgggcaaccaagaagagcaactactgttccca 1715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2113 GCCGTAAACAAGTCCCAAGATGACTTCGTGTCATATGAGAACACACCTCTCGATTGCC 2172
QY 1716 cgcacgggtgaggtctgtgctgtgcatgaaccatctcttgggtgtaataagcagctaac 1775
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DB 2173 AAGAGATCGAGTTTCTGTCTGTGAAGAGCCCTTTGGGATCGCACTACCTCTTGGCC 2232
QY 1776 acgctatgtctgtctgtgtgtgtgagctgtgcccctgttgcctgtgcatttcacaca 1835
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DB 2233 GTGCTGGGACTTTTCCGACAGCCTTTGCTGGGTGTGTTATCAAGTTCCGGAACACA 2292
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2293 CCCATTGTCAAGGCCACCAACCGAGAGCTCTCACTCTCTCTCTCTCTCTCTCTGCG 2352
QY 1896 ggaagtgagcgtctctatagttcttggggagcccaagtgcccggtgtgtctgtggt 1955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2353 TGTCTTCACACTCCCTGTTTATCGGAGGCCGCCGAGACTGGACCTGGCGCTGGCG 2412
QY 1956 cagccccccttctctcgtgggttgagccatctctcctcctcgtgacaatcagctcttc 2015
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2413 CAGCGGCGCTTTGGCATCAGCTTGTGCTGTGCATCTCATGATCCTGCTGAAAAACCAAC 2472
QY 2016 caactgtgcatcatcttcaagtcttctaccaaagtgcccaatcttaacgtacctggcc 2075

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DB 2473 CGTGTCTCTCTGCTGTGTGAG---GCCAAGATCCCCACGACTTCCACCGCAAGTGGTG 2529
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QY 2076 caaacaatggttgaggtgcatctatctgtcatctgtcagctccacaggttccatctgt 2135
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DB 2530 GGGCTCAACCTCGACTGCTGCTGTGTGTCTGTGACCTTCAATGAGATGTGATCTGT 2589
QY 2136 ctcaacagcttgtaatgtgagcccccacagaccacacaggaataacacagcttccccc 2195
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DB 2590 GTGATCTGGCTCTACACCGGGCCCTCAAGTACCGCAACGAGCTGAGGATGAG 2649
QY 2196 ctggtgattctgaggtgacagaggttaactctgttaggttctgttgccttccaccac 2255
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DB 2650 ATCATCTTCAATCAAGTCCGACGAGGGGCTCCCTGATGGCCCTGAGGCTTCCGATCGGCTAC 2709
QY 2256 aacattctcttccatcaatcttctgttgcagctgaactggtgtaaggaactggcagag 2315
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DB 2710 ACGTGGCTGCTGGCTGCACTGCTTCTTCTTGTGCTTCAAGTCCGGAAGCTGGGAG 2769
QY 2316 aactataatgaagccaatgtgtacaccttcagcctgctcctcaactctgtatcctgagtc 2375
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DB 2770 AACTTCAATGAGGAGTCACTACCTTCAAGTCACTGATGCTCATCTTCAATGCTGTGATC 2829
QY 2376 gcttcttccatgagcagcatttaccagaggaagctactgctgctggtcaatgtgtc 2435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2830 TCCTTCATTCAGGCTATGCGACGACCTATGCGAAGTTTCTCTGCTGCTGAGGTGAT 2889
QY 2436 gcaaggtgtgacacacacgtgagcggcgcttcaagcgttacttctcccaagtgctatgt 2495
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DB 2890 GCCATCTTGCGAGCGACTTGTGGCTGTGCTGCGTGCATCTTTCACCAAGATCTTACATC 2949
QY 2496 attctgcctgtccagaactcaacaatacaga 2527
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2950 ATTCTTCAAGCATCCCGCAACACCATCGA 2981

```

```

RESULT 6
US-08-485-588-1
Sequence 1, Application US/08485588
Patent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESS: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994

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PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 36,119  
REFERENCE/DOCKET NUMBER: 213/006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 515..3769  
OTHER INFORMATION:  
US-08-484-565-1

Query Match 6.4%; Score 176.4; DB 2; Length 5275;  
Best Local Similarity 49.0%; Pred. No. 1e-36;  
Matches 530; Conservative 0; Mismatches 546; Indels 6; Gaps 2;

QY 1479 ctggacataaataagacaaaatccagtcgacggaagaagaacatccagtcgtgtca 1538  
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QY 1539 gtgtgtccacgagcgtctgtgtgacgggacac--cacagggtgtgtgtgtgtccacac 1595  
DB 2138 AACTGCAGTGCAGACTCTCTGCGACGACGACGAAAGATCATTGAGGGGAGCCACC 2197  
QY 1596 tgcgtctttagtgtgtccctgcgaagctgtgaccccttccacatgagtgtgtc 1655  
DB 2198 TGTGCTTTGAGTGCTGTGATGCTGTGATGAGGAGTACAGCAGACAGATGCAAGT 2257  
QY 1656 atctgcagcctgtgtgaagaagaatgtggaccccaagaagaagactactgttccca 1715  
DB 2258 GCCTGTATAGTGCCTGTGATGATCTGTGCTCATAGAACCACTTCTGTGATGCC 2317  
QY 1716 cgcacggtgagtcctgtgtgtgacatgaaacccatcttgtgtgtaataagcagctaac 1775  
DB 2318 AAGGAGATCAGATTCTGTGTGTGACGAGCCCTTGGGATGACGACGCTTTTGTCT 2377  
QY 1776 acgctatgt 1835  
DB 2378 GTGCTGGGCAATTTCTCAGACGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2437  
QY 1836 cctgt 1895

DB 2438 CCCATGCTCAGGCGACCAACCGGAGCTCTCTATCTCTCTCTCTCTCTCTCTCTCTCT 2497  
QY 1896 ggaagtgcagctctcatagctctctccgggagccacagctgtccgcgctgtgtgtgtgt 1955  
DB 2498 TGTCTTCCAGCTTCT 2557  
QY 1956 caagccctcttctctcgt 2015  
DB 2558 CAGCGGCGCTTGTGATCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2616  
QY 2016 caactgtatcatcttcaagtttctacaaagtgccacattctaccgtactgtgtgt 2075  
DB 2616 -ATCGGCTCCTCTGT 2674  
QY 2076 caaacaatgtgcaggtctatctatctatctatctatctatctatctatctatctatctat 2135  
DB 2675 GGGCTCAACTGCAGTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2734  
QY 2136 ctacatgt 2195  
DB 2735 GCATTTGGCTCAATACAGGCGCCCTGTGAGCTACCGACACGAGCTGGAGAGAG 2794  
QY 2196 ctgtgtatctctgagtgacagagtgacactgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2255  
DB 2795 ATCATCTTCATCACCTGTGACGAGGCGCTGCTCATGCGCTGTGCTGTGATGCGCTAC 2854  
QY 2256 aacattctctctccatcagctacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2315  
DB 2855 ACCTGTCTGTGCGCGCATCT 2375  
QY 2316 aactataatgaagcaaatgt 2435  
DB 2915 AACTCATATGAACCAAGTATCATCT 2495  
QY 2376 gccttctacatgt 2455  
DB 2975 TCTTTATCCCGCTACGCGACGCACTTACGCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCT 3034  
QY 2436 gcaaggctgtgacacactgtgagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2495  
DB 3035 GCCATCTGTGCGCGCATCTTGT 3094  
QY 2496 attcttgcctgt 2555  
DB 3095 ATCTCTTCAAGCTTCCGAGACACATGAGAGGTGGCTGACACCGCGGACAC 3154  
QY 2556 ac 2557  
DB 3155 GC 3156

RESULT 8  
US-08-480-751-1  
Sequence 1, Application US/08480751  
Patent No. 5858684  
GENERAL INFORMATION:  
APPLICANT: Edward F. Nemeth  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: Forrest H. Fuller  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071







```

: STREET: First Interstate World Center
: STREET: Suite 4700
: STREET: 633 West Fifth Street
: City: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: FASTSEQ
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,986
: FILING DATE: 03-OCT-1997
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/484,565
: FILING DATE: 7-June-1995
: APPLICATION NUMBER: 08/353,784
: FILING DATE: 9 December, 1994
: APPLICATION NUMBER: PCT/US/94/12117
: FILING DATE: 21 October, 1994
: APPLICATION NUMBER: U.S. 08/292,827
: FILING DATE: 23 August, 1994
: APPLICATION NUMBER: U.S. 08/141,248
: FILING DATE: 22 October, 1993
: APPLICATION NUMBER: U.S. 08/009,389
: FILING DATE: 23 February, 1993
: APPLICATION NUMBER: U.S. 08/017,127
: FILING DATE: 12 February, 1993
: APPLICATION NUMBER: U.S. 07/934,161
: FILING DATE: 21 August, 1992
: APPLICATION NUMBER: U.S. 07/834,044
: FILING DATE: 11 February, 1992
: APPLICATION NUMBER: U.S. 07/749,451
: FILING DATE: 23 August, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Heber, Sheldon O.
: REGISTRATION NUMBER: 38,179
: REFERENCE/DOCKET NUMBER: 213/006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 955-0440
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5275 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 515..3769
: OTHER INFORMATION:
: US-08-943-986-1

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Query Match 6.4%; Score 176.4; DB 4; Length 5275;  
 Best Local Similarity 49.0%; Pred. No. 1e-36;  
 Matches 530; Conservative 0; Mismatches 546; Indels 6; Gaps 2;

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QY 1479 ctgacataaataagaacaaatcagtgacaggaagaacatcagtcgtgtgac 1538
DB 2078 ctcttcacatgatagaataatctgtgagtgattctcagaaggagctctttcc 2137
QY 1539 gtgtgtacaggaactgtgtgacaggaacac--cacaggtgtgtgtgtgtccaccac 1595
DB 2138 aacttcacatgcagactgctgtgacaggaacacagaaagaaatcattgagggagccacc 2197
QY 1596 tgcgtccttgagtggtgtgcccctgcgaagcttgagacccttccaacatgagtgaagcttac 1655

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DB 2198 tgcgtccttgagtggtgtgagatgctcctgatggagagatcagcagcagacagatgcagat 2257
QY 1656 atctgcacagccttggtgaaacagaagaatgggcaacccaagaagagacactctgtcccca 1715
DB 2258 gccttgatataagtgccctgatgacttctgtccaaatgaaacacacacttctcattccgcc 2317
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DB 2438 cccatgcgtcaaggccacacacacggagacttcttattctcttcttcttcttcttcttctgc 2497
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DB 2498 tgcgttcacagctcccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2557
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DB 2558 cagccgctcttgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2616
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DB 2616 -atcgsgtctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2674
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QY 2256 aacattctcttccatcagtaacttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2315
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QY 2376 gcttcttcaacatgacagcatttaccagggcagctaccctgtgtgtgtgtgtgtgtgtgtgt 2435
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QY 2556 ac 2557
DB 3155 gc 3156

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RESULT 10  
 US-08-353-784-1  
 Sequence 1, Application US/08353784  
 Patent No. 6011068  
 GENERAL INFORMATION:  
 APPLICANT: Edward F. Nemeth, Edward M.



APPLICANT: Brown, Steven C. Hebert,  
APPLICANT: Bradford C. Van Wagenen, Manuel  
APPLICANT: F. Balandrin, Forrest H. Fuller,  
APPLICANT: Eric G. Delmar, and Scott I. Moe  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,784  
FILING DATE: 9 December, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 8  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 209/069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 515..3769  
OTHER INFORMATION:  
US-08-353-784-1  
Query Match 6.4%; Score 176.4; DB 5; length 5275;  
Best Local Similarity 49.0%; Pred. No. 1e-36;  
Matches 530; Conservative 0; Mismatches 546; Indels 6; Gaps 2;  
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QY 1539 gtgttaccacgagactctctgacaggac--cacagggtgtgtgttccaccac 1595  
DB 2138 AACTGCAGTCAAGCTGCTCTGGCAGGACCCAGAAAGAAATCATTTAGGGGAGCCACC 2197  
QY 1596 tgcctcttgatgtgtgtccctgcgaagctggagcccttctcaaatgagtgaattcac 1655  
DB 2198 TGCTGCTTTGAGTGTGTGAATGTCTGATGGGAGTACAGCAGAGACAGATGCAAGT 2257  
QY 1656 atctgcagccttgtaaacagaatgggaccccaaggagagactactgttccca 1715  
DB 2258 GCCTGTGATGATGCTCCTGATGACTTGTGTCATGAGAACCACTTCTGATGCTGCC 2317  
QY 1716 cgaaggtggaggtctctgctgcatgaaccctcttggtggtcaatgaagctaac 1775  
DB 2318 AAGGATCGAGTTCGTGCTGGACCGAGCTTCGGATCGACATCAGCTTTTGTCT 2377  
QY 1776 acgctatgctgctgctgctgtgttgagactgctgctgttggccttgcatltaacaca 1835  
DB 2378 GTGCTGGGCAATTTCTTCACAGCCTTGCTGGCGGTCTTCATCAAGTTCCGACACG 2437  
QY 1836 cctgtagtgaagtcagctggggtagctgtgtctctcatgtcgggttccctgtggcc 1895  
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QY 1896 ggaagttgcaactctctatagcttcttggggagcccaagggcccggtgtcttgct 1955  
DB 2498 TGCTTCTCAGCTCCCTGTTTTCATCGGGAGGCCACGAGCTGAGATGCGCTGCGC 2557  
QY 1956 cagccccccttctctctggtgttgcacatctctctctctctctcgcgaacatcgctcttc 2015  
DB 2558 CAGCGGCGCTTTGGCATCAGCTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 2616  
QY 2016 caactgtcatcatcttcaagtttctacaaagtgccacatctacgtacctggcc 2075  
DB 2616 -ATGGGCTCCTCTGTTGTGAGGCGCAAGTCCACACACTTCCACCGGAAGTGGTG 2674  
QY 2075 caaaacctgtgagctcttctgtatgtgagctcccaaggtcttctatctgt 2135  
DB 2675 GGGCTCAACCTGCAATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2734  
QY 2136 ctcaatgctgttaatgtgaccccaagcccaaggaatacagcgctcccccacat 2195  
DB 2735 GCCATTTGCTCATACAGCGCCGCCCTCGAGCTACCGCAACCAAGCTGGAGACGAG 2794  
QY 2196 ctgtgattctcaggtgcacagaaggtcaactctgtaagctccgtgtgttcaaccac 2255  
DB 2795 ATCATCTTCATCAGCTGCGCAGAGGGCTGCTCATGCGGCTGGGCTTCTGATGGGCTAC 2854  
QY 2256 aacatctccctctcatagtaacctgtgtcagcgtaccgggtlaagaaactgcgaag 2315  
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DB 2915 AACTTCATGAAGCAAGTATCATCCTTCAGCATGCTCATCTTCTTATGCTGTGATC 2974  
QY 2376 gctctctacacatgccaagatttaccagaagcagctacctgctgcygtaaatgtgtg 2435  
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DB 3095 ATCTCTTCAGAGCTTCCCGGAACATGAGAGAGTGGCTGAGACCGCGGCAACAC 3154  
QY 2556 ac 2557  
DB 3155 GC 3156







RESULT 12  
US-08-484-565-2  
Sequence 2, Application US/08484565  
Patent No. 5763569  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,565  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hebert, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 488-1500  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5006 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 436..3699  
OTHER INFORMATION:  
US-08-484-565-2

Query Match 6.1%; Score 170.2; DB 2; Length 5006;  
Best Local Similarity 49.5%; Pred. No. 4,1e-35;  
Matches 498; Conservative 0; Mismatches 503; Indels 6; Gaps 2;

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Qy	1581	gtgtgttcccaacacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1640
Db	2131	GAGGGGAGCCCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2190
Qy	1641	atgagtgaagcttccacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1700
Db	2191	GAGACAGATGCCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2250
Qy	1701	actactgttcccaacagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1760
Db	2251	ACCTCTGATTTGCAAGAGATGAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGT	2310
Qy	1761	ctaatagaagcttaacacagctattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1820
Db	2311	CTCACCTCTTTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2370
Qy	1821	tggcattttcacacacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1880
Db	2371	AAGTTCCGCAACACACCACTTGTCAAGGCCACCAAGAGCTCTCTTACTCTCTC	2430
Qy	1881	gttccctgt	1940
Db	2431	TTTCCCTGTCTCTGT	2490
Qy	1941	gcgt	2000
Db	2491	ACGTCGCGCTGT	2550
Qy	2001	acaatcgccttcccaacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2060
Db	2551	CTGTGTAACCAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2610
Qy	2061	taccgtaccttggt	2120
Db	2611	CACCGCAAGT	2670
Qy	2121	cattgtctatctgt	2180
Db	2671	CAGATTGATCTGT	2730
Qy	2181	caggtgttcccaacactgt	2240
Db	2731	GAGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2790
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Db	2791	TTCTGATGCGCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2850
Qy	2301	aaggaactgccaggaataatgaagccaatgtgtgtgtgtgtgtgtgtgtgtgtgtgt	2360
Db	2851	CGGAAGCTGCCGAGAGACTTCAATGAAGCCAAAGTCACTACCTTACAGATGCTAT	2910
Qy	2361	ttgctatcctgt	2420
Db	2911	TTCTGCTGT	2970
Qy	2421	gcgttcaatgt	2480
Db	2971	GCGGTAGAGGTGATGCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3030
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Db	3031	AACAAGATCTACATCATCTCTTCAAGCCATCCGCAACACCAATGCA 3074	



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QY	1524	caggtgcgtctgtcagtggtgtacacagagactgtctggcaggagac--cacagggttggt	1580						
Db	2071	CAGGGCCCTTCTCCAACTGCAGCCGAGACTGCTGGCAGGACCAAGAAAGGATCATTT	2130						
QY	1581	gtgggttcccaacactgtctgttgtagtgtgtgtccctggcgaagcttggaacttctcaac	1640						
Db	2131	GAGGGGAGCCACACTGCTGCTTTGAGTGTGTGAGTGTCTGTATGGGAGTATAGTAT	2190						
QY	1641	atgagtgagcttcacatctgcagcgccttgttgaaacagaagaattggcaccacaaagagagc	1700						
Db	2191	GAGACAGATGCCAGTATGCTGTATACAGAGGCCACAGATATGATCTGTGTCATATGAGAACAC	2250						
QY	1701	actactgtctcccaagcagcagtgtagttcttggcttggcatgaaccatctcttggtg	1760						
Db	2251	ACCTCTGTCATTGGCCAGAGAGATGAGATTGTGTCTGTGAGAGGACCCCTTTGGGATGCCA	2310						
QY	1761	ctaataagcagtgtaacagcgtatgtctgtgtgtgtgttgtagactgtcgtgaccttggcc	1820						
Db	2311	CTCACCCCTTTGGCCGTGCTGGCATTTTCTGTACAGCCTTTGTGCTGGGTGTATTATC	2370						
QY	1821	tgagcatcttcacacactgttagtgaggtlcaagcttggagtgagcgtgtcttcatagtctg	1880						
Db	2371	AAGTTCGCACACACACCATTGTCTAAGGCCACCAACGAGAGCTCTCTACCTCTCTCTC	2430						
QY	1881	gtctccctcgtgtggccggaagcttcagctctcatatgctctctcggggagcccaagtgacc	1940						
Db	2431	TTTCTCCCTGCTCTGCTGTTCTTCAGCTCCCTGTTCTTCATCTGGGAGACCCCAAGACTGG	2490						
QY	1941	ggcgtgtcgtcgtgcagccccctcttctctcgtgttgacatctctctcgtcgtg	2000						
Db	2491	ACGTGCCCTGTGCCGACGCCGCTTTGGCATAGCTTCGTGATCTGATCTCATATGCATC	2550						
QY	2001	acaatccgctctctccaactgtcatcatcttcaagtcttaccaaagtgccacatc	2060						
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QY	2061	taccgtacctgggcccacaaacatcgtgtgcaagtatctgtcatgttgagcttcacaggtc	2120						
Db	2608	CACCGCAAGTGTGGGGGCTAACCTGCAAGTCTCTGCTGTTTCTCTGCACTTCATG	2667						
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QY	2181	cagagcttcccccactctgtgtatctctgtagagtcagaaagtcgaactctgttaggttctgt	2240						
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QY	2241	ttgagcttcacacacaaactctctctccacatgacttacctcgtctgagcttacctggt	2300						
Db	2788	TTCTCGATCGGCTACACTGCTGCTGCTGCTGCATATCTCTTTCTTTGCTTCAGATCC	2847						
QY	2301	aaggaactgcagagagaactataatgaagcacaatgtgtacacctcaagcgtctctcctaac	2360						
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QY	2421	gcgggtlcaatgtgtcgtgcagaggtctgacacacacttgacggtcttcagcaggttactcttc	2480						
Db	2968	GCCGAGAGGTGATTTGCCATCTGTGCAGCCAGCTTTGGCTTGTGCGGTGATCATCTTCTTC	3027						
QY	2481	cccaaggtctatgtgatctctgcccgtccagaactcaacaatacaga	2527						
Db	3028	AACGAGATCTACATCATCTCTTCAAGGCACATCCGCAACACACATTCGA	3074						



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US-08-943-986-2
RESULT 14
Sequence 2, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCF/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5005 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 436..3699
OTHER INFORMATION:
US-08-943-986-2

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Query Match Similarity	6.1%	Score 170.2	DB 4	Length 5006;
Best Local Similarity	49.5%	Pred. No 4.1e-35;		
Matches 498;	Conservative 0;	Mismatches 503;	Indels 6;	Gaps 2;
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Db	2191	GAGACAGATGCCAGTGCCTGTATCAAGTGCCTCCAGATGTACTTGTGTCATATGAAACAC	2250	
QY	1701	actattgtcttccacagcaggttggatgtctgtgcttggcatgtaaacatctcttgggtg	1760	
Db	2251	ACCTCTGTCATTTGCCAAGAGATTCAGATTTCTGTGTGGACGAGACCTTTGGATGCGA	2310	
QY	1761	ctaatagcagctcaaacagcgtatgttgtctgtcgtgtgttgagctcgtgcgttgttggc	1820	
Db	2311	CTACACCTCTTTGCCGTGTGGGCAATTTTCCGTACAGCCTTTGTGCTGGGTGTGTTATC	2370	
QY	1821	tggcatcttcacacacccctgttagtgagtgacgttggggtagctgtgtctgtctcatgtctg	1880	
Db	2371	AGTTCGCCGACACACCCTATGTCAAGGCCAACACGACGAGACTCTCTACCTCTCTC	2430	
QY	1881	ggctccctcggcggccggaagttgcagctctctatagcctctcttggggagaccaggtgcc	1940	
Db	2431	TTCTCTCTCTCTGTGTGTCTTCTCCAGCTCTCCGTCTTCATCGGGGAGCCCAAGACTTGG	2490	
QY	1941	gggtgtctgtgtgtgcagagccctctctctctccggcttgccattctctctccctcgtgcgtg	2000	
Db	2491	ACGTCCCGCTGTGCGCACCGCGCTTTTGGCAACACACTTCTGTGATCTCATATGATC	2550	
QY	2001	acaatccgctcttccaactgtgtcatcatctcaagttcttaccagaatgtgccaatctc	2060	
Db	2551	CTGGTGAAGAACCAACCGGTCTCTCTGTGTGTAGG---CCAAATATCCCCACACGACTTC	2607	
QY	2061	tacgttactgtggcccacaacacattgtgtgaagttcatctgttcatgttgatcctcaagctc	2120	
Db	2608	CACCCCAAGTGGTGGGGGCTCAACCTGCAGATTTCTGCTCGATTTCTCTGCACTTTCATG	2667	
QY	2121	catctgtcatctctctcacaatgtgttgaatgttgaccaccaagaccacaagaggaatatc	2180	
Db	2668	CAGATTGTCAATGTGTGTATGTGCTTACACCGCGGCCCTCTCAAGTACCGCACACG	2727	
QY	2181	caggcttcccacatctgtgtctctctgagtgccagaaggttcaactctgttagcttctgt	2240	
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QY	2241	tgtgtcttaccacaazacattctctctctctcactagctactactctgttgcagctactggst	2300	
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Db	2848	CGAAGCTGCGCGAAGACTTCATTAAGCGCAAGTTTCATCACTCTTCAAGCATGCTCATCTTC	2907	
QY	2361	tctgatactgtatgtgccttcttcaacatgtgcagcatcttaccagaagagctactgctt	2420	
Db	2908	TTTCATCTGTGGATGTCTCTTCATTCACAGCTATGCGAGACCTATAGGCAAGTTGTCTCT	2967	
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1      RESULT 1577
2      US-08-353-784-2
3      Sequence 2, Application US/08353784
4      Patent No. 6011068
5      GENERAL INFORMATION:
6      APPLICANT: Edward F. Nemeth, Edward M.
7      APPLICANT: Brown, Steven C. Hebert,
8      APPLICANT: Bradford C. Van Wageningen, Mannel
9      APPLICANT: F. Balandrin, Forrest H. Fuller,
10     APPLICANT: Eric G. Delmar, and Scott T. Moe
11     TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
12     MOLECULES
13     NUMBER OF SEQUENCES: 20
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Lyon & Lyon
16     STREET: First Interstate World Center
17     STREET: Suite 4700
18     STREET: 633 West Fifth Street
19     CITY: Los Angeles
20     STATE: California
21     COUNTRY: USA
22     ZIP: 90071
23     COMPUTER READABLE FORM:
24     MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
25     COMPUTER: IBM PC compatible
26     OPERATING SYSTEM: PC-DOS/MS-DOS
27     SOFTWARE: FASTSEQ
28     CURRENT APPLICATION DATA:
29     APPLICATION NUMBER: US/08/353,784
30     FILING DATE: 9 December, 1994
31     CLASSIFICATION: 514
32     PRIOR APPLICATION DATA:
33     PRIOR APPLICATION DATA: Including application
34     PRIOR APPLICATION DATA: described below: 8
35     APPLICATION NUMBER: PCT/US/94/12117
36     FILING DATE: 21 October, 1994
37     APPLICATION NUMBER: U.S. 08/292,827
38     FILING DATE: 23 August, 1994
39     APPLICATION NUMBER: U.S. 08/141,248
40     FILING DATE: 22 October, 1993
41     APPLICATION NUMBER: U.S. 08/009,389
42     FILING DATE: 23 February, 1993
43     APPLICATION NUMBER: U.S. 08/017,127
44     FILING DATE: 12 February, 1993
45     APPLICATION NUMBER: U.S. 07/934,161
46     FILING DATE: 21 August, 1992
47     APPLICATION NUMBER: U.S. 07/834,044
48     FILING DATE: 11 February, 1992
49     APPLICATION NUMBER: U.S. 07/749,451
50     FILING DATE: 23 August, 1991
51     ATTORNEY/AGENT INFORMATION:
52     NAME: Heber, Sheldon O.
53     REGISTRATION NUMBER: 38,179
54     REFERENCE/DOCKET NUMBER: 209/069
55     TELECOMMUNICATION INFORMATION:
56     TELEPHONE: (213) 489-1600
57     TELEFAX: (213) 955-0440
58     TELEX: 67-9510
59     INFORMATION FOR SEQ ID NO: 2:
60     SEQUENCE CHARACTERISTICS:
61     LENGTH: 5006 base pairs
62     TYPE: nucleic acid
63     STRANDEDNESS: single
64     TOPOLOGY: linear
65     MOLECULE TYPE: cDNA to mRNA
66     FEATURE:
67     NAME/KEY: CDS
68     LOCATION: 436..3699
69     OTHER INFORMATION:
70     US-08-353-784-2

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Best Local Similarity 49.58; Pred. No. 4.1e-35;  
Matches 498; Conservative 0; Mismatches 503; Indels 6; Gaps 2

OY	1524	cagggtgcctgtgcagtgatgtatccacgagcctctcgcaggagcaca--cacaggttgatt	1580
Db	2071	CAGGTGCCCTTCTTCCAACTGCACGCGCAGACTGCTCTGCGAGGACCAAGMAAGGATCA	2130
OY	1581	gtgggttcccaacacatgtgctctttgagtgatgtgccctgcgaagctgggaccttctcaac	1640
Db	2131	GAGGGGAGGCCCACTTCGCTCTTGTAGTGTGTGGAGTGTCTCGATGGGAGATATAGTAT	2190
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OY	1701	actactgtctcccaacgaacgagtgagagttcttgagcttgatgaatgaacccatctctgtg	1760
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Db	2608	CACGCGAAGTGGTGGGGGCTCAACCGTAGCTTCGTGCTGTTCTCTGCACTTCATG	2667
OY	2121	catctgtcatctgtctcacatgactgtttaaagtgaaccccaagcaccacaaggagataac	2180
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OY	2181	cagagctcccccacatctcgtgatacttcgcaggtgcagaaagtcaactctgtatgagctctcgt	2240
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• Sun Mar 26 09:26:19 2000

us-09-361-652-4.mri

Page 17

Search completed: March 19, 2000, 18:06:40  
Job time: 1199 sec







GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 18:09:57 ; Search time 185.6 Seconds  
(without alignments)  
3735.357 Million cell updates/sec

Title: US-09-361-652-4  
Perfect score: 2771  
Sequence: 1 attcacatcagaagctgtcgt.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY\_NUC

Searched: 311585 segs, 125096042 residues

Database: N\_Geneseq\_36:\*

Word size: 0

Number of hits that pass the threshold: 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	181.6	6.6	3809	1	T61382	Parathyroid calcitri
2	181.6	6.6	3809	1	T95859	Human parathyroid
3	181.6	6.6	3809	1	V26964	Human parathyroid
4	181.6	6.6	3809	1	V82485	Human parathyroid
5	176.4	6.4	5275	1	T95857	Bovine parathyroid
6	176.4	6.4	5275	1	V26962	Bovine parathyroid
7	176.4	6.4	5275	1	V82483	Bovine parathyroid
8	170.2	6.1	5006	1	T61381	Parathyroid calcitri
9	170.2	6.1	5006	1	T95858	Human parathyroid
10	170.2	6.1	5006	1	V26963	Human parathyroid
11	170.2	6.1	5006	1	V82484	Human parathyroid
12	160.6	5.8	4131	1	T95860	Rat kidney cell ca
13	160.6	5.8	4131	1	V26965	Rat kidney calcium
14	160.6	5.8	4131	1	V82486	Rat parathyroid ca
15	154	5.6	4131	1	T89290	Dogfish shark kidn
16	138.2	5.0	3384	1	T86165	Nucleotide sequenc
17	137	4.9	4000	1	T86166	Nucleotide sequenc
18	113	4.1	2148	1	Q73222	BOPCAR 1, bovine p
19	87.4	3.2	2361	1	X05808	Mouse pheromone re
20	86.6	3.1	2821	1	X05812	Mouse pheromone re
21	85	3.1	3080	1	X05801	Mouse pheromone re
22	85	3.1	2550	1	X05840	Mouse pheromone re
23	84	3.0	2907	1	X05803	Mouse pheromone re
24	84	3.0	2409	1	X05842	Mouse pheromone re
25	81.6	2.9	2732	1	X05810	Mouse pheromone re
26	81.6	2.9	2962	1	X05811	Mouse pheromone re
27	78.2	2.8	1644	1	X05856	Rat pheromone rece
28	78.2	2.8	2811	1	X05817	Rat pheromone rece
29	73.6	2.7	2961	1	X05802	Mouse pheromone re
30	73.6	2.7	2434	1	X05841	Mouse pheromone re
31	73.2	2.6	3919	1	O80418	Human mglur3 DNA
32	73.2	2.6	3410	1	T03887	Human mglur3 DNA
33	73.2	2.6	3108	1	X05814	Mouse pheromone re
34	73.2	2.6	2412	1	X05853	Mouse pheromone re
35	71	2.6	2619	1	T16710	Metabotropic gluta
36	71	2.6	2619	1	T29408	Human metabotropic
37	71	2.6	2734	1	X05809	Mouse pheromone re
38	71	2.6	2773	1	X05813	Mouse pheromone re
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44	67.8	2.4	4085	1	O80419	Human mglur5a cDNA
45	67.8	2.4	4181	1	O80420	Human mglur5b cDNA

RESULT 1  
T61382  
ID T61382 standard; cDNA to mRNA; 3809 BP.

AC T61382;  
DE 22-ARR-1997 (first entry)  
KW Calcium receptor; human parathyroid gland adenoma tumour; pRo2CAR1;  
KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;  
KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;  
KW variant; untranslated region; alternative polyadenylation; probe;  
KW alternative transcription initiation; pRupCAR5.2; pRupCAR4.0;  
KW human Car gene; isoform; ss.  
OS Homo sapiens.  
FH Key  
FT cds  
FT Location/Qualifiers  
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FT /\*tag= a  
FT /product= Calcium receptor  
FT /note= "Pages 94-95 are missing from the specification,  
sequence information was obtained from the Epo"

MO9612697-A2.

PD 02-MAY-1996.  
PF 23-OCT-1995; U13704.  
PR 21-OCT-1994; WO-U12117.  
PR 08-DEC-1994; US-353784.  
PI (NPS-) NPS PHARM INC.  
PI Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC,  
DR WPI: 96-230520/23.  
DR P-PDB: W1889.

PT New di-arylalkyl amine cpds. useful for modulating inorganic ion  
PT receptor activities - esp. for modulating effect of extracellular  
PT calcium on cell surface calcium receptors, useful for treating e.g.  
PT hyperparathyroidism, Paget's disease or osteoporosis  
PS Example 1: Page 93-100; 231pp; English.

CC The sequences given in T61381-82 encode functional calcium receptors.  
CC These sequences were isolated from human parathyroid gland adenoma  
CC tumour using pRo2CAR1 as a hybridisation probe. mRNA was isolated from  
CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism  
CC and two clones of approx. 5 and 4 kb were identified. These cDNA's were  
CC injected into Xenopus oocytes which were assayed for the presence of  
CC functional calcium receptors. Both clone types gave rise to functional  
CC calcium receptors as assessed by the stimulation of calcium-activated  
CC chloride currents upon addition of appropriate calcium receptor agonists,  
CC e.g. NPS R-467 and NPS R-568. Sequence analysis of the two cDNA clones  
CC indicated the existence of at least two sequence variants differing in  
CC the 3' untranslated region and which may result from alternative  
CC polyadenylation. Sequence variation also exists in the 5' end of the  
CC inserts. These sequence differences may have arisen due to alternative  
CC transcription initiation and/or splicing. Three additional sites of  
CC sequence variation occur within the coding regions of cDNA clones  
CC pRupCAR5.2 and pRupCAR4.0 demonstrating that they encode distinct  
CC proteins. Sequence analysis of the human Car gene indicates that the  
CC additional 30 bp in clone pRupCAR5.2 as compared to pRupCAR4.0, results  
CC from alternative mRNA splicing. This alternative splicing is predicted  
CC to insert 10 additional amino acids into the Car protein encoded by  
CC pRupCAR5.2 between residues 536 and 537 of the protein encoded by  
CC pRupCAR4.0. In addition pRupCAR4.0 encodes Gln at position 925 and Gly  
CC at position 990, whereas pRupCAR5.2 encodes Arg at both equivalent  
CC positions. The human Car gene encodes for Gln and Arg respectively at  
CC these positions. These two receptor isoforms may be functionally and/or  
CC pharmacologically distinct.

Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;



Query Match	6.6%;	Score 181.6;	DB 1;	Length 3809;
Best Local Similarity	49.6%;	Pred. No. 4.1e-35;		
Matches 522;	Conservative	0;	Mismatches 524;	Indels 6;
				Gaps 2;

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QY	1539	gtgtgtacacacagcgtctctgacagggac--caagsgtggttgtgtgtccacac	1595
Db	1993	AACGTACGCGAGCTGCTCGGACGGAGACCAGAAAGGATCATTTGAGGGAGGCCACC	2052
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Db	2233	GTGTGTGGGCAATTTCCGACAGCCTTTGTGTGGGTGTATTATCAAGTCCGCACACA	2292
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QY	2076	caaaacatggtgcaggtctatctgcgtcatgtgtcagctccaggtctcatgtctatgt	2135
Db	2530	GGGCTCAACTGCAGTTCCTGTGGTGTTCCTCTGTGACCTTCATCAATTTGATCTGT	2589
QY	2136	ctcacatgcttgtaatgtgaccccaagcaccacacaggaatacagcgtctcccat	2195
Db	2590	GTGATGTGGGTACACCGCGGCCCTCAAGCTACCGGAACACAGAACTGGAGATGAG	2649
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QY 2496 attctctgcgctccagaactcaatacaga 2527  
 ||||| | | ||| | ||  
 Db 2950 ATTCTTCAAGCCATCCCGCAACCATCGA 2981

Query Match	6.6%	Score 181.6	DB 1	Length 3809
Best Local Similarity	49.6%	Pred. No. 4,1e-35		
Matches 522	Conservative 0	Mismatches 524	Indels 6	Gaps 2
DB 1933	CTCTTCACTCAACGAGGAAATCCCTGTGAGTGGTTCCTCAGGAGGAGTGCCTTCTTCC	19922		
DB 1539	gtgtgtacacagagactgtctgtgagagcaac---cacagggtgtgtgtgtgtgtgtccaccac	15958		
DB 1993	AACGTGACGCGGACGACGTGCGGACGAGGACGAGGAAAGGATCATTTAGAGGGAGCCAC	20522		
DB 1536	tgctgtctttagt	16555		
DB 2053	TGCTGCTTTAGGT	21122		
DB 1656	atctgtacagagctgt	17155		
DB 2113	GCTGT	21727		
DB 1716	gcacaggt	17755		



[illegible]

	PR	11-FEB-1992:	US-834044.	
	PR	21-AUG-1992:	US-934161.	
	PR	12-FEB-1993:	US-017127.	
	PR	23-FEB-1993:	US-009389.	
	PR	22-OCT-1993:	US-141248.	
	PR	19-AUG-1994:	US-292827.	
	PR	21-OCT-1994:	WO-012117.	
	PR	08-DEC-1994:	US-353784.	
	PA	(BGHM ) BRIGHAM & WOMENS HOSPITAL.		
	PA	(NPSP-) NPS PHARM INC.		
	PI	Brown EM, Garrett JE, Hebert SC;		
	DR	MPI: 98-347412/30.		
	DR	P-PDSB; W54846.		
	PT	Calcium receptor poly:peptide(s) - useful for drug screening or		
	PT	antibody production		
	PS	Example 27: Fig 49: 174pp: English.		
	CC	The human parathyroid calcium receptor gene encodes a 1078 amino acid		
	CC	protein. The tissue from which the receptor and receptors from bovine		
	CC	parathyroid and rat kidney are derived, respond to changes, and control		
	CC	changes, in calcium ion concentration, e.g. parathyroid hormone regulates		
	CC	Ca2+ homeostasis in blood and extracellular fluid, and kidney function		
	CC	alters through changes in Ca2+ levels in juxtaglomerular and proximal		
	CC	tubule cells in the kidney. The purified receptors (produced		
	CC	recombinantly) can be used to screen for compounds that modulate calcium		
	CC	receptor activity, especially those that can be used to treat diseases		
	CC	associated with the receptors in these tissues. They can also be used		
	CC	to raise antibodies for use in detection assays.		
SQ	Sequence	3809 BP; 910 A; 1071 C; 979 G; 849 T;		
	Query Match	6.6%; Score 181.6; DB 1; Length 3809;		
	Best Local Similarity	49.6%; Pred. No. 4.1e-35;		
	Matches 522; Conservative	0; Mismatches 524; Indels	6; Gaps	2
QY	1479	ctggacataatagaagcaaaatccacgtygcccggaagaacaatcagtgcttcgttca	1538	
DG	1933	ctctttcatcacagagagaaaaatccgtgcactgggtctccaggagagtgccctttccc	1992	
QY	1539	gtgtgtaccacggaactgtctggcagagcac--cacaggttgttgtgtgttccaccaac	1595	
DG	1993	aactgcagccgaacctgcctggcagagcagacaggaalaggaatttgaggsggaccac	2052	
QY	1596	tgtctgttttaagtgtgtccctgtggaagcttggaaccttctcaaatagtgtaccca	1655	
DG	2053	tgcgtgctttgagtggtgcagtgctcctgatgggagatmagatgacacagatgccagt	2112	
QY	1656	atctgcacagctctgtgtgacagagaagaatgtggaccccaggaagacacttgttccca	1715	
DG	2113	gctctgtatmacaagtgcccaaatgactttgtgtccaaatgaaacacacactccttgattg	2172	
QY	1716	cgcacgtgtgagttctgttgcttggcattgaaccacactttgtgtgtaatatgagccta	1775	
DG	2173	aaggaatgcagattttgtgtgcgtgcagcagacccctttgggatgcgacgtacccctttg	2232	
QY	1776	acgctatgtctgtgtctgtctgtgttggaactgtgcgcctgttgcctggcaattccaca	1835	
DG	2233	gtgctggcgcattttcctgtacagacgctttgctggtgtgtgttatcaaatgcgaacaca	2292	
QY	1836	cctgtatgtaggtcagagctgtgggtgtagtgctgtctccacatgtgtggttccctgtg	1895	
DG	2293	ccccattgtcacaggccacacacagcagagcttcttccctcccttcttctctctgtgc	2352	
QY	1896	ggaagtgtgagctgtctatagctcttctcgagagaccagagcgcccgctgtgtcgt	1955	
DG	2353	tgcgttccacagctccctgtttcttcatcgggagacccccacagatggacgtgcgccttc	2412	
QY	1956	cagoccccttctctctgtggtttgcacatcttccctctctcctgtgacaatccgtcttc	2015	
DG	2413	cagcggcgccttttggaatcagcttgcgtgctgtgcatactatcgttcgttgaamaaac	2472	
QY	2016	caactgtatcatcttcaagltttcttaccagaagtgtccacattcatccgttacctgg	2075	
DG	2473	cgtgtcctctctgtgtgttttag--gcgaagaatccccacacactttccacacgaatgtgtg	2529	



QY	2076	caaaacatggtgtaggctcatcttcgcatctgtagagctccaaggtccattgctcatgct	2135
Db	2530	GGGCTCAACCTGCAAGTTCCTCGTGGTTTTCCTGTGCACCTTCATGCATATGTCATCTGT	2589
QY	2136	ctcacatgagcttgaatgctgtagaccaccagagccaccaggaataaccagagcttcccccat	2195
Db	2590	GTGATCTGGCTCTACACCGGGCCCCCTCAGCTACCGCAACGAGAGCTGGAGATGAG	2649
QY	2196	ctggtgattctcgaggtgcagaagggccaactctgtatgagcttcctgttggcttaccacac	2255
Db	2650	ATCATCTTCATCACTACGTCGCAAGAGGGGCTCCCTCATG6CCCTGGGCTTCCTGATCGCTAC	2709
QY	2256	aacattccctccatccatcagctactcgtctgtcagctactcctggtaaagaaatgcacag	2315
Db	2710	ACCTGGCTGGTGGGTGGCCATCTGCTCTTCTTTGGCTTCAATCCCGGAAGCTGCCGGAG	2765
QY	2316	aactataatgaagcacaatgctgtaaccttaacgctgtcctcaactctgtaacctgta	2375
Db	2770	AACCTCATGTAAGGCACAGTTCATCACCTTCAGATGCTCATCTTCATCTGCTGGATC	2829
QY	2376	ggctcttcaacaatgccaacatttaacagggagcttacctgctcgcggtcaatgtgctg	2435
Db	2830	TCCCTCAATCCAGCCATAGCCACACCTAAGGCAAGTTGTCTCTGCGCTAGAGGTGATT	2889
QY	2436	gcaagaggtgcacacaactgagcggcggtcttaacgcygttacctctctcccaagtgcatg	2495
Db	2890	GCCATCTCTGGGAGGACACTTTGGCTGTGGGGGTGCATTTCTTCAACAAAGATCTACATC	2949
QY	2496	attctctgcggtccagaacatccaacaatacaga	2527
Db	2950	ATTCTCTTCAAGCCATCCCGCAACACCATCGA	2981

AC	ID	VS2485	standard; cDNA to mRNA; 3809 BP.
DT	19-MAR-1999	(first entry)	
DE	Human parathyroid calcium receptor	PhuPcar 4.0 encoding cDNA.	
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; KM spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neonatal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle tension; depression; anxiety; ss.		
KW	depression; anxiety; ss.		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension; depression; anxiety; ss.		
OS	Homo sapiens.		
FN	Key	Location/Qualifiers	
FT	CDS	373..3609	
FT		/tag= a	
PN	US5856684-A.		
PD	12-JAN-1999.		
PD	07-JUN-1995.	480751.	
PR	07-JUN-1995.	US-480751.	
PR	23-AUG-1991.	US-749451.	
PR	11-FEB-1992.	US-834044.	
PR	21-AUG-1992.	US-934161.	
PR	12-FEB-1993.	US-017127.	
PR	23-FEB-1993.	US-009389.	
PR	22-OCT-1993.	US-141248.	
PR	19-AUG-1994.	US-282827.	
PR	21-OCT-1994.	WO-012117.	
PR	08-DEC-1994.	US-353784.	
PA	(BGMH ) BRIGHAM & WOMEN'S HOSPITAL.		
PA	(NPSP-) NPS PHARM INC.		
PI	Balandin MF, Brown EM, Del Mar EG, Garrett JE, Hebert SC, Nemeth EF, Van Wagenen BC;		
DR	WPI; 99-119871/10.		
DR	P-PSDB; W89565.		
PT	Screening for calcium receptor-active compounds - by recombinant expression of nucleic acid encoding calcium receptor and determining the effect of nucleic acids on calcium receptor activity		
US	Claim 1; Fig 49; 176pp; Engl15h		

A method has been developed of screening for a compound able to affect one or more activities of a calcium receptor (CR) comprising: (A) contacting a recombinant cell with a test compound, where the recombinant cell comprises a recombinant nucleic acid expressing the CR, provided that the cell does not have functional CR expression from endogenous nucleic acid; (B) determining the ability of the test compound to affect one or more activities of the calcium receptor; and (C) comparing the ability with the ability of the test compound to affect the one or more CR activities in a cell not comprising the recombinant nucleic acid. The present sequence encodes human parathyroid CR, designated a pHPaCR 4.0. The nucleic acid sequence of pHPaCR 4.0 can be used as part of the recombinant nucleic acid in the method described above. The compounds identified can be used to treat diseases or disorders characterised by abnormal calcium homeostasis, e.g. hyperparathyroidism, osteoporosis and other bone and mineral-related disorders. They can also be used for the treatment of diseases and disorders associated with disrupted Ca2+ responses, e.g. seizures, stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in cardiac arrest or neonatal distress, epilepsy, neurodegenerative diseases such as Alzheimer's disease, Huntington's disease and Parkinson's disease, dementia, muscle tension, depression, and anxiety. Sequence 3809 BP, 910 A, 1071 C, 979 G, 849 T.

Query Match	6.68;	Score 181.6;	DB 1;	Length 3809;
Best Local Similarity	49.68;	Pred. No. 4.1e-35;		
Matches 522; Conservative	0;	Mismatches 524;	Indels 6;	Gaps 2

QY	1479	ctgcaataatgaagcaaaaatccatccatctggcaagggaagaacatcaggtgcgtgca	1538
Db	1333	ctcttcttcaacagcagagaaatccctgttgagatgggtttctcagggaagtgcccttcttc	1932
QY	1539	gtgtgtaccacgactgtctctggcaaggca--cacagggtgtgtgtgtgtccaccac	1595
Db	1993	aactgcacgcgaagactcctggcagggaccaggaaaggatcattgaggggagccacc	2052
QY	1596	tgcgtcttgagtggttgccttcggcaagcttggaaccttctcaaatgagtgagcttac	1655
Db	2053	tgcgtctttagtggttgagtgctcctgattgggagatgtagtaagaacacagatgcagt	2112
QY	1656	atctgcacgccttgtagaacagaaatgttgacccaaaggagagacactactgttccca	1715
Db	2113	gcctgtaacagtgagccacagatgactctctggtccattgagaacacacctcctggattgcc	2172
QY	1716	cgcacgttgaggtctcttgctcttgcatgaaccactctcttggtgtctaatagcagctaac	1775
Db	2173	aagagatcagattttctgtcgttgagacggacccttggagatgcactacacctctttggcc	2232
QY	1776	acgtatgtgtgtcgtcgtgtgttggaactgtgcgcctgtgttgccttgcatcttaaca	1835
Db	2233	gtcgtgggcattttcctgacagocctttgtcgtgggtgtgtttatcaatttccgcaacaca	2292
QY	1836	ccctgtagtgagtcagcgtcgtgggtgaagcgtctctctcctcaatgctgggttccctgtggcc	1895
Db	2293	cccatgtgtcagagccacacacgagacgactctcactcctcctcctcctcctcctgtgc	2352
QY	1896	ggaagtgcagcgtctctatagctctcttcggggagaccacagtgcccggtgtgttgctggt	1955
Db	2353	tgcgtctccacgctcctcctgtttcttcatcggggagccccaagactggacactgccctgcgc	2412
QY	1956	cagcccccctctctctctcgtggttgcaactctcctctccctcgtctacaaatccgctcttc	2015
Db	2413	cagccgccttttgcatcagctcttgcgtctgcattctatgatcattcgtggtaaaacacac	2472
QY	2016	caactggtatcatctctcaagtcttcttaaccaagtgccccacatcttaacgttaactggcc	2075
Db	2473	cgtgtcctcctctgtgtttgag--gcacaagatccccaccagcttccacccgaagtggtgg	2539
QY	2076	caaaaccaaigtgcaggtctatctgcgtacatgtcagcgtccaaagtcattgtctatcgt	2135
Db	2530	gggcctcaacctgcagttcctcgtctgttttccctctgcaccttcatgacaattgtctatcgt	2589
QY	2136	ctcaatggtcttgtaatgtggaaccocacagaccacacaggaataaccagcgtctccocat	2195







QY	2496	attctctgcgcgcgaactcaacatcagagaccttctgagctcattcagacacac	2555
Db	3095	ATCCCTTCAAGACCTTCCCGGACACATCGAGAGGTGCTGCAACGACCGGCGACAC	3154
QY	2556	ac 2557	
Db	3155	GC 3156	
RESULT	6		
ID	V26962	standard; cDNA to mRNA; 5275 BP.	
AC	V26962		
DT	01-SEP-1998	(first entry)	
DE	Bovine parathyroid calcium receptor 1 gene 5kb fragment.		
KW	ss; calcium ion concentration; parathyroid hormone; homeostasis;		
OS	kidney; calcium receptor; detection.		
FS	Bos sp.		
FT	Key	Location/Qualifiers	
FT	CDS	515..3772	
FT	/*tag= a		
FT	/product=	"BOPCAR 1 5kb fragment"	
PN	US5763569-A.		
PD	09-JUN-1998.		
PR	07-JUN-1995; 484565.		
PR	07-JUN-1995; US-484565.		
PR	23-AUG-1991; US-749451.		
PR	11-FEB-1992; US-834044.		
PR	21-AUG-1992; US-934161.		
PR	12-FEB-1993; US-017127.		
PR	23-FEB-1993; US-009389.		
PR	22-OCT-1993; US-141248.		
PR	19-AUG-1994; US-292827.		
PR	21-OCT-1994; WO-012117.		
PR	08-DEC-1994; US-353784.		
PA	(BGM ) BRIGHAM & WOMENS HOSPITAL.		
PA	(NPS-) NPS PHARM INC.		
PI	Brown EM, Garrett JC, Hebert SC;		
PI	WPI; 98-347412/30.		
DR	P-PSDB: W54844.		
PT	Calcium receptor poly:peptide(s) - useful for drug screening or		
PT	antibody production		
PS	Example 25; Fig 47; 174pp; English.		
CC	The bovine parathyroid calcium receptor gene encodes a 1085 amino acid		
CC	protein. The tissue from which this receptor and receptors from human		
CC	parathyroid and rat kidney are derived, respond to changes, and control		
CC	changes, in calcium ion concentration, e.g. parathyroid hormone regulates		
CC	Ca2+ homeostasis in blood and extracellular fluid, and kidney function		
CC	alters through changes in Ca2+ levels in juxtaomericular and proximal		
CC	tubule cells in the kidney. The purified receptors (produced		
CC	recombinantly) can be used to screen for compounds that modulate calcium		
CC	receptor activity, especially those that can be used to treat diseases		
CC	associated with the receptors in these tissues. They can also be used		
CC	to raise antibodies for use in detection assays.		
SD	Sequence 5275 BP; 1277 A; 1475 C; 1516 G; 1207 T;		
Query Match	6.4%;	Score 176.4;	DB 1; Length 5275;
Best Local Similarity	49.0%;	Pred. No. 8.9e-34;	
Matches 530; Conservative	0;	Mismatches 546;	Indels 6; Gaps 2;
QY	1479	ctggaacataaataagaacaaatccatgagcagcggaagaacaatcaggtgcctgtgtca	1538
Db	2078	CTCTTCATCAACATGAGTGAAGAAAAATTTGTGAGATGATTCTCAAGGAGGTGCTTCTCC	2137
QY	1539	gtgttaccacagagatgtctgtgcagagcacc--cacaggtgtgtgtgtgtccacacc	1595
Db	2138	AACCTCAGTCCGAGATGCTGCTGCGACGGACCCAGAAAGCATATTATGAGGGAGCCAC	2197
QY	1596	tgtgtcttgaagatgtgtgtccctgcgaagcgtggagaccttctcaaatagtgtagcttca	1655
Db	2198	TGCTGCTTTGAGTGTGTGGAATGTCTCTGATGGGAGATACAGCAGCAGACATGCAAGT	2257

QY	1656	atggccagcgcctgtggaacaagaatgagaccaccaaggagagagactactgtgtcca	1715
Db	2258	GCCTGTATTAAGTGTCCCTCATGTACTTCTGTGCAATGAAACACACATCTCTGGATGCC	2317
QY	1716	cgacaggtggaagctcttggtcttgacatgagaccacatctcttggctgtaataagacgtaac	1775
Db	2318	AAGAGATGAGATTGTGTGTGTGGACCGAGCCCTTGGGATGGACATCAGCTCTTTGCT	2377
QY	1776	acgctatgtcgtcgtcgtcgtcgtcgttggaactgctgcgtcgttgccttgacattcaaca	1835
Db	2378	GTGTGTGGGCAATTTTCCATCACAGCCTTCGTGCGGGCGCTTCATCAAGTTCCGCAACAG	2437
QY	1836	ccttagtgaagtcacgtggyggtaagctgtgtccctcaatcagtgtgtccctgtagtgc	1895
Db	2438	CCCATGCTCAAGGCGACACAAACGGAGAGCTCTCATCTCTCTCTCTCTCTCTCTCTCTGCG	2497
QY	1896	ggaagttgcagctctcatagctctcttcggygagcccaagtgcccgcgtctgtcgt	1955
Db	2498	TGCTTCTCCAGAGCTCCCTGTCTTCTATCCGGGGAGCCCGAGATGAGCTGCGCGCTGCGC	2557
QY	1956	cagcgcctctctctcgtcgttggtgcacatcttcctcctcgtcgtcgtcaatcgccttc	2015
Db	2558	CAGCGGCGCTTTTGGCATACAGCTTCGTGCTCTGCAATCTGTGATCTTGTAANAACA--	2616
QY	2016	caactgtgtacatctctcaagtttctacaaagtgycacaatctacacgtacgtgagcc	2075
Db	2616	-ATCGGGGCTCCGNGHTTGGAGGCCAAGATTCCACACAGCTTCCACGGAGNGHGG	2674
QY	2076	caaaacatggtgcaggtcctatcgtcatgtcagctcagctcaggtcattgtctatcgt	2135
Db	2675	GGGCTCAACCTGCAAGTTCCGTGCGTGTCTCTCTGTGACCTTTCATGCAATTGTATCTGT	2734
QY	2136	ctcacatggtctgtaaltgtagaaccccaacagccacacaggaatlacagcagctccocat	2195
Db	2735	GCCATTTGGGTCAATACAGAGGCCCCCTCGAGCTACCGGAACAGAGAGCTGAGAGAGAG	2794
QY	2196	ctgtgtatctctgaaatgacagaaggtcaactgttagcttccgttgyctttcaaccac	2255
Db	2795	ATCATCTTCATACACCTCCACGAGGGGCTGCTCATAGGCGCTGGGCTTCTGATGGCTAC	2854
QY	2256	aacatctccctccatcagtaactacctctcgtctcgtcagctacgttgytaagaaactgcagag	2315
Db	2855	ACCTGCTGCTGGCGCGGCACATCTGCTTCTTCTTGCCCTTCAATCCCGGAGACTGCGAGAG	2914
QY	2316	aactataagaaagccaatgtgtcacctcaacgtcgtctccctcaactcgtatccgtgac	2375
Db	2915	AACCTCATGAGGCCAAGTTCATCACCTTCACATGCTCATCTTCTTCATGCTGTGATC	2974
QY	2376	gcctcttcaacaatgacagcaattcaacagggagagctacgtcgtcgtgtaatgtgctg	2435
Db	2975	TCTTTATCCCGGCTACAGCCACACTTACGGCAGATTGTGTCTTGCCGTGAGGTGATC	3034
QY	2436	gcagaggtgcacacaactgagcagcgtgcttcaacggttactcctccccaagtgtcatgtg	2495
Db	3035	GCCATCCGAGGGGCGACACTTGTGCTTGTGCGGTGATCTTCTTCACAGAGGTGATATC	3094
QY	2496	attctctgcgtccagaactcaacatcacagaacatttcagcgtctcatccaggtacac	2555
Db	3095	ATCCTCTTCAAGCCTTCCCGGAACCCATTCAGAGAGTGCGCTGAGCACCAGCGGACACAC	3154
QY	2556	ac 2557	
Db	3155	GC 3156	
RESULT 7			
ID V82483 standard: cDNA to mRNA: 5275 BP.			
AC V82483:			
DE 19-MAR-1999 (first entry)			
KW Bovine parathyroid calcium receptor BoPar 1 encoding cDNA.			
parathyroid calcium receptor; inorganic ion receptor; osteoporosis;			
calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;			



Query Match	6.4%	Score 176.4	DB 1	Length 5275
Best Local Similarity	49.0%	Pred. NO. 8.9e-34		
Matches 530:	Conservative 0	Mismatches 546	Indels 6	Gaps 2
QY 1479	ctggaacataataagaacaaaatccagctgacggaagaacaaatcagctgtgtca	1538		
DB 2078	ctcttcacatcgaatgaaataaattctgtgagctgcattctcaaggagtgctttcttc	2137		
QY 1539	gtgtgtacacagagctgtctgtgcgaagc---cacaggtgtgtgtgtgtccaccac	1595		
DB 2138	aactcagctgcagactgctcttgccagggacacgaagaagatcatttgaggggagccacc	2197		
QY 1596	tgtcgtcttgaatgtgtgtccctgcgaagcttggaaccttccaatgtgtagcttacc	1655		
DB 2198	tctctgttgaatgtgtgtgaatgtcttcttatgtgggagctaaaggacagacaaatgcacct	2257		
QY 1556	attctgcagccttgtgtgaacagaagaatgtggaccccaaggaagagactactgtcttcca	1715		

Db	2258	GCCTGTATTAAGTGCCCTGATGACTCTTCTGTCCAAATGAGAACCAACTTCTCGATCGCC	2317
Qy	1716	cgcaaggctggagctctctgcctctgcacagaccatctcttggctaatagaaagctaac	1775
Db	2318	AAGAGATCGAGTTTCTGTGTGGACGAGCCCTTGGATGGCACTCAGCGTCTTTCT	2377
Qy	1776	aagctaatgctgctgctgctgctgcttggagactgctggcctgttgcctgcaatttcaaca	1835
Db	2378	GTGCTGGGCAATTTTCTTCACAGAGCCCTTCGTGCTGGGGCTCTTCATCAAGTTCGGACACAG	2437
Qy	1836	cccttagtagagcgcaagctgggggttagcgtgtctctctcatgctgctgctgctgtagcc	1895
Db	2438	CCCATCGTCAAGGCGACCAACCGGAGCTCTCTATCTCTCTTCTCTTCTCCCTGCTGTGC	2497
Qy	1896	ggaagttgcagctctctataagctctcttcgsgagaccacagtgctcccgctgct-tgtgct	1955
Db	2498	TGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGAGATGGACATGCGCGCTGGCG	2557
Qy	1956	caagccctctttctctcctgggtttgccaactctctctctctctctgacctgacaatccgctcttc	2015
Db	2558	CAGCGGCGCTTGGCATTACACTCTCGTGTCTGCAATCTCGTCATCTCTGTGAAACCA--	2616
Qy	2016	caactgtcatcatctctcaagctttctaccagagtgcccacacttaccgtactcgtggcc	2075
Db	2616	-ATGGGGTCTCTCGTGCTGTTTGAAGGCAAGATTCCACCAAGCTTCCACCGGAAAGTGCG	2674
Qy	2076	caaacacatgctcgaagctctatcgtctatcgtcatctgcagctccacgtcatctgctatcgt	2135
Db	2675	GGGCTCAACTGCAAGTTCTCGTGGTCTTCTCTGCACTTATGCAATTTGTCATCTGT	2734
Qy	2136	ctcacatgctgtttaatgtagaccaccaagaccacacaggaatacaagcgtctcccccat	2195
Db	2735	GCAATTGGCTCAATACAGAGGCCCTCTGGAGCTACCGCAACCAAGACCTGGAGGACGAG	2794
Qy	2196	ctgtgtgactctcgaagtgacagaaggtcacaactctgaagcttccgtgtgccttaaccac	2255
Db	2795	ATCATCTTCATACCTGCGCACGAGGGCTGCTCATGCGCGCTTGCGTTCGATCGGCTAC	2854
Qy	2256	aacactctctctccatcagtaacctctcgctcgtcagctgacctggtgaagaaactgcagag	2315
Db	2855	ACCTGCTTGGCTGGCGGCATCTGCTTCTTCTTGCGCTTCAAGTCCCGGAAGCTGCCAAG	2914
Qy	2316	aactataatgaagccaatgtgtcaccttcaagctgcttccctaactcgtatccctgagtc	2375
Db	2915	AACCTCATGAGCAAGTTCATCACCTTCACAGATGCTATGTTCTCATGCTGTGAGATC	2974
Qy	2376	gcctctctccacatgcccagcaacttaacagsgcagctacactgctcgtggctaatgtcgt	2435
Db	2975	TCTTTCACTCCCGCCCTACGCGCACACTTTCAGGCAAGTTGCTGTGCGGTGAGGTGATC	3034
Qy	2436	gcgaaggtgacacacacgacgagcgagcttcacaggttactctctctcccaagtgtcatgtg	2495
Db	3035	GCAATCTCTGGGGGCGACGCTTTGGCTGTGCTGGCTGTGATTTTTCACAAAGGCTCAATC	3094
Qy	2496	attctctgcctccagaactcaactcaaatlaagaacacttcaagcctctacacagactac	2555
Db	3095	ATCTCTTCAAGCTTCCCGGAACACATCATGAGGAGGTGCGTGGAGACCGCGGCGACAC	3154
Qy	2556	ac 2557	
Db	3155	GC 3156	
RESULT 8			
ID T61381 standard; cDNA to mRNA; 5006 BP.			
T61381			
AC T61381;			
DT 22-APR-1997 (first entry)			
DE Parathyroid calcium receptor coding sequence clone plupcar5.2			
KW Calcium receptor; human parathyroid gland adenoma tumour; pBOPcar1;			
KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;			
KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;			
KW variant; untranslated region; alternative polyadenylation; probe;			



















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Db 2614 CAGCTGCTTTGGCATGAGCTTTGCTCTATCTGTCATCTTGGTGAAGCAAT 2673
QY 2016 caactgcatcatcttcaagttcttcaagaagtcacacatctacagtcctggcc 2075
Db 2674 CGCGTCTGCTGATTTGA---AGCAAGATACCCACAGGTTCCACCGAAGGGTGG 2730
QY 2076 caaaccatgctgagcttctatctgcatctgcaagtcacagctcattgtctatct 2135
Db 2731 GGGCTCAACCTGACATTCCTGCTGTTTCCCTCACCCTTCATCAGATCTCTATGCG 2790
QY 2136 ctacatgctgcttgaatctgagaccacagaccacaggaatatacagctctcccat 2195
Db 2791 ATCATCTGGCTTACACGGCGCCGCCCTCTAGCTACCGCAACCAAGATGGAAGAGAA 2850
QY 2196 ctggtgattctcgatgacagaaggtcaactctgtagctctctctgtgcttccacac 2255
Db 2851 ATCATCTTATCATGCTGCATGAGGGCTCATCATGAGCACTTGGCTCCCTGATCGGCTAT 2910
QY 2256 aacattctctctcactcaagtaactctgctgctgacagctacacgtggaaggaactgcagag 2315
Db 2911 ACCTGCTGCTGGCTGCGCATCTGCTTCTTCTTGGCTTCAAGTCCAGGAAGTTACCAAG 2970
QY 2316 aactaatgaagcaaatgctgacacttgaagctgctgctcctcaacttgtaactctgagtc 2375
Db 2971 AACTTCAAGCAAGCCAAAGTTCAATACCTTACAGATGCTCATCTTCTCATGCTTGAGTC 3030
QY 2376 gctctcttcaacatgctgacagcaacttcaagagcaactacactgctgctgctcaatgctg 2435
Db 3031 TCGTTCAATCCAGCTTATGCGACGACCTACGCAAGTTGTGTGCGGTAGAGTGAATC 3090
QY 2436 gcaaggtgacacacactgaagcggtctcagcggttactctctcccaagtgctatgtg 2495
Db 3091 GCCATTTTGGCAGCGCTTGGCTTACTAGCTTCATCTTCTTCAAGGCTTACATTT 3150
QY 2496 attctctgctgctgacgaactcaacatacagaacacttcaagctctcatc 2556
Db 3151 ATCTCTTCAAGCTTCCCGAAGACCATGTGAGAGTCCGCTCCAGCAACC 3201

RESULT 13
V26965
ID V26965 standard: cDNA to mRNA; 4131 BP.
AC V26965;
DT 01-SEP-1998 (first entry)
DE Rat kidney calcium receptor 3A gene 4Kb fragment.
KW ss; calcium ion concentration; parathyroid hormone; homeostasis;
KM kidney: calcium receptor; detection.
OS Rattus sp.
FH Key Location/Qualifiers
FT 574..3813
FT CDS /tag- a
FT /product= "PRAKAR 3A 4Kb fragment"

US7635569-A.
09-JUN-1998.
07-JUN-1995. 484565.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGMH) BRIGHAM & WOMENS HOSPITAL.
PA (NPS) NPS PHARM INC.
PI Brown EM, Garrett JE, Hebert SC;
DR P-PSDB; W54847.
PT Calcium receptor poly(peptide)s - useful for drug screening or
PT antibody production
PS Example 30; Fig 50; 17app; English.

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CC The rat kidney calcium receptor gene encodes a 1079 amino acid protein.
CC The tissue from which this receptor and receptors from bovine parathyroid
CC and rat kidney are derived, respond to changes, and control changes, in
CC calcium ion concentration, e.g. parathyroid hormone regulates Ca2+
CC homeostasis in blood and extracellular fluid, and kidney function alters
CC through changes in Ca2+ levels in juxtaglomerular and proximal tubule
CC cells in the kidney. The purified receptors (produced
CC recombinantly) can be used to screen for compounds that modulate calcium
CC receptor activity, especially those that can be used to treat diseases
CC associated with the receptors in these tissues. They can also be used
CC to raise antibodies for use in detection assays.
SQ Sequence 4131 BP; 988 A; 1170 C; 1052 G; 921 T;

Query Match 5.8%; Score 160.6; DB 1; Length 4131;
Best Local Similarity 48.2%; Pred. No. 6e-30;
Matches 516; Conservative 0; Mismatches 549; Indels 6; Gaps 2;

QY 1479 ctgacataaataagacaaaatcagtgacagcggaagaacatcagctgctgtgca 1538
Db 2134 CTCTTCAATCAATGAGAGAAAGATCTTGAGAGTGGTTCTCCAGAGAGTGCTTCTCC 2193
QY 1539 gtgtgacacagagctgtctgacagggcacacaggtgtgtt---ggattccacacac 1595
Db 2194 AATTGCAAGCCGGGACTGTCAAGGACGAGCAAGAGGGGATCATCAGGAGAGAGCCACCC 2253
QY 1596 tgcgtcttgatgtgtgcccctgcaagctggagaccccttcaacatgagtgaacttcac 1655
Db 2254 TGCGCTTTTGAAGTGTGAGAGTGTCTGATGAGATGAGATGAGAGACAGATGCGAGT 2313
QY 1656 atctgcaagcctgttgaaacaaagaatgggacccaaggaagaaactactgtgtccca 1715
Db 2314 GCGTGTGACAAGTCCCGAGATGACTTGCTGCTCAATGAGAACCACTTCTTGATGCGC 2373
QY 1716 cgcacggtgaggttctggtgtgcatgaacacatccttgtgtcctaagaagcctaac 1775
Db 2374 AAGGAGATGTAGTTCTGGCGTGAGCGAGCGACCTTGGAATCGCTCACTCTTTGCG 2433
QY 1776 acgctatgctgctgctgctggtgagctgctgctgttgcgtgcaatttcacaca 1835
Db 2434 GTGCTGGGCAATTTCTCGACCGCTTGTGTGCTGGGTCTTTCATCAAGTTCCGAACACA 2493
QY 1836 cctgtagtgaagtcagctggtggtgagctgtgtcttctcaatgctggttccctgtggtc 1895
Db 2494 CCRATGCAAGGCGACCAACCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2553
QY 1896 ggaagttgacgctctatagcttctcgggagagccacaggtgcccgtgtctgtgtcgt 1955
Db 2554 TGCTTCTCAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2613
QY 1956 cagccctcttctctcgggttgcacatctctctcctcctgacctgaatccgctcttc 2015
Db 2614 CAGCTGCTTTCGGGATCAGCTTGTGCTGTATCTGTGATCTGTGATGAGAGCAAT 2673
QY 2016 caactgcatcatcttcaagtttcttcaagaagtcacacatctacgcgttaccgtggcc 2075
Db 2674 CGCGTCTGCTGATTTGA---AGCAAGATACCCACAGGCTTCCACCGAAGTGGTGG 2730
QY 2076 caaaccatgctgagcttctatctgcatctgcaagtcacagctcattgtctatctgt 2135
Db 2731 GGGCTCAACCTGACATTCCTGCTGTTTCCCTCACCCTTCATCAGATCTCTATGCG 2790
QY 2136 ctacatgctgcttgaatctgagaccacagaccacaggaatatacagctctcccat 2195
Db 2791 ATCATCTGGCTTACACGGCGCCGCCCTCTAGCTACCGCAACCAAGATGGAAGAGAA 2850
QY 2196 ctggtgattctcgatgacagaaggtcaactctgtagctctctctgtgcttccacac 2255
Db 2851 ATCATCTTATCATGCTGCATGAGGGCTCATCATGAGCACTTGGCTCCCTGATCGGCTAT 2910
QY 2256 aacattctctctcactcaagtaactctgctgctgacagctacacgtggaaggaactgcagag 2315
Db 2911 ACCTGCTGCTGGCTGCGCATCTGCTTCTTCTTGGCTTCAAGTCCAGGAAGTTACCAAG 2970

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OY	2316	aataatgagcaaaatgtgcatactggccttccctaactcgatcctgacac	2375
Db	2971	AACCTCAACGAGACCAGCATTTACTTACCTTCAGCATTGCTATCTTTTCATCGTGTGGATC	3030
OY	2376	gcctcttcaccatgycgaagcatltaacaggagcagctacctgcgtggtcaatgtgcgt	2435
Db	3031	TCCCTCATTTCCAGGCCTATGCCAGACACCTACGGCAAGTTGTCGTGGCGTAGAGTGATC	3090
OY	2436	gcagggcctgaccacacgcagcgcgcgcgttacccggttaactctcccagaagtctatgc	2495
Db	3091	GCCATTTTGGCAGGCAGCTTTGGCTTACTAGCCATCTTCTTTCACAACGAAGTCTCATTT	3150
OY	2496	attctcgcgcgtccagaactcacacaatafagaagaacttaagccttcacac	2546
Db	3151	ATCCTCTTAAGCCTTCGCCGAAACACCATTTGAGAAATCGCTTCCAAGACC	3201
RESULT	14		
ID	V82486		
AC	V82486	standard; cDNA to mRNA; 4131 BP.	
DT	19-MAR-1999	(first entry)	
DE	Rat parathyroid calcium receptor prakcar 3A encoding cDNA.		
KW	Parathyroid calcium receptor; Inorganic ion receptor; osteoporosis;		
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;		
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;		
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;		
KW	depression; anxiety; ss.		
OS	Rattus sp.		
FH	Key	Location/Qualifiers	
FT	CDS	574..3813	
ET		/tag= a	
PN	US5858684-A.		
PD	12-JAN-1999.		
PF	07-JUN-1995; 480751.		
PR	07-JUN-1995; US-480751.		
PR	23-AUG-1991; US-749451.		
PR	11-FEB-1992; US-834044.		
PR	21-AUG-1992; US-934161.		
PR	12-FEB-1993; US-011727.		
PR	23-FEB-1993; US-009389.		
PR	22-OCT-1993; US-141248.		
PR	19-AUG-1994; US-292827.		
PR	21-OCT-1994; WO-012117.		
PR	08-DEC-1994; US-353784.		
PA	(BGM ) BRIGHAM & WOMENS HOSPITAL.		
PI	(NPSF-) NPS PHARM INC.		
PI	Balandin MF, Brown EM, Del Mar EG, Garrett JE,		
DR	Hebert SC, Nemeth EF, Van Wagenen BC;		
DR	WPI: 99-119871/10.		
PT	PFSDB: W89565.		
PT	Screening for calcium receptor active compounds - by recombinant		
PT	expression of nucleic acid encoding calcium receptor and determining		
PT	the effect of compounds on calcium receptor activity		
PS	Claim 1: Fig 50: 176pp. English.		
CC	A method has been developed of screening for a compound able to affect		
CC	one or more activities of a calcium receptor (CR) comprises: (A)		
CC	contacting a recombinant cell with a test compound, where the		
CC	recombinant cell comprises a recombinant nucleic acid expressing the		
CC	provided that the cell does not have functional CR expression from		
CC	endogenous nucleic acid; (B) determining the ability of the test		
CC	compound to affect one or more activities of the calcium receptor; and		
CC	(C) comparing the ability with the ability of the test compound to		
CC	affect the one or more CR activities in a cell not comprising the		
CC	recombinant nucleic acid. The present sequence encodes rat		
CC	parathyroid CR, designated a PrakCar 3A. The nucleic acid sequence of		
CC	PrakCar 3A can be used as part of the recombinant nucleic acid in the		
CC	method described above. The compounds identified can be used to treat		
CC	diseases or disorders characterised by abnormal calcium homeostasis, e.g.		
CC	hyperparathyroidism, osteoporosis and other bone and mineral-related		
CC	disorders they can also be used for the treatment of diseases and		

CC	disorders associated with disrupted Ca <sup>2+</sup> responses, e.g. seizures,
CC	stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in
CC	cardiac arrest or neonatal distress, epilepsy, neurodegenerative
CC	diseases such as Alzheimer's disease, Huntington's disease and
CC	Parkinson's disease, dementia, muscle tension, depression, and anxiety.
SQ	Sequence 4131 BP; 988 A; 1170 C; 1052 G; 921 T;

Query Match	5.8%	Score 160.6;	DB 1;	Length 4131;
Best Local Similarity	48.2%;	Pred. No. 6e-30;		
Matches 516;	Conservative 0;	Mismatches 549;	Indels 6;	Gaps 2;
QY	1479	ctggacataataaaagacaaaaatccaggcgcgaaggaagaacacacagtggtctgtgta	1538	
Db	2134	CTCTTATCAAGAGAGAGAAGATTGTTGGAGATGGGTTCCTCCAGAGAGTGCTTTCTCC	2193	
QY	1539	gtgttacacagactctctgtgcaaggacccaagaagt-gtgtt---ggattcccaccac	1595	
Db	2194	AATTGCACCGGAGATGTCACAGCAGGACCAAGAAAGGGATCATCGAGGAAAGGCCACC	2253	
QY	1596	tgtctcttgaagtgtgttcctcgcaagaatggaaacctttctaacaatgatgagttcac	1655	
Db	2254	TCTGCTTTGAAGTGTGGAGTAGTGTCTGATGAGAGTACAGTGGAGAGACATGGAGT	2313	
QY	1656	atctgcceagccctgtggaacagaaaatgaggacaccaagaagagagactactgtctcca	1715	
Db	2314	GCTTGTGACAAAGTCCCGGATGACTTTCGTGCTCAATGAGAACACACTTTCGCAATGCC	2373	
QY	1716	cgcacgtagagttcttgcttgtagcatbaaaccatctcttfgtgctaaatagcagtaac	1775	
Db	2374	AAGGAGATTGAATTCTGTGCGTGGACCGAGCCCTTTGGAATGCTCTCACTCTTTTGGC	2433	
QY	1776	agcctatlgctgtcgtcgtgtltggaactgtgcgcgtgtlgtccctggcatlltcaaca	1835	
Db	2434	GTGTGGGGGATTTTCTCTGACGCCCTTTGTCGTGGGTGTCTTATCAAGTCCGAAACA	2493	
QY	1836	cctgtatgtagagtcacgctggggatgagctgtgct+ccctaaatgctgggttccctgtgcc	1895	
Db	2494	CCTATCGTCMAAGGCCACCAACCGAGAACTGTCCTACTCTCTTCCCTACTCTGTC	2553	
QY	1896	ggaagtltgagttctatatagctctcttgsgygagcccaaggtgccccgtgtctgttgcgt	1955	
Db	2554	TCTTCTTCAGTCTCTTGTCTTCAATGGGGAGCCCCAAGACTGAGCGTCCGCTGGCA	2613	
QY	1956	caagccctctttctctcgggttttgcacatctccctcccgctgaacaatccgcctcttc	2015	
Db	2614	CAGCCTGCTTTGGGATCAGCTTTGTGCTCTATCTGCTGATCTTGGTGAAGACAAAT	2673	
QY	2016	caactgylcatcatlctcaagt+tttctaccaagtgccacaatlctaccgtacctgggcc	2075	
Db	2574	CGCGTCTCTCTGGTATTGTA--AGCCAAGATAACCCACAGCTCCACGGGAAGTGGTG	2730	
QY	2076	caaaaccaaagtgcaggtcttatctgtcatlgtlcagctcccaagtlccattgtctatcgt	2135	
Db	2731	GGGCTCAACCTGCAGATCTCTGCTGTTTTCTCTCACACTTCATCAGATCTCTACTGTC	2790	
QY	2136	ctcatatgagcttgaatgtggaaccacagaccacaaaggaataacagagctctcccat	2195	
Db	2791	ATCATCTGGCTTAACAGGCGCCCCCTCTTACTTACCTTCCGCAACATGAGCTGGAAGACGA	2850	
QY	2196	ctggtgatctcgaatgcaagaggtlcaactlgtgagcttccgtltgtgctttcacccac	2255	
Db	2851	ATCATCTTCATACAGTGCATGAGGGCTCACATCATGAGCACTTGGCTCCCTATGGGCTAT	2910	
QY	2256	aacatctccctcccatcaagtaectctgtctcgagctacatggttaagaaactgtccagag	2315	
Db	2911	ACCTCCCTGCTGGCCATCTGCTTCTTCTTTCCTTCATCATCAGGAAGATTACAGAG	2970	
QY	2316	aactaataagagaacaatgtgtaaccttcaagccctgc+cctcaactctgtatccggatc	2375	
Db	2971	AACCTTCAAGGAAGCCAAAGTTCATTACCTTACGATGCTCATCTTTTTCATGCTGGATC	3030	
QY	2376	gcctcttccacatgycagcagcatllaccagaggaagctlaactgtccgtggtaeatlgtcy	2435	



Db	3031	TCCTATTCCAGGCTATGCGCAGACCTACGGCAAGTTGTCTGTGGCCTAGAGTGATC	3090
Oy	2436	gcaggcgtcaccacactgacggcgcggtcctcaagcgcttactctccccaagtgcata	2495
Db	3091	GCCATTTTGGCAGCGACGACTTTGGCTACTAGCCTGCATCTCTTCACACAGGCTACACAT	3150
Oy	2496	attctcgcgcgtccagacactcaccaataacagacacttcaggccctccatc	2546
Db	3151	ATCCTCTTCAAGCCTTCCGGGAACACCATTTGAGAGAGTCCGCTCCAGCAC	3201
RESULT	15		
ID	T89290		
AC	T89290:	standard: cDNA: 4131 BP.	
DT	27-MAR-1998	(first entry)	
DE	Dogfish shark kidney calcium receptor related protein cDNA.		
KW	dogfish receptor related protein; Car-RP; dogfish shark; SKCa-RP;		
KW	polycation-sensing receptor; aquaculture; fish farming;		
KW	salinity tolerance; ss.		
OS	Squalus acanthias.		
PH	key	location/Qualifiers	
FT	CDS	439..3519	
FT		/*tag= a	
FT		4076..4113	
FT		/*tag= b	
PN	MO9735977-A1.		
PD	02-OCT-1997.		
PF	27-MAR-1997:	U05031.	
PR	27-MAR-1996:	U05622738.	
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.		
PI	Brown E, Harris HW, Hebert S;		
PI	WPI: 97-489640/45.		
DR	P-SDB: W32059.		
PT	New isolated Aquatic polyvalent cation-sensing receptor - used to		
PT	develop products for increasing or decreasing the salinity tolerance		
PT	of fish for use in aquaculture		
PS	Claim 2: Fig 4A-F: 57pp: English.		
CC	This cDNA clone codes for dogfish shark kidney calcium receptor		
CC	related protein (SKCa-RP, see W32059), an aquatic polyvalent		
CC	cation-sensing receptor (PVCaR). It was isolated from a shark		
CC	kidney cDNA library using a rat kidney calcium receptor cDNA as		
CC	probe. Also claimed are: a probe comprising the 4131 bp SKCa-RP		
CC	sequence. An isolated PVCaR present in the plasma membranes of		
CC	aquatic species, especially on the apical membrane of epithelial		
CC	cells of elasmobranch fish, particularly from cells found in the		
CC	collecting duct or late distal tubule in the kidney, intestine,		
CC	gill, rectal gland, gonad or brain; an antibody that specifically		
CC	binds to a PVCaR; and a method of screening for aquatic PVCaR		
CC	agonists and antagonists. Modulation of the expression of the		
CC	aquatic PVCaR activates or inhibits aquatic PVCaR mediated ion		
CC	transport and endocrine changes that permit fish to adapt to fresh		
CC	or salt water. The method facilitates the aquaculture of marine		
CC	fish and can provide for the development of marine fish that are		
CC	easily adaptable to fresh water aquaculture.		
CC	Sequence 4131 BP: 1028 A; 1161 C; 1019 G; 923 T;		

Query Match	5.68;	Score 154;	DB 1;	length 4131;
Best Local Similarity	47.78;	Pred. No. 2.5e-28;		
Matches 516; Conservative	0;	Mismatches 560;	Indels 6;	Gaps 2

QY 1479 ctgacctaataagcaaaaacacacagctgcaacggagaagaacaacacagctgctgtgca 1558  
Db 2020 CTCACACTCAACGAAAGAAAATCCTCTGTGAGTGGCTTCTCCAAAGTGCTCTTTCTCC 2079  
QY 1539 gctgtatccacggactgtctctgacagggac--cacaggtgtgttctgttccaccac 1595  
Db 2080 AACTGCAGTGCAGACGTGTGCGCGGGACACAGGAAGGGATCATGAGGGGGAGCCACAC 2139  
QY 1596 tctctgctttgagtgtgtgtccctcggaagcttggaccttctcaacatgaatgaagcttcac 1655

D	2140	TGCTGCTTTAAATGATGGATGTGTGACGAGGGAGAGTTCAATGATGAAAGATGCAAGT	2139
Q	1556	atctgcagccctgtgtggaacagaatgtggacacccaaagagaactacttgcctcca	1715
D	2200	GCGTGTCAAAAGTGCCCGGAATGATTTCTGTGTGAATGAGAACACATCGTGATCGCC	2259
Q	1716	cgacaggtgaattcttgcgttggttgacatgagaccactctcttggctgtataagactaac	1775
D	2260	AAGGAGATCAGTAACTGTGTGTGAGAGGAGCCCTTGGGATGCTTCAACCATCTTGCC	2319
Q	1776	acgcatattgctgtcgtcgtcgtgtgtggaactgtgcgcgtgttgccttggcatattcacaca	1835
D	2320	GTACTGGGATCCTGATCAACACTCTCTCGTGCTGGGGGCTCTTCATCAAGTTAGGAACACT	2379
Q	1856	cccttagttaggttcaagctgtgggttaggtcgtgtcttccctcaagctgtgttccctgttgcc	1885
D	2380	CCCATCTGTGAAGGCAACAAACGGGAGTGTCTCACTGTGCTCTCTTCTCCTCATCTGC	2439
Q	1896	ggaagtgcagcgtctctatagctctcttcggtggagacacagtggtcccggtgtgttcgtgt	1955
D	2440	TGCTTTCACAGCTCGCTCATCTTCATCGGCGAGGCCAGGAGTGAACCTGTGCGCTCGC	2499
Q	1956	caagccctctttctctcgtggttttgcaactcttcctccgtgcctgacacacgcgtcttc	2015
D	2500	CAACGGCGCTTTGGATCAACCTTCGTGCTGATCTCTGATCTCTGATCTCTGTGAAGCAAC	2559
Q	2016	caactgtcatcatcttcaagcttcttaccagaagtggtcccaattaccgttaacttgggc	2075
D	2560	CGGTTGTGTGTGCTTCGAG--GCCAAGATGCCACACAGCTCCACCGCAAGTGGGTG	2616
Q	2076	caaaacatgttgcaagctcatctgcgtcatctgtgcacgtccagtgctcatcttgcactgt	2135
D	2617	GGCCTCAACTGAGTTCCTCCCGTGCTTCCTGTGATCTCTGTGAATGTCAACTCGC	2676
Q	2136	ctcaatgtgctttaaitygagaccocagacccacacaggaaatacagcgcttccccat	2195
D	2677	ATCATCTGCGCTACACCGCGCTCCCTCCACATCAAGAACCAAGACTGGAGACGAG	2736
Q	2196	ctgtgtgtctctgagtgagacagaggtgcaactctgtgagcttctcgttgcgttcttaaccac	2255
D	2737	GTCATCTTCAACCTGTCCAGCGAGGGCTGTGCTATGCGCGCTTGCGCTTCATGCGCTAC	2796
Q	2256	aacatctccctccacacagtaactctgcgtctgcagtaactgtgtaagaaactgcagag	2315
D	2797	ACCTGCGCTCTCGCGCGCATCTGCTCTTCTTGCGCTTCATGCCGTAAGCTGCGGAG	2856
Q	2316	aactataatgaagccaaatgtgtcaccttcagcctgtcctcctaactctgtaactcgtgact	2375
D	2857	AACCTCAACAGAGCTAAGTTCAATCAACCTTCACAGCATGTGATTTCTTCATGTGTGATC	2916
Q	2376	ggcctcttgaacatgccaagcatattacagggcagcctacgtccctggtggttaatgtgtg	2435
D	2917	TCTCTTCACTCCCGCATATGTCAACCACTTCGGCAAGTTGTGTCCGCGGTGAGGTGATT	2976
Q	2436	gcagagtgtagccacacttgaagcgtggtcttcagcpgtlaactcctcccaagtgtcatgtg	2495
D	2977	GGCATCTCTGGCGTCAAGCTTGGCGGCGTGTGGGCTGCATTTACTTCAACAAGTTACTC	3036
Q	2496	attctctgccttccagaaactcaacaatatagaacactttcaggtctccatccaggaactac	2555
D	3037	ATCTCTGTTCAAGCGGTGCGGTAAACACATCAAGAGAGGTGTGCGCTGCAGACGGCGCCAC	3096
Q	2556	ac 2557	
D	3097	GC 3098	

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Job time: 2882 sec



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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 00:19:26 ; Search time 3521.68 Seconds  
(without alignments)  
-2389.150 Million cell updates/sec

Title: US-09-361-652-4  
Perfect score: 2771  
Sequence: 1 attcacatcagagctgtgct.....aaaaaaaaaaaaaaaaaaaaa 2771

Scoring table: IDENTITY\_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenBank.\*

Word size: 0

Number of hits that pass the threshold: 1642386

1: gb\_bal:\*  
2: gb\_ba2:\*  
3: gb\_om:\*  
4: gb\_ov:\*  
5: gb\_pac:\*  
6: gb\_ph:\*  
7: gb\_p11:\*  
8: gb\_p12:\*  
9: gb\_p13:\*  
10: gb\_p14:\*  
11: gb\_p15:\*  
12: gb\_ro:\*  
13: gb\_sts:\*  
14: gb\_sy:\*  
15: gb\_un:\*  
16: gb\_vl:\*  
17: em\_fun:\*  
18: em\_hum1:\*  
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20: em\_in:\*  
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28: em\_sts:\*  
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32: gb\_hg1:\*  
33: gb\_hg2:\*  
34: gb\_in1:\*  
35: gb\_in2:\*  
36: em\_bal:\*  
37: em\_ba2:\*  
38: em\_hum3:\*  
39: em\_hum4:\*  
40: gb\_p14:\*  
41: gb\_hg3:\*  
42: gb\_hg4:\*  
43: gb\_hg5:\*  
44: gb\_hg6:\*  
45: gb\_hg7:\*  
46: em\_hg1:\*  
47: em\_hg2:\*  
48: em\_hg3:\*  
49: em\_hum5:\*

50: gb\_p13:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2520	90.2	2520	12	AF127389	AF127389 Rattus no
2	447.6	16.2	2529	12	AF127390	AF127390 Rattus no
3	185.8	6.7	270	13	G09859	G09859 human STS C
4	181.6	6.6	3809	5	AR012624	AR012624 Sequence
5	181.6	6.6	3809	5	AR028467	AR028467 Sequence
6	181.6	6.6	3809	5	I75053	I75053 Sequence 3
7	181.6	6.6	3361	9	HUMCASR	D50355 Human mRNA
8	181.6	6.6	3783	10	HSU20759	U20759 Human parat
9	181.6	6.5	3234	10	S83175	S83175 CaSR-calcitri
10	180	6.4	5249	3	HSPCAR1	X81086 H. sapiens
11	176.4	6.4	5249	3	S67307	S67307 Ca(2+)-sens
12	176.4	6.4	5275	5	AR012622	AR012622 Sequence
13	176.4	6.4	5275	5	AR028465	AR028465 Sequence
14	176.4	6.4	5275	5	I75051	I75051 Sequence 1
15	172.4	6.2	4319	12	AF110179	AF110179 Mus muscu
16	170.2	6.1	5006	5	AR012623	AR012623 Sequence
17	170.2	6.1	5006	5	AR028466	AR028466 Sequence
18	170.2	6.1	5006	5	I75052	I75052 Sequence 2
19	170.2	6.1	5009	10	HSU20760	U20760 Human extra
20	170.2	6.1	5009	13	G28586	G28586 human STS S
21	169.8	6.1	4550	12	AF110178	AF110178 Mus muscu
22	168.2	6.1	3569	12	AF128842	AF128842 Mus muscu
23	160.0	5.8	4131	5	AR012625	AR012625 Sequence
24	160.0	5.8	4131	5	AR028468	AR028468 Sequence
25	160.5	5.8	4131	5	I75054	I75054 Sequence 4
26	160.6	5.8	3761	12	RNU20289	U20289 Rattus norv
27	160.6	5.6	3106	10	HSU20289	U20289 Rattus norv
28	154	4.8	798	40	HSU20289	U20289 Rattus norv
29	133.2	4.8	798	40	S81755	S81755 human Krupp
30	114.4	4.1	2815	4	AF083081	AF083081 Carassius
31	113	4.1	2148	5	A73577	A73577 Sequence 1
32	107.6	3.9	4981	4	AB008859	AB008859 Fugu rubr
33	107.2	3.9	761	12	AB027140	AB027140 Mus muscu
34	105.2	3.8	2568	12	AF053985	AF053985 Mus muscu
35	98.8	3.6	2785	4	AF083080	AF083080 Carassius
36	98.4	3.6	4781	4	AB008860	AB008860 Fugu rubr
37	98.2	3.5	4743	4	AB008862	AB008862 Fugu rubr
38	90.2	3.3	3506	4	AB008857	AB008857 Fugu rubr
39	90.2	3.3	2739	12	AF053986	AF053986 Mus muscu
40	89.4	3.2	1786	4	AF083084	AF083084 Carassius
41	88	3.2	927	4	AB009044	AB009044 Fugu rubr
42	87.4	3.2	2561	12	AF011418	AF011418 Mus muscu
43	86.6	3.1	2821	12	AF011422	AF011422 Mus muscu
44	85.6	3.1	753	4	AB009041	AB009041 Fugu rubr
45	85	3.1	3080	12	AF011411	AF011411 Mus muscu

## ALIGNMENTS

RESULT 1  
AF127389 AF127389 2520 bp mRNA ROD 04-MAR-1999  
LOCUS Rattus norvegicus putative taste receptor TRL mRNA, partial cds.  
DEFINITION AF127389  
ACCESSION AF127389  
VERSION AF127389.1 GI:4337085  
KEYWORDS  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 2520)



AUTHORS	Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J. and Zuker,C.S.
TITLE	Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity
JOURNAL	Cell 96 (4), 541-551 (1999)
MEDLINE	99159821
REFERENCE	2 (bases 1 to 2520)
AUTHORS	Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J.P. and Zuker,C.S.
TITLE	Direct Submission
JOURNAL	Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA
FEATURES	Location/Qualifiers
source	1. .2520

CDS

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/cell_type="Circumvallate papilla"
1..>2520
/note="G protein-coupled receptor"
/codon_start=1
/product="putative taste receptor TR1"
/protein_id="F04916.0"

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BASE COUNT	479 a	749 c	676 g	616 t
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Query Match	90.9%;	Score 2520;	DB 12;	Length 2520;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2520;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	1	ATGCTCTTTCGGGCTGCTCACTCTCTCAAGCTTGCAGTTGGTCTACTGCTGGGCTTTC	60
OY	117	agctgcacaagagacagatcctctccaggcttcagccttactctgggagcttcctctctgca	176
Db	61	AGCTGCACAAAGACAGAGATCCTCTCCAGGGCTTCAGCCTTCTGGGGACTTCCTCTTGA	120
OY	177	ggtctgtttctccctccaatggtgatgtgtctgaaagtggacacagactctgtgtgcaagt	236
Db	121	GGTGTGTTCTCCCTCCACATGGTGACTGTGAGGTGAGACACACACCTCTGGTGACAAAT	180
OY	237	tgtgacaagcccgacagcttcaacgagcattgctacacacctctctcaagcatalgacgttc	296
Db	181	TGTGACAGGCCCGACAGCTTCAAGGGCGATGGCTACACACCTTCCAGAGCATGGGTTTC	240
OY	297	actgttgagagataaacaactcctctggccctgtctcccaacatcacctctggggtatgag	356
Db	241	ACTGTTGGGAGAAATAACATCTCTCGGCCCTCGTCTCCCAACATCACCTCTGGGGTATGAG	300
OY	357	ctgtacagacggtgctctcaagaatctggcacaatgtgatatcacacccctgagaggtcttgccctg	416
Db	301	CTGTACGACGtGTGCTCAGATTCGTGCCAATGTGATGCACACCTCGAAGGAGTCTTGCCCTG	360
OY	417	caagggcccccgcacatagagatatcaagaagacctctgcaacacacactctctcaagtgatg	476

Db	361	CAAGGCCCCGCACATAGAGATACGAAAGACCTTCGAAACCACTCCTCCAAAGTGGTG	420
QY	477	gcttcaatcgggacctgacaacaactgacacagcgtgtaactaccgctgacctgctggtlect	536
Db	421	GCGTTACATGCGGCGCTGACAACTGACACACGCGTGCATACCGGTGCGTTGGTGGTCTT	480
QY	537	ttctctgatgcacctgtgtcagctatgagcgcaagcagcgtgtactaagtgtgccaaagcgcaag	596
Db	481	TTCTCGATGCCCCCTGGTCACCTATGAGGCAACAGGTGTCTCATGAGCCAAAGGCGAAG	540
QY	597	ttccgcgcttccctctgttaacgcgtcccccagtgagccgacacaggtggaagtcatgtgtgag	656
Db	541	TTCCCGGCTTTTCTCTGTAACCGTCCCACTGACCGGACACAGGTGGAAGTCAATGTTGACG	600
QY	657	ctctgtcagaagtttgggtgtgtgtgtatcgtcgtcaattgtgagcctaaagctagtgatgacgg	716
Db	601	CTCGTGCAGAGTTTGGGTGGGTGTGTGATCTGCTCATTTGGCAGCTTAGCGATTAACGGG	660
QY	717	cagctgtgtgtgtcgaagcgctgtgagaagctgtgcccgtgcccggtggacatctgtcgcttc	776
Db	661	CAGCTGGGTGTGCAAGGCGCTGTGAGAGCTGTGGCGCTGTGCCCGGGCGATGTGGTGCCTTC	720
QY	777	aaggaacgtgtgctctctctctctgcccgggtgtgggtgacccgagatcagacatgattgacg	836
Db	721	AAGGACATCGTGCTTTCTCTGCCCCGGGTGGGTGACCCGAGATCAGACATGATTGACG	780
QY	837	catctgtgctcaaggccaggaacacacgctgtgtgtgtgtctctcacaacccggcacctgtgtaga	896
Db	781	CATCTGGCTCAGGCGCAGGACCAACGATGTGTGTGTCTTCTAACCGGACACTGGCTAGA	840
QY	887	gtgtttcttcaggttccgt	956
Db	841	GTTGTTCTTCAGGTCCTCGTGTGCTGTGGCCAACTGACTGGCAAGGTGTGGGTGCGCTTCACAA	900
QY	957	gaatgggacatctccaaagtacatccaccagcgtgactgggagatccaaagatctgggaaggtgt	1016
Db	901	GACTGGGCACTTCACAGTACATCACACAGTGAAGTGGATCTCAAGGCAATTGGAGCGGTG	960
QY	1017	ctcgtgtgtggccgttccagcagaagacacccctgtggtctgaagagtttgaggagttcttat	1076
Db	961	CTCGGTGTGGCCGTCACAGCAAGACAAAGTCCCGGGCTTAAGAGATTTGAGGAGGTCTAT	1020
QY	1077	gtcagggcgttaacaagctgtctccagcgctgtgccggagggttccctgtgtgcaagcaataac	1136
Db	1021	GTCAGGGCTGTAAACAGCTGCTCCACACGCGTTGCCGAGAGGGTCTCTGTGACAGCACTAAC	1080
QY	1137	cagctgtgtccgggaagtgtcccaacggttcaagaatctgtaaacatcccaagcttggagaccttc	1196
Db	1081	CAGCTGTGGCGGGAGTGCACACAGTTCACAGACTCGTAACATCCCAACGCTTGGAACTTTC	1140
QY	1197	tccaatgagtcgcccactcaagagtataatgagcgtgtgtactgcgtgtgtgtgccacgacctcac	1256
Db	1141	TCCATGAGTCCCGCTACAAAGTATGAGAGGTGTATACGTGTGGCCCAAGGCGCTCAC	1200
QY	1257	caagctccvggaatgtactcttgagatcgtgtccagaagcccaagctctaacccctgtgacgtt	1316
Db	1201	CAGCTCTCGGAATGTACTTCTGTGAGTCTGTCCAGAGGCCAGTCTACCCCTGGACGCTT	1260
QY	1317	cttaagaagatctacaagtgtaatttctcttaaatggaataacgtgtgaattgtatgac	1376
Db	1261	CTTAGAGAGATCTAACAGGTGAATTTTCTTACATGAGAAATACGTGGCATTTGATGTAC	1320
QY	1377	aacgggacaactaaagtattactacagcatcatcgcctgtgagactgtgaatggagacctgaatgtg	1436
Db	1321	AACGGGACACTAGTATCTACTACGACATCATTCGCTGGGACTGGAATGGACTGTAAAGG	1380
QY	1437	acctttgagatcaltgtgtctgtccatcgtgtccagtltcatcaltgtgacataataataagaca	1496
Db	1381	ACCTTTGAGATCATTTGGCTCTGCGCTCACTGCTCCAGTTCATCTGGACATTAATTAAGACA	1440
QY	1497	aaaatccagtgtgcaagcggaagaacaatactcaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1556
Db	1441	AAAATCCAGTGGACGCGGAAGCAATCAAGGTGCGCTGTCTCATGTGTGTACCAACGACGACT	1500



[illegible]

DEFINITION	Rattus norvegicus putative taste receptor TR2 mRNA, partial cds.
ACCESSION	AF127390
VERSION	AF127390.1 GI:4337087
KEYWORDS	.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 2529)
AUTHORS	Hoon/M.A., Adler/E., Lindemeier/J., Battey,J.F., Ryba,N.J. and Zuker,C.S.
TITLE	Putative mammalian taste receptors: a class of taste-specific GPCRs with distinct topographic selectivity
JOURNAL MEDLINE REFERENCE AUTHORS	Cell 96 (4), 541-551 (1999) Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J.P. and Zuker,C.S. Direct Submission Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA
FEATURES	location/Qualifiers source 1..2529 /organism="Rattus norvegicus" /strain="Wistar" /db_xref="taxon:10116" /cell-type="circumvallate papilla" 1..>2529 /note="G protein-coupled receptor" /codon_start=1 /product="putative taste receptor TR2" /protein_id="AA18070.1" /db_xref="GI:4337088" /translation="MGPOARTLLLSJLHVLPKGLVENSDEHLADYDLGGLEFTLVNANKSHSLYLQVPCKNEPTMKVSGYNMQAKRFVEELNNSSLLPVLIGYEWDVCNLNSHGILGFPAODDDLDPLIKDYOIMHYAVAGPNSEALIVSNLSHF LIPOTTSAISDKLRDRHRHPKSRLTPSATSRTHLEANVOLMVRÖNMWIVLVSDDT GRENSHLSORLTSTDSICIAFOEVLIPESSEOQRÖDNLIIDRIKRTSARVV VPESELTSFSEFEHEVLWMVFMLASSMDAPVLNTLETHTGELEGVIQHVV SIPEOSFRVRROKPGYPVNITNLRTCCNDCACLNTKSFENILLGERERVSV YSAIYAVALHRLRGNRCTOKXYPMÖLBREIHVMVTTLGNRLFDOGDMPML LDIIOMQMDSONPROSIASYSPTSRLTYINNVSXPTNNITYVMCSKCSCQGOM KKSJLHCPCEBLCDCMPGYLYLNABEFNCLOPSGSMSKYNDTCÖRPYLENH KEPIPVAILLAALAEFSFLAILEFWRHFGT PWRVASGGECFLMVPLLATGMVPP YVGSPTEASCRCQAEPFTCVFCISLCISTYRSFYGVCFMARLPSAYSMRYHQPY VFVAETIALKVALLVGNMLATTNPGRIDDOPNMTLICBNYNGLFNTSMÖL LVSATGFPAMKEKLPTNNNAKFILLSWFESTSISICTEWGVHDVLVTIMDLL VTYNFLAIGLGIRGPCKYMILPFPEPNTSAFNMSIQGTTRMS"
CDS	BASE COUNT 497 a 826 c 623 g 583 t ORIGIN
Query Match	16.2%; Score 447.6; DB: 12; Length 2529;
Best Local Similarity	51.6%; Pred. No. 1,4e-93;
Matches 1266; Conservative	0; Mismatches 1144; Indels 42; Gaps 9;
OY	142 cagagctcagcccttccttggaacctccccttgcaggctgctttccctcatagttagat 201
DB	83 CTGATTTCCACTGCAGCGGGAGCATCCTTGCGTAGGCCCTTTTACCCTCCATGCCAACG 142
OY	202 gtctgcaggtagagaca--cagaaccttgtgtgacaaagtltgtacagggcccgacagctca 258
DB	143 TGAAAGAAGATCTCCCACCTCAGCTACCTGACGAGGTGCCCAAAGTGAATAAGATTACAACATGA 202
OY	255 aeggccaaigcctaacaccctttccaagccaaigcggttacctggttgaggaagataaacact 318
DB	203 AGGTGTGGGCTACAACTCATGACGAGGCATGCGCTTGCTGTGAGGAGAAGATCAACAACACT 262
OY	319 ccctggscctgcttcaccaaatcacccctggsgtatcaagcttlacagacttgcttaagatat 378
DB	263 GTAGCTCCCTGCTACTCCGGCGGCTGCTGCGGTACGAGATAGTGGATGTCGTGTAACCTCT 322
OY	379 ctggcaaatgtgtatgccacccctgaggtgtcctgtcccttcagaaggggcccgccacatalagaga 438



DB 323 CCAACAATATCCACCTGGGGCTTACTTCTGGACAGGAGC---ACGACCTCTTGCCCA 379  
QY 439 tacaagaagaccttcgaacacactccccaaggtggtgcttcatactggcctgagaca 498  
DB 380 TCTCAAGACTTACAGCACTGATGCTCCCAAGGTGGCTGATTTGGCCCGCACT 439  
QY 499 ctgacacagctgtcaactacagcttgcttggtggttccttcctgatatccctgtcaact 558  
DB 440 CTGAGTCCGCAATATACCGTGTCCAAATCTCTCTCATTTCTCTATCCACAGATCAT 499  
QY 559 ataaggaagacaggtgtgtactcaagtgcgaagcgcaagttccgctcttcctgtaacg 618  
DB 500 ACAAGCGCAATCTCGACMACTGGGGACAAGCGCACTTCCTCCAGCATCTACGCAAG 559  
QY 619 tcccacatgacgagcaccaggtggaggtgatgtgacagctgcgcagagtttggtggg 678  
DB 560 TGCCCAAGCCGACCCACCAATCAATGAGCCATGGTGAAGTGAATGTTCACTTCCAAATGA 619  
QY 679 tgtgatactgcctcaatgtgacgtacgtgtatgagagc---agctgtgtgtgagagcgc 735  
DB 620 ACTGATTTGTGTGTGTGTGAGCAGACGATTAAGGCGCGAGAACAGCACACCTGTTGA 679  
QY 736 tgaagagagctgagccgtgtgccccggagactgtgcgtccctcaaggaacatgtgcttct 755  
DB 680 GCCAGGCTGTGACCAAAACAGAGCACTGTGATTTGCCTTCCAGAGAGTTCTGCCATAC 739  
QY 796 ct-----gcccgggtgggtgagccgagga-----tgcagagcatgatgagc 837  
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QY 838 atctggtcagagcgaagacacagctgtgtgtgtctctctctaaacggcaccctgtgagag 897  
DB 800 AGCTGGGGCGAGCTCTGGCCGCGTGTGTGTGTCTGCCGACCTGAGCCTGATA 859  
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DB 860 GCTTCTTTCAAGAGGTGCTCGCTGTAACGTTACGGGTTTGTGTGTGTGTGTGTGTGTGT 919  
QY 958 actgggacatcccaacgtatcacacagcgtgagctgagctaccaaagcattggagagctgc 1017  
DB 920 CCGGGGTATCAACCCAGCTTCTGATTAACCTCAGAGAGCTGCGCACAGGGATACTTTTC 979  
QY 1018 tccgtgtgtgcgtccagcagagaacatccctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1077  
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QY 1138 agctgt 1197  
DB 1094 AGGACGTGTGAGGCTGTGTTAACAACCAAGTCTTCAACACATCTTATACTTTTCG 1153  
QY 1198 ccaatgtgtgcgtccatacagaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1257  
DB 1154 GGGAGGCGGT 1213  
QY 1258 agcttctgt 1317  
DB 1214 GACTTCTGGCTGTAAACGGGTCGCTGACCAAGAAAAGTCTTACCTCGAGAGCTAC 1273  
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DB 1394 CTTTCCAAAGCATGCGCTCTTATTTCTC---CCACCAAGAGAGGCTAACCTATTAACA 1450  
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DB 1451 ATGTGTCTGT 1510  
QY 1558 tggcagagcaccacaaggt 1617  
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QY 1618 gcaagctgt 1674  
DB 1571 GTATGCCAGGACACTTCAACCAACCGCTCAGAGATGATTACTGTCTGTCTGCCCG 1630  
QY 1675 cagaagaatgggacaccagaaggaaggaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1734  
DB 1631 GTTCCATGT 1690  
QY 1735 ctgtgatatgaaccatctcttctgt 1794  
DB 1691 AGTGGACGAAGTGGCCACCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1750  
QY 1795 tgt 1854  
DB 1751 CACTGGCAATTTCTTTCATCTCTGTGAGACATTTCCAGACCCATGAGTGTGCGCTGCG 1810  
QY 1855 ggggt 1914  
DB 1811 GTGGCCCATGT 1870  
QY 1915 gcttctcggggagcccaagctgt 1974  
DB 1871 TGTATGTGGGGGCCCCCAGGCTTCTTCATGCTTGTGCGAGAGGCTTCTTACCGCT 1930  
QY 1975 ggttctcacttct 2034  
DB 1931 GCTTCTTCATCTGTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1990  
QY 2035 agttcttcaacaagtggtccacatcttcaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2094  
DB 1991 AGATGGCCAGAGCGGCTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2050  
QY 2095 taticgtatgt 2151  
DB 2051 TCTTGT 2110  
QY 2152 tgt 2211  
DB 2111 CCACCATCAACCCCATTTGGCCGAGCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2170  
QY 2212 gcaagaggtcaactctgt 2271  
DB 2171 GCCACCTTAACATCCGCAAGGGCTACTGTTCACACCAAGATGAGTGTGTGTGTGTGTGT 2230  
QY 2272 tcaagacttctgt 2331  
DB 2231 TGCTGT 2290  
QY 2332 aatgt 2391  
DB 2291 AGTTTCACTCTCAAGCATGAGCTTCTTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCT 2350  
QY 2392 ccagacttaccagagcagctacgt 2451  
DB 2351 TGCTGT 2410  
QY 2452 tgaagcgt 2511  
DB 2411 TCTGTGCAATGCGCTTGGGATATTGGCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2470  
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DB 2471 AGCGAACACCTCAGCTTCTTCAATGATGATGATCAGGGCTTACACCATGAG 2522



RESULT	3
G09859/c	
LOCUS	G09859 270 bp DNA STS 15-AUG-1995
DEFINITION	human STS CHIC.GCT15G02.P16729 clone GCT15G02.
ACCESSION	G09859
VERSION	G09859.1 GI:941708
KEYWORDS	STS sequence; primer: sequence tagged site. human vector;pJcPl host=E.coli dltung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
SOURCE	Homo sapiens Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
ORGANISM	Catarrhini; Hominoideae; Homo. 1 (bases 1 to 270)
REFERENCE	Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buelow,K.H. Cooperative Human Linkage Center Unpublished (1995) Synonyms: GCT15G02, CHIC.GCT15G02.T16713 Contact: Dr. Jeffrey C. Murray ucf
AUTHORS	The University of Iowa Department of Pediatrics, Iowa City, IA 52242, USA Tel.: (319) 356-3508 Fax: (319) 356-3347 Email: jeff-murray@uiowa.edu
JOURNAL	
COMMENT	Primer A: CTCACCACAGCGGTCTCTAG Primer B: TGGTGTTTGCTTGCC STS size: 124 PCR Profile:  denature: 30 seconds at 94 degrees C annealing: 75 seconds at 55 degrees C extension: 15 seconds at 72 degrees C PCR cycles: 27 extension: 6 minutes at 72 degress C  Protocol:  Template: 30ng genomic DNA Primer: each 1.5 pmole dNTPs: each 200 uM Tag polymerase: 0.3 units Total Vol: 10 ul  Buffer:  MgCl2: 1.5mM KCl: 50mM Tris: 10mM pH: 8.3.  Location/Qualifiers 1..270 /organism="Homo sapiens" STS primer_bind 95..218 primer_bind 95..114 complement(201..218) BASE COUNT 66 a 90 c 75 g 39 t ORIGIN
FEATURES	
source	Location/Qualifiers 1..270 /organism="Homo sapiens"
STS	95..218
primer_bind	95..114
primer_bind	complement(201..218)
BASE COUNT	66 a 90 c 75 g 39 t
ORIGIN	
Query Match	6.7% Score 185.8; DB 13; Length 270;
Best Local Similarity	80.7%; Pred.No.6.ee-33;
Matches 217; Conservative	0; Mismatches 52; Indels 0; Gaps 0;
OY	1671 ggacagaagaattggagcccaaggagagcacactactgtcttccacagcaggttgagtgc 1730
Db	270 GGGAAGAAGATGGGCACCTGAGGAAAGCCAGACTGCTTCGCCGCACTGTGRTT 211
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DEFINITION	Sequence 3 from patent US 5763569.			
ACCESSION	AR012624			
VERSION	AR012624.1	GI:3970614		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 3809)			
TITLE	Brown,E.M., Herbert,S.C. and Garrett,J.E. Jr.			
JOURNAL	Calcium receptor active molecules			
FEATURES	Patent: US 5763569-A 3 09-JUN-1998;			
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Query Match 6.6%; Score 181.6; DB 10; Length 3783;  
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ACCESSION S83176
VERSION S83176.1 GI:1836093
KEYWORDS human medullary thyroid carcinoma cell line TT.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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REFERENCE 1 (bases 1 to 3234)
          Freichel,M., Zink-Lorenz,A., Holltschl,A., Hafner,M., Flockert,Z.V.
          and Rane,F.
          Expression of a calcium-sensing receptor in a human medullary
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          JOURNAL Endocrinology 137 (9), 3842-3848 (1996)
          MEDLINE 96343808
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          This sequence comes from Fig. 6.
          Compare X81086.
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ACCESSION	SEQUENCE	1	from patent	US 5765569.		
VERSION	AR012622					
KEYWORDS	AR012622.1	GI:3970612				
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 5275)					
TITLE	Brown,E.M., Hebert,S.C. and Garrett,J.E. Jr.					
JOURNAL	Calcium receptor-active molecules					
FEATURES	Patent: US 5763569-A 1 09-JUN-1998;					
SOURCE	Location/Qualifiers					
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BASE COUNT	1277 a 1475 c 1316 g 1207 t					
ORIGIN	"/organism="unknown"					

Query Match	6.4%;	Score 176.4;	DB 5;	Length 5275;
Best Local Similarity	49.0%;	Pred. No. 1e-30;		
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DEFINITION AR028465
ACCESSION AR028465
VERSION AR028465.1 GI:5940438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5275)
AUTHORS Nemeth,E.F., Brown,E.M., Hebert,S.C., Garrett,J.F. Jr., Van
Wagenen,B.C., Balandrin,M.F. and Del Mar,E.G.
TITLE Method of screening calcium receptor-active molecules
JOURNAL Patent: US 5858684-A 1 12-JAN-1999;
FEATURES
source 1..5275
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BASE COUNT 1277 a 1475 c 1315 g 1207 t
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RESULT 14
I75051 I75051 5275 bp DNA PAT 03-APR-1998
LOCUS Sequence 1 from patent US 5688938.
DEFINITION I75051
ACCESSION I75051
VERSION I75051.1 GI:3011192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5275)
AUTHORS Brown,E.H., Fuller,F.H., Hebert,S.C. and Garrett,J.F. Jr.
TITLE Calcium receptor-active molecules
JOURNAL Patent: US 5688938-A 1 18-NOV-1997;
FEATURES
location/Qualifiers

```







Query Match	6.2%;	Score 172.4;	DB 12;	Length 4319;
Best Local Similarity	45.8%;	Pred. No. 8.7e-30;		
Matches 1055;	Conservative	0;	Mismatches 1146;	Indels 105;
				Gaps 9;

OY	251	cagcttcaaggccatgctgtctacccacctcttccaagccatgaggttcaactggttgagagat	310
Db	707	CAGGATTAACCTTCGGTGATTCGGATGTGCGATGTACAAAGCCATGATCTTTGGCATGAGAGAAAT	766
OY	311	aaacaacccctcgggacctgtctctccaacatcacaccctggggtatgagctgtacgagctg	370
Db	767	AAACAGAGCCCCCCTTCTTCCCAACATGACTCTGGGATATAGGATATTGACACCTG	825
OY	371	--ctcagaatctgccaatgtgtatgtgccaacctgaaggtgtcttgccctgcaagggccccg	427
Db	837	TAAACCGCTCTCCAAAGCCTCTGGGAGCCACTTGATGTTTGTGGCCAGAAACAAATGGA	886
OY	428	ccacatagagataagaagaagaccttgcgaaccactctcccaaggtgtgtgagcttcatcg	487
Db	887	TTCTCTGAACCTGATGATGATGTTGTGCAACTCTCTCCAGACATCTCTTCAACCATGTGCGT	945
OY	488	gcttcgacaacacttaccacagctgtctacactgctg-----ccttgcgtgggtccttct	541
Db	947	GSTGGACCAACCGGCTCCGGTGTCTCTCCACAGCGGTAGCCAACTGTCTGGGACTTTTCTA	1006
OY	542	gattccccctgttgcagctatgaggaagcaagcgtgtgtactcaagtgtccaaagcggaaattcc	601
Db	1007	TATCCCCAGGTGAGCTTACGCTTCCTCTCTACAGAGCTTCTACCAATTAAGAACCACTTCA	1066
OY	602	gtcttctctcttgtaacgtgtccccaaggtbaacggaaacgggtgtgaggtgtcatgtgtgagctgt	661
Db	1067	GTCCTCTCTCCGACACCTTCCCAACGACGACACCGGACCGGAGTGGCTGACATTAT	1126
OY	662	gcaagaattcttggtgtgtgtgtgtatctctgcatactgtgcagctacgtgtgattcaagggcagct	721
Db	1127	CGAGTATTCCGTTGGAACTGGGTGGGACAAATGCAACCCGACGACGACTATGGGAGGCC	1186
OY	722	gggtgtgcagagcgtctggaagagctgtgcgcgtgtgccggggaatctgcgtgcctccaaga	781
Db	1187	TGGCAATTGAGAAAGTTCCGAAGAGGAACCCGAGGAGAGGACATCTGCATTGACTTCAGGA	1246
OY	782	catcgtgcctctctcctgcgggtgtggtgcacccgagatgtcagagcatgtatgtcagcatct	841
Db	1247	GCTCATCTCCCACTACTCTATGAGGAAGA-----GATCCAGCAGGTGTGTGGAAGTAT	1300
OY	842	ggtctcagggccaagaccacgctgtgtgtgtgtctctctcttcaacgggcacactgtgctagaagt	901
Db	1301	CCAGACACTCTACACCCTCAAGSTCAATGTCGTTTCTCCACGGGCCACGACTAGAACCTCT	1360
OY	902	cttcaaggtccgt	961
Db	1361	CATCAAGAGATTTGTGGCCGTGAACATCAACAGGCAGAGATCTGGCTGGCCAGCGAGGCTGT	1420
OY	962	ggccatctcccaagtaataccacagcgctgactgtgagatcaagggcatgttgagagcggtgtcgg	1021
Db	1421	GGCCAGTTCCTCCTGATTGCTATGCTCTAGTACTTCCATGTAGTCGGGGGTACCATTTGG	1480
OY	1022	ttgtgcgcgtccagcagagacaagaatccccctgggtcgtgaagagatttgagaggtcttatgtcag	1081
Db	1481	GTTGGGTCTGAAAGCTGGGCGAGATCTCAGGCTTCCAGAAATTCTTACAG---AAAGTCA	1537
OY	1082	ggcgtgtaaagctgtgtctcccgcgctgtgccggaggggtctctgtgtcagagcttaaccagct	1141
Db	1538	TCCCAAGAACTGTCCACATATGTTTTCGCAAAAGGTTTGGAAAGAAACCTTTAATG	1597
OY	1142	gtgcgggagatgtccacaacggttctacgaactgttaacatgtcccaagcgtctgagccttccat	1201
Db	1598	CCACCTCGAAGAGCGGCCAAAGACCTTTATCCCGTGGACA-----CCTTGTGTAG	1648
OY	1202	gagtgtccgcgtctcaagagtgtatgtagagcgtgtgtacgctgtgtgccacggccttcaacagct	1261
Db	1649	AAGTCACAGGAAGGCGGCAACAGTTTACTCATATCTCATCTGCTTCCACACCTCTGT	1708

OY	1252	cctgtagcgtactcttcgtgagctcgtgtccaaaggcccaactctcaoccttgcagctcttca	1321
Db	1709	CACGGGGGATGAAACA--CMAATAGGTGTGAGACCCCTTACATGGGCTACGAAACATTACG	1768
OY	1322	gcagaatccaaaggagaaattctctctctacagagaa--actgtgacatttgatacaacg	1381
Db	1769	GATATCTTACAAACGTGTACTTAGCCGTTACTCCATTCCGCAACGCCCTTGCAAGATATA--	1827
OY	1382	ggacacttaagttactacgaacatcatcgctcgtgagcttgaaatgtaacttgaaacctt	1441
Db	1827	-----TACACCTGGTTACCCGGGAAGAGGGCTTTCACCAACGGGTCTCGT	1870
OY	1442	tgaagtaacttggctctcgtccctacgtctctccagttcaatctggaataaaataagacaaaat	1501
Db	1871	TGCACACAT-----	1880
OY	1502	ccagtgagcagggaaagaacaatcagtgctcgtgtgcagtgtgttaccagaagctgtctggc	1561
Db	1880	---CAAGAAAGTTGAGGCTTGCAAGTACCCTTCTCCAACTGCAACCGGAGATGTCAGGC	1936
OY	1562	aggagacacacagg--Tggtttgtggttcccaacacacgtcgtcttgagtggtccctg	1618
Db	1937	AGGGACCAAGGAAGGCAATCATTTGAGAGGAGACCCACGCTCGTGTTTGATGTGTGAGTGTG	1995
OY	1619	cgaagcttgggaaccttctcaacaatgagtgaagcttcaactctgcagacctgttgaacaga	1678
Db	1997	TCTTACACGGCAGATACAGTGTGTGAGACAGATGCGAGTGCCTGTGACAGTGCCTCCGATGA	2056
OY	1679	agaatgggcaccccagaagagagacacttgccttcccacgcagcgtggaggtcttctgcttg	1738
Db	2057	CTTCTGGTCCAAATGGAACATACACTCTCTGATTTGCCAAGAGATTGAGTTCTGGCGTG	2115
OY	1739	gcaatgaacccactctcttgggtgataagaaagctaacaagcattgtgcgtgcgtctggt	1798
Db	2117	GACTTAGCCCTTTGGAATCGCTCACCTCTCTTGGGTGCTGGGCAATTTTCTTCAACGC	2176
OY	1799	tggagctgcgtgcctgtttgccttgacatttcaacacccgttagtgaggtcaagctgaggg	1858
Db	2177	CTTGTGCTGGGCGCTCTCATCAAGTTCCGAACACGCCCATTTGCAAGGCCACCAACCG	2236
OY	1859	taggtgtggtcttccatagctcgggttcccttggctggccggaagctgcagcttctaagctt	1918
Db	2237	AGAGGTGTCCTACCTCCCTGCTTCTTCACTCTCTGCTGCTTCTCCACCTCCCTGTTCTT	2296
OY	1919	cttgcggagagcccaagggtgcccgcggtgtgtgtgcgtcaagcccttctctcgggtt	1978
Db	2237	CATTGGGAACCCCAAGACTTGAGACTCGCCGCTGCGAAGCCCGCTTCGGCATAGCTT	2356
OY	1979	tgcacattctctctcctcgtcgtcaaatccgctctcttcaactgtgtcatcatcttaagtt	2038
Db	2357	CGTGCTTGTATTCGTGTGCATCTTGTGTGAAAGCAATGAGTCTGCTGATTTAG--	2415
OY	2039	tcttcaacaaggtgcccaattctacgttaacctgggcccacaaacatggtgcaggtctatt	2098
Db	2415	-GCCAAATTAACCAACACACTTCCACCCGGAATGGGGGACTCAACCTGCAAGTTCTCTCT	2473
OY	2099	gctaatgtgagcttcccaagggtcccaattgtcatctcgt--ctcaatggcgttgtaagtgac	2158
Db	2474	GCTTTTCTCTGCACTTTCATGCAATGTGATGTGATCTGATCTAATGTGGCTCTACAGGCAC	2533
OY	2159	cccaagacccacagggagatccagagcgtcttcccacatctgttgatctcgaatgacaga	2218
Db	2534	CCCCGTCAGTACCGCAACCAAGAGCTGGAAGAGGAATATCTTTCATCAGCTGCGCATGA	2593
OY	2219	ggtcaactctttaggcttctcgttggctt--aacccaacaattctcctctccatcagtaac	2278
Db	2594	GGGCTCACTCATGGGCTCGGCTCCCTGATGGGTGTACACCTCGCTCCGTGGCTGCATGTG	2653
OY	2279	cttgcgttcgagcttaccctgggttaaggaaactccagagagacatataagagccaatggt	2338
Db	2654	CTTCTCTTTCTTCCCTTCAAGTGTGGAAAGTCCCAAGAACTTTCAAAGAGCCAAAGTTCAT	2713
OY	2339	caccttaagcctgtctctcaactctgtatcccttgatagcccttcttcacacagagccagat	2398



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Db 2714 TACCTTCAGCATGCTTCATCTTCTCATGCTGTGATCTCCTTCATTCACGCTATGCCAG 2773
QY 2399 ttaccagggcagcctacactgcctgggtcaatgctgcaaggctgaaccaactgaagcgg 2458
Db 2774 CACCTACGGCAAGTTGTCTCTGCGGTGAGGTGATGCGCATCCCTGGCAGGCCAGCTTTGG 2833
QY 2459 cggctcagcggttacttcctcccaagtgtatgtatctctgcggtccagaactcaa 2518
Db 2834 CTGTAGCCTTCATCTTCTTCACAAGGTCTACATCATCTCCTTTCAGAAGCTTCACGGAA 2893
QY 2519 caatacagaacacttcaaggcctcca 2544
Db 2894 CACCATCGAGGAGGTGCGCTCCAGCA 2919
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Search completed: March 19, 2000, 01:20:07  
Job time: 3641 sec











RESULT 2  
AI562167/c  
LOCUS AI562167 298 bp mRNA EST 25-MAR-1999  
DEFINITION vw3d10.1 Strataegene mouse heart (#937316) Mus musculus cDNA clone  
IMAGE:1260595 3' similar to SW:CaSR\_HUMAN P41180 EXTRACELLULAR  
CALCIUM-SENSING RECEPTOR PRECURSOR ; mRNA sequence.  
ACCESSION AI562167  
VERSION AI562167.1 GI:4513512  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 298)  
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Steptoe,M., Theisling,B., Allen,M., Bowers,Y.,  
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,  
Ritter,E., Rohm,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterson,T. and Wilson,R.  
TITLE The Mashu-NCI Mouse EST Project 1999  
COMMENT Unpublished (1999)  
On Mar 10, 1998 this sequence version replaced gi:2948814.

This clone was previously sequenced on the 5' end only, this new date is from the 3' end  
Possible reversed clone: similarity on wrong strand  
Possible reversed clone: polyT not found  
High quality sequence stop: 286.  
MGI:661347  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Email: mouseest@watson.wisl.edu

FEATURES	Location/Qualifiers
source	1. .298

```
/organism="Mus musculus"  
/strain="NIH/Swiss"  
/db_xref="taxon:10090"  
/clone_1="IMAGE:1260595"  
/clone_lib="Stratagene mouse heart (#93731c)"  
/sex="pooled"  
/tissue_type="heart"  
/dev_stage="13 day embryos"  
/lab_host="SOLR (Kanamycin resistant)"  
/note="Organ: heart; Vector: pluscript SR-; Site:1:  
ECORI; Site:2: XhoI; Cloned unidirectionally. Primer  
Oligo dt. 93 pooled NIH/swiss 13 day embryo hearts.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'  
adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor  
sequence: 5' GCGGTACCTTCA 3'
```

BASE COUNT	59 a	101 c	87 g	51 t
ORIGIN				

Query Match	11.48;	Score 294.8;	DB 48;	Length 298;
Best Local Similarity	99.38;	Pred. No. 1.3e-68;		
Matches 296; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

QY 686 gttcaagcgccttgaaagactctgcaactccaaagggacatcgcgtcccttaagaactg 745  
Db 118 gTCAAGCGCCTGAGAGACTGCGCACCTCAAGGAGGACATCTGCGTCCGCTTCAAGAGACTG 59  
QY 746 gttcctctcttcgcccaagcaggtgtgacccaagatgcacgcctgaatgtcgtcttgg 803  
Db 58 gTCCCTCTCTCCGCCAAGCGGAGTGAACCAAGATGAGAGCGCATGATGCTGGTGGTGG 1

RECEIPT	3	562 bp	EST	21-JUN-1999
LOCUS	A1742401/c			
DEFINITION		562 bp	EST	21-JUN-1999
	wg4602.x1 Soares NSF F8.9v.OT PA.p.S1 Homo sapiens CDNA clone			
	IMAGE:367578.3			
	similar to TR:093557 093557 PUTATIVE ODOURANT			
	RECEPTOR ?; mRNA sequence.			

ACCESSION	AI742401
VERSION	AI742401.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

JOURNAL Unpublished (1997)  
COMMENT On Dec 20, 1995 this sequence version replaced gi:1130951.

Email: Robert\_Strausberg@nih.gov  
This clone is available royalty-free through LINT; contact the IMCE Consortium ([info@imce.llnl.gov](mailto:info@imce.llnl.gov)) for further information  
Seq primer: -40UP from Gldo  
High quality sequence stop: 468.

FEATURES	Location/Qualifiers
source	1. .562

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/organism: "Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2367578"
/clone.lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clonesIDs: Soares NBHF pool 1:
3200384-310919, 323208-325895 Soares NBHF pool 1:
4450532-14735, 347720-148303, 148872-149255, 15002
150407, 151176-152327 Soares NBHF-9W pool 1:
758280-760583, 772104-774407 Soares NBHF pool 1:
304776-305311, 320136-322823, 325280-32663 Soares NBOT
pool 1: 723270-726407, 739080-740939 Soares NBOT
poares and M.Feltriina Bonaldi."

```

BASE COUNT	116 a	161 c	167 g	117 t	1 others
ORIGIN					

Query Match	10.8%	Score	279.2	DB	51	Length	562
Best Local Similarity	83.2%	Pred. No.	3e-54				
Matches	317	Conservative	0	Mismatches	64	Indels	0
						Gaps	0

[illegible]



[illegible]

RESULT	4
A1415100/c	
LOCUS	
DEFINITION	
ACCESSION	A1415100
VERSION	A1415100.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

A1415100	421 bp	mRNA	EST	09-FEB-1998
mb96801.x1	Soares mouse p3MNF19.5	Mus musculus cDNA clone		
IMAGE:3374d1.3	similar to SW-CASR_RAT P48442	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR ;,	mRNA sequence.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 421)	Marra, M., Hillier, L., Kueba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepec, M., Theising, B., Allen, M., Bowers, J., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schirk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	The WashU-NCI Mouse EST Project 1999	Unpublished (1999)	On Apr 21, 1998 this sequence version replaced g1:3073000.

**FEATURES**  
**SOURCE**

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:337441"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT7SD (Pharmacia) with a modified
polylinker. site_1: Not I; site_2: Eco RI; 1st strand cDNA
was primed with a Not I...oligo(dT) primer."
TGTTACCAATCTGATGAAGGGAGGCGCGGATTTTTTTTTTTTTTTT 3'1,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7SD vector
(Pharmacia). Library was through one round of
normalization to a Cot = 5. Library constructed by Bento

```

Soares and M. Patima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

Query Match	10.58;	Score 270.2;	DB 46;	Length 421;
Best Local Similarity	98.98;	Pred. No. 6.5e-62;		
Matches 272;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0;

Oy	2276	aactataagaagccaatattgcaacttcgaagcgtctctccaactcgtatccgagtc	2335
Db	421	AACATATACGAAGCAAAATGTGTACACTTCAGCGCTCTCTCTCACTTGTGTATCTGGATC	362
Oy			
Oy	2336	gcttcttcacacatgctcagcaattaccagggcagctaccccgagtcagtctg	2395
Db	361	GCTTTCTTACACATGTCCACCAATTATCCAGGGCAGCTACTCTCCCGCGGTCAATGTCTG	302
Oy	2396	gcagagcctggcgaactctgaatgfcgagcttcagcgagctattctctcccaatgtaagtg	2455
Db	301	GCAAGGCTGGCCACTCTGAAATGGCGGGCTTACGCGGTATTCTCTCTTAATGCTACTG	242
Oy	2456	attctctgcgctcagaactcaacaacacagaacacittcagcgctccatccagactac	2515
Db	241	ATTCTTCGCGGTCCAGAACTCAACAACAACAAGAACTTTCACAGCCCTCATCCAGACATAC	182
Oy	2516	acagagcgctfcgscgaactactcaagcggcttgccg	2550
Db	181	ACGAGGCGCTGGCGCACTACTGTAATCCGCTGGGGC	147

RESULT	5
AA853967/c	
LOCUS	
DEFINITION	AA853967 496 bp mRNA EST 31-DEC-1998
	a351e0.s1 Soares_testis_NRT Homo sapiens CDNA clone IMAGE:1339866
	3 similar to SW:CASR_RAT P48442 EXTRACELLULAR CALCIUM-SENSING
	RECEPTOR PRECURSOR ; mRNA sequence.
ACCESSION	AA853967
VERSION	AA853967.1 GI:2941505
KEYWORDS	EST.
SOURCE	human.

ORGANISM Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (Bases 1 to 496)  
REFERENCE NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP)  
TITLE Tumor Gene Index  
JOURNAL unpublished (1997)  
COMMENT On Jan 14, 1998 this sequence version replaced g4:1797381.

Tel.: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bernaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bdpr/image/image.html](http://www-bio.llnl.gov/bdpr/image/image.html)  
 Possible reversed clone: similarity on wrong strand  
 Insert length: 878 Std Error: 0.00  
 Seq primer: 40ml3 fwd. ET from Amersham  
 High quality sequence: stop: 223.

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FEATURES
  source
    location/Qualifiers
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      /db_xref="taxon:9606"
      /clone="IMAGE:1393866"
      /clone_1db="Scars_testis_NHT"
      /sex="male"
      /lab_host="DH10B"
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/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCCGCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5 and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 102 a 145 c 148 g 100 t 1 others

ORIGIN

Query Match 7.9% Score 204.4; DB:39; Length 496;  
Best Local Similarity 81.5% Pred. No. 3.3e-44;  
Matches 260; Conservative 0; Mismatches 57; Indels 2; Gaps 2;

2221 cctcctccatcagcaacttctgtctgagctactcgtgtaagaaactgcggaacta 2280  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
494 CCTCTTCCCATCAGAGGCTTCCCTGCAGCTACTGGTAAAGACTGCCAGAACTA 435  
2281 taacgaagccaatgtgtcactctcagcctgcctccacttcgtatcctgagctt 2340  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
434 CAAGAGGCAAAATGTCTACCTTCAGCTCTCTTCAATTCGTCTGATCGCTT 375  
2341 cttaacatgtccagacttccacaggagactactaccgcggtcaatgtcgtcagg 2400  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
374 CTACCAAGGCGCTCTACGAGGCAAGTA-ANCTTTCGGGCAACATGATGTC- 317  
2401 gctgcccactgagtgagcgtctcagcgtctatctctccctaatactcagctatct 2460  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
316 GCTAGCAAGCCTGAGCAAGCGGCTTGGTGGTATTTTCTGCTAAGTCTACGTATCT 257  
2461 ctgcgtccagaactcaacaacagaaacttcaaggcctccatccagaaactacag 2520  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
256 CTGCGGCCACAGACTCAACAGACAGAGACTTCAGGCTTCATTCAGGACACAGAG 197  
2521 gcgctgagcactcactccta 2539  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 196 GCGCTGCGCTCACCTTA 178

RESULT 6  
LOCUS W18663 247 bp mRNA EST 10-SEP-1996  
DEFINITION m986d01.t1 Soares mouse p3NMF19.5 Mus musculus cDNA clone  
IMAGE:337441 5', mRNA sequence.  
ACCESSION W18663  
VERSION W18663.1 GI:1294371  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 247)  
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
On May 9, 1995 this sequence version replaced gi:802427.  
Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.  
M91:218841  
Seq primer: mob. REGA-ET  
High quality sequence stop: 225.  
Location/Qualifiers

FEATURES  
source  
1. 247  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:337441"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Vector: pT73D (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCCGCCAATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Ximora Ko (Wayne State University)."

BASE COUNT 44 a 89 c 42 g 72 t

ORIGIN

Query Match 7.5% Score 192.2; DB:26; Length 247;  
Best Local Similarity 98.5% Pred. No. 4e-41;  
Matches 194; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1904 tgctgtcgtcgtcagccctcttctctcgtggttcacatttccctctcgtctgaca 1963  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
46 TTCTTGCTGCTCACGCCCTTTTCTCTCGGTTTGCAATTTCTCTCTGTCTGACA 105  
1964 atccgctctcttcacactggtcatcatctcaagtcttctcaacaaagracacattcac 2023  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
106 ATCCGCTCTCTCAAGTGTATCATCTTCAAGTTTCTTCAAGGATACCAATCTTAC 165  
2024 cacacttgagcccaaacatagtgccgggaatctctcatctgcaactccaggtccat 2083  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
165 CACACTTGGGCCCAAAACAGGTGCGGAATTCGTCAATGTCAGCTCCACGGTCCAT 225  
2084 ttgttcctc-gtctcac 2100  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
226 TTGTTCTCTGTCTTCTCAC 242

RESULT 7  
LOCUS AA937218/c 464 bp mRNA EST 09-JUN-1998  
DEFINITION OK134f08.s1 Soares NSF\_F8\_9W\_OT\_PA\_2-S1 Homo sapiens cDNA clone  
IMAGE:1507719 3 similar to SW:CA5R\_HUMAN P41180 EXTRACELLULAR  
CALCIUM-SENSING RECEPTOR PRECURSOR; mRNA sequence.  
ACCESSION AA937218  
VERSION AA937218.1 GI:3095329  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 464)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Jan 19, 1998 this sequence version replaced gi:2150441.  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert length: 1252 Std Error: 0.00

JOURNAL  
COMMENT







TITLE	Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and Hood, L.
JOURNAL	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
MEDLINE	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT	99380589
	Contact: Mahairas GG, Wallace JC, Hood L

Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>) or from Research Genetics (<http://inforesgen.com>). BAC end Web Server: <http://www.htsc.washington.edu>  
Plate: 714 Row: F Column: 8  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 514.

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                /sex="male"
                /note="Vector: pBACE3.6; Genomic sequence of BAC ends
122 a 153 c 174 g 104 t
BASE COUNT
ORIGIN

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Query Match	2.9%	Score 74.4	DB 105	Length 514
Best Local Similarity	63.7%	Pred. No. 2.7e+09		
Matches 128	Conservative 0	Mismatches 72	Indels 1	Gaps 1

[illegible]

QY 1468 gcaagggaagaacaatcaggtgcctgtgtcagtggttacaggactgtctgaaggca 1527

1528 ccacacatctatcatctatgattccaccac-tacttacttccaadtatcatatccctatgaacta 1584  
 369 gcccttctggcttttaccaggiccaaagctctgctggttccagccacacttgccttgaaggcca 310

Db 309 CCAGCGAGTGTAAACGGGTTTCATCACATGCTTGCTTGGAGTGTGTGCCCTGTGGGCTG 250

Db 249 GGACCTTCCTCATCAGAGTG 229

RESULT	10		
LOCUS	AV278654		
DEFINITION	AV278654	260 bp	mRNA
ACCESSION	AV278654		EST
VERSION	AV278654.1		05-NOV-1999
KEYWORDS			
SOURCE	house mouse,		
ORGANISM	Mus musculus		

REFERENCE  
1 (Pages 1 to 260)  
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Haratsun, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Ito, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusaka, M.,

Mitsuyma, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
 Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,  
 Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
 Suzuki, H., Suzuki, Y., Takahashi, F., Tachino, Y., Tomihata, N.,  
 Tsunoda, Y., Watanishi, A., Watanabe, S., Yamamura, T., Yasunishi, A.,  
 Yokota, Y., Yoshiki, A., Yoshino, M., Yamatsutsu, M., and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al.)  
 Unpublished (1999)  
 On Mar 10, 1998 this sequence version replaced g1:2948605.  
 COMMENT  
 TITLE  
 JOURNAL  
 COMMENT

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: +81-298-36-9013  
Fax: +81-298-36-9098  
Email: genome-res@rtc.riken.go.jp  
URL: <http://genome.rtc.riken.go.jp/>  
Sasaki, N., Izawa, M., Watabiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,  
Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y., and  
Hayashizaki, Y.  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. *Proc. Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998)  
Itoh, M., Kitsumi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. *Genome Res.* 9 (3), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,  
19-44 (1999)

FEATURES	Location/Qualifiers
SOURCE	1. .260

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BASE COUNT      64
ORIGIN           a
                  55 c          74 g          67 t
clone.lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site.1: Sall; Site.2: BamHI; CDNA library was
prepared and sequenced in Youssef Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5']
GAGAGAGAGAGATCCAAAGACCTCTTTTCTTTTTTTTNN 3'). cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5']
GAGAGAGAGATCGAGGTATTAAATTATCCCCCCCCCCC 3'}. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified p Bluescript KS(+/-) after bulk excision from Lambda
EUC.I. Cloning Sites, 5' end: Sall; 3' end: BamHI.
```

[illegible]



[illegible]

BASE COUNT	136 a	152 c	137 g	147 t	1 others
ORIGIN	control.				
Query Match	2.4%: Score 63; DB 49; Length 573;				
Best Local Similarity	54.0%: Pred. No. 3.3e-06;				
Matches 129; Conservative	0; Mismatches 110; Indels 0; Gaps 0;				
Qy	437 gcaactcattggccctgataaactgacacgacgctgtacacactgctcgtcgtgagcct 496				
Db	206 GCAATCCTGGGAGAAACATACACTGTAGCTATTCATTCATTCGCTATGGCCAAAGCTCCTCAGCCTC 265				
Qy	497 ttcttgatgccccctggtctagctatgagcgagcgagcgctgatactctagtggggaagcgcaag 556				
Db	266 TACCTCGTCTCTCAGAGTACAGCAGCTCCCTCTTCTCCGGTCTGATGATTAAGTGGCGC 325				
Qy	557 ttccgcgtctctcttcgacacatccccacgacgaataagtaacagctggaagtaagtacg 616				
Db	326 TACCGCTCTTCATACGCGTGTATTCCTCCAGTATGTGTACACAGCTCAGCGCTGCTCAAG 385				
Qy	617 ctgcctcagagccttcgcgtgctgatactcgcctcgtcttggcaagctatggtactaagg 675				
Db	386 CTCATGTCCTCATTTCTCTCCTGGAACACTGGCTCGGTGCTGTACGAGATGATGACTATGG 444				
RESULT 12					
FR0044379	619 bp DNA GSS 22-OCT-1999				
LOCUS	Fugu rubripes GSS sequence, clone 184F17aE5, genomic survey				
DEFINITION	sequence.				
ACCESSION	AL131871				
VERSION	AL131871.1 GI:6113817				
KEYWORDS	GSS; genome survey sequence.				
SOURCE	Fugu rubripes.				
ORGANISM	Fugu rubripes				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.				
AUTHORS	Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K., Umranda, Y., Williams, G., and Brenner, S.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB. UK Email: biolhelp@mp.mrc.ac.uk				
COMMENT	Vector: pBluescript II KS V_Type: phagemid PRIMER: KS				
DESCR:	One pass dye-terminator sequencing of cosmid cloned genomic sequence.				
FEATURES	Location/Qualifiers				
SOURCE	1..619 /organism="Fugu rubripes" /db_xref="taxon:31033" /clone_id="cosmid 184F17" /clone="184F17aE5" /clone="184F17aE5"				
BASE COUNT	166 a	126 c	132 g	187 t	8 others
ORIGIN					
Query Match	2.4%: Score 62.2; DB 80; Length 619;				
Best Local Similarity	54.1%: Pred. No. 5.7e-06;				
Matches 124; Conservative	0; Mismatches 105; Indels 0; Gaps 0;				
Qy	2255 aactgcggagaaactataacgaagccaatgtgtacattcaagctgctctccactctcg 2324				
Db	46 AACGCCCGAATATTTCAACAGCAAGCAAGATGACCTTCAGCATGCTGATATTTCTGG 105				



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QY 2325 tatcttgatcgccttcttccacatgctccagcatltaaccaggcagctaccgccg 2384
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 CCGTCTGATACACTTATCCCTTACGTACAGCTCTCCGGAAATTCACCGTGGCCG 165
QY 2385 tcaatgtgc-tggcaggcctgcccactctgagtgccgcttcagcgctattccctccta 2444
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 166 TCGAGATCTTGGCATTTGGCTCCAGTTTGGACATCATCTGTGCATTTTCTGCTCAA 225
QY 2445 aagctcagcgatctctgcgcgtccagaactcaacaacagacactt 2493
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 226 AATGTTTATTATTATTATTAAAGCAGAGAAATACANNAAACACTT 274

RESULT 13
LOCUS AL040113 732 bp mRNA EST 29-SEP-1999
DEFINITION DKFZP434C2213.1 434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION AL040113
VERSION DKFZP434C2213.5, mRNA sequence.
KEYWORDS AL040113.2 GI:5935280
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
TITLE 1 (bases 1 to 732)
JOURNAL Eutheria; Primates; Catarrhini; Homiidae; Homo.
COMMENT Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehler, et al.)
On Jul 7, 1999 this sequence version replaced gi:5409080.
Contact: Koehler K
MIPS
Am Kiofierspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcententrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..732
location/Qualifiers
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/db_xref="taxon:9606"
/clone="DKFZP434C2213"
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/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Vector: pSport1; Site-1: Not; Site-2: SalI"
BASE COUNT 125 a 245 c 191 g 169 t 2 others
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Query Match 2.38: Score 60.2; DB 64; Length 732;
Best Local Similarity 45.18: Pred. No. 2.2e-05;
Matches 264; Conservative 0; Mismatches 318; Indels 3; Gaps 1;

QY 1769 ggcctgttccctgcctctccacagcgcctgtgtgaggtcagctggggtagcctgc 1828
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19 GGGTCTCTTTGTGGGCGCAATGCCACACAGTGTCAAGGCTTCAAGTCCGGAGCTTGC 78
QY 1829 tctccatgctgggtctcctctgtagcctgggaagtgcagcctctacagcctcttcgggaag 1888
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 79 TACATCTCTGCTGGTGGTGTCTCTCTCTACATGACCTTCATCTCATTTGCCAAG 138
QY 1889 cccaagctgcgcgctgctgcgcgcgcagccctctctcgcgggtttgcatttc 1948
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 CCAATCCAGGCGACATGTACTTACGGCGTCTGTGGTGGACACTGCTTCTGTCTGC 198

```

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QY 1949 ctctcctgtctgacaaatccgctccctccacatggtca-cattctcaagttcttaccag 2008
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Db 199 TACTCACCCCTCGTCACCAAGAACCAACCGCATTCGATCGGTGGGCGCGGAG 258
QY 2009 gtaccacatcttcaacacttggcccacaaacca-vgtgcgggaatattcg-cattgtc 2068
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 2069 agctccaggttcatttgttccctctgtctcagtgagcttgcaattgagcccaaggccc 2128
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Db 319 ATCT--CGGGCCAGCTGCTCATCTGTGTGCTGTGCTGTGTGTGAAGCAGCGGCACA 375
QY 2129 accagagagtaaccagcgcctcccccattc-egttattcttgagtgcaagaaggtcaacttc 2188
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Db 376 GGCAAGAGAGACACCCCGGACAGCGCGGAGAGTGTACACATGGCTGTGCACACACCGCAT 435
QY 2189 gtgggtcttcgttggccttcgcacacaacatccctctccatcagcacttggctgc 2248
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QY 2249 agctactcgtgtaagaactgcgcggagactataagaagccaagtgc-actctcgc 2308
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Db 496 GCCTTCAAGACTGCAAGTGCCTCCGAAAACTTCACGAGGCCAGTTCAATTGGCTTACC 555
QY 2309 ctgctcctccactctgatactcgatcgcttcttccacatgctc 2353
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Db 556 ATGTACACACACTGCATCATCTGGCTGCGCATTTCTCCCATCTTC 600

RESULT 14
LOCUS AI434785/c 602 bp mRNA EST 30-MAR-1999
DEFINITION t120c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131025 3'
ACCESSION AI434785
VERSION AI434785.1 GI:4298607
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 602)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On May 7, 1998 this sequence version replaced gi:3121344.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Insert Length: 1217 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 453.
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a modified polylinker; Site-1: Not I; Site-2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

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```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-485-588-3

Query Match      6.4%; Score 166.2; DB 1; Length 3809;
Best Local Similarity 46.3%; Pred. No. 1.9e-37;
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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QY 266 gagataaacaactccacagctctctcccaacatcacccctgggtatgaactgtatgac 325
DB 610 GAGATTAACAGCAGCCGCCCTTTCCCACTTGACGCTGGGATACAGGATTTTGAAC 669
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QY 557 ttcccgctctcttgcgacccatcccccagcgaatgaatgaagtggaatgaatgaagc 616
DB 910 TTCAAGTCTTTCTCTCGAACAATCCCAATGATGACGACCAACGCAATGCAATGCAAC 969
QY 617 ctgtctcagaagcttgcgctgtgtgacgtcgtctgttgcagctatgtgtgactacgg 676
DB 970 ATCATGAGTATTTCCGTGGAGCACTGGGTGGGCAATTTGACACTGATGACGATTTGG 1029
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QY 737 aagagacgtgtgctctcccgcccgagcggtgtgacccaaggaatgaagcgtatgagc 796
DB 1090 AAGTA-----ACTCATCTCCCACTGACTGATGAGGAAGATTCAGCATGTGTAGAG 1143
QY 797 cgtctgtcgtcagcaggaaccaacgtgtgtgtgtctcttcaacggcaccctgtgtga 856
DB 1144 GTGATTCAAATATCCAGCGGCAAAATGATCGTGTGTTTCCGATGGGCCAAGATCTTAG 1203
QY 857 ggtgttctcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 916
DB 1204 CCGCTCATAGAGAGATTGTCCGCGCAATATACGCGCAAGATCTGCGTGGCCACGAG 1263
QY 917 gactgtggcatctccacgtacacacatgtgtccggatccaggaactgtgtgaagtg 976
DB 1264 GCCTGGGCAAGCTCTCCGATGCGCAATGCTCACTTCCACGTGTTGGGGGACCC 1323

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QY 977 ctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1024
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QY 1024 -----tgaaagctctatgttcagcagtgatg----- 1052
DB 1384 CATCCAGCAAGTCTGTCACAAATGTTTGGCAAGGATTTTGGAGAAACATTAAAC 1443
QY 1052 -----ggtgtcccaagacttgcacagaggggtctgtgtgtgtgtgtgtgtgtgt 1096
DB 1444 TGCCACCTCCAAAGAGTGCAAAAGACCTTACTGTGTGACACCTTTCTGAGAGTAC 1503
QY 1097 -----cagctgtcagagag 1111
DB 1504 GAAGAAAGTGGGACAGTTTNGCAACAGCTCGACAGGCTTCGACCCCTCTGTACAGG 1563
QY 1112 tgtcagcgttcaagacatgtgaacatgcgcaggttgaagccttcacatgaagcgtgc 1171
DB 1564 GATGAGAACATCAGCAGTGTGAGACCCCTTACATAGATTACACGCAATTTACGATATCC 1623
QY 1172 tacaatgtgtatgaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1231
DB 1624 TACAATGTGTACTTACAGCTACTCTCAATGCCCCAGGCTTGCAAGATATATATACCTGC 1683
QY 1232 accctctggagacctg-----tgccagagggccagctacccc 1267
DB 1684 TTACTGGGAGAGGGGCTGTTCACCAATGGCTCTGCAACATCAAAAGTTGAGGCG 1743
QY 1268 tggcagctcttcacagacatctacaagtgaaatccctctacataaga--agactgt 1324
DB 1744 TGGCAGGTCTCCAAACACCTACGCACTTAACTTACAAACAAATATGGGGAGCAGGTG 1803
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DB 1804 ACTTTGATGATGTGTGTGACCTGTGGGAGACTTTTCATCATCATATGACCACTCTCC 1863
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US-08-484 2
US-08-484-565-3
Sequence 3, Application US/08484565
Patent No. 5763569
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: James C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM type: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION DATA: including application
described below: 9

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APPLICATION NUMBER: 08/353,784  
 FILING DATE: 9 December, 1994  
 APPLICATION NUMBER: PCT/US/94/12117  
 FILING DATE: 21 October, 1994  
 APPLICATION NUMBER: U.S. 08/292,827  
 FILING DATE: 23 August, 1994  
 APPLICATION NUMBER: U.S. 08/141,248  
 FILING DATE: 22 October, 1993  
 APPLICATION NUMBER: U.S. 08/009,389  
 FILING DATE: 23 February, 1993  
 APPLICATION NUMBER: U.S. 08/017,127  
 FILING DATE: 12 February, 1993  
 APPLICATION NUMBER: U.S. 07/9934,161  
 FILING DATE: 21 August, 1992  
 APPLICATION NUMBER: U.S. 07/834,044  
 FILING DATE: 11 February, 1992  
 APPLICATION NUMBER: U.S. 07/749,451  
 FILING DATE: 23 August, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hebet, Sheldon O.  
 REGISTRATION NUMBER: 38,179  
 REFERENCE/DOCKET NUMBER: 213/006  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3809 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
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 OTHER INFORMATION:  
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RESULT 3  
 US-08-480-751-3  
 ; Sequence 3, Application US/08480751  
 ; Patent No. 5858684  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edward F. Nemeth  
 ; APPLICANT: Edward M. Brown  
 ; APPLICANT: Steven C. Hebert  
 ; APPLICANT: Forrest H. Fuller  
 ; APPLICANT: James E. Garrett, Jr.



TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,751  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3809 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
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NAME/KEY: CDS  
LOCATION: 373..3606  
OTHER INFORMATION:  
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RESULT 4  
US-08-943-986-3  
Sequence 3, Application US/08943986  
Patent No. 5962314  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,986  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,565  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 3:







Db 2464 AAAACCAACCGTGTCCCTCCGCTGTTTACG---GCCAAGATCCCAACACACTTCCACCGC 2520  
QY 2027 acttgagcccaaaacacatggtgcaggaatattgcatctgacgtccacagagccatttg 2086  
Db 2521 AAGGAGGGGGGCTCAACCTGCAGATTCTCTGTTTCTCTGACCTTCAATGAGATT 2580  
QY 2087 ttctctgtctcagtggtctgcaatgtgagcccaagagcccaagagagtaaccagcgc 2146  
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QY 2147 ttcccccattgtgattcttctgagtgacagaggtcaactctgtgggtctctgtggtc 2206  
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Db 2941 ATCTACATCATCTCTTCAAGCCATCCCGCAACCATCA 2981

RESULT 5  
US-08-353-784-3  
Sequence 3, Application US/08353784  
Patent No. 6011068

## GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth, Edward M.  
APPLICANT: Brown, Steven C. Hebert,  
APPLICANT: Bradford C. Van Wagonen, Manuel  
APPLICANT: F. Balandrin, Forrest H. Fuller,  
APPLICANT: Eric G. Delmar, and Scott T. Moe  
TITLE OF INVENTION: CALCIUM RECEPTOR ACTIVE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,784  
FILING DATE: 9 December, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 209/069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO. 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3809 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 373..3606  
OTHER INFORMATION:  
US-08-353-784-3

Query Match 6.4%; Score 166.2; DB 5; Length 3809;  
Best Local Similarity 46.3%; Pred. No. 1.9e-37;  
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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Dh 2881 GAGGTATTTGCCATCTGTGCGAGCCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940  
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RESULT 6  
US-08-485-588-1  
: Sequence 1, Application US/08485588  
: Patent No. 5688938  
: GENERAL INFORMATION:  
: APPLICANT: Edward M. Brown  
: APPLICANT: Steven C. Hebert  
: APPLICANT: Forrest H. Fuller  
: APPLICANT: James E. Garetz, Jr.  
: TITLE OF INVENTION: MOLECULES  
: NUMBER OF SEQUENCES: 20  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Lyon & Lyon  
: STREET: First Interstate World Center







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QY	2086	gttctctgtctcctcagcgtggtcttgcaatctgtagcccccaagcccaacagggagtaccag	2145
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Db	2785	GGAGAGAGAGATCATCTTTCATCACTGCGCACAGAGGGCTGCTCATGCGCGCTTGCT	2844
QY	2206	tttcgcacaaacatccctctctccatctcagcaccttgcctgtcgaactaactcgtgtaaga	2265
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QY	2326	atctctgatatccttcttccacatgctcagcaatttaccagagcaagctaacacccggt	2385
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Db 3085 GGCTCAATATCTCTCTCAAGGCTTCGCCGAACACCATCGAAGAGTGCCTGCAGCAG 3144
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Db 3145 CCGCGCACACGC 3156

RESULT 7
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; Sequence 1, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; City: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/934,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hebert, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELE: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs

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? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 515..3769
? OTHER INFORMATION:
US-08-484-565-1

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Query Match	6.1%	Score 157.2	DB 2	length 5275
Best Local Similarity	46.0%	Pred. NO. 8e-35		
Matches 1136, Conservative	0	Mismatches 1168	Indels 168	Gaps 11

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US-08-480-751-1  
Sequence 1, Application US/08480751  
Patent No. 5858684  
GENERAL INFORMATION:  
APPLICANT: Edward F. Nemeth  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: Forrest H. Fuller  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,751  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/351,784

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1      FILING DATE: 9 December, 1994
2      APPLICATION NUMBER: PCT/US/94/12117
3      FILING DATE: 21 October, 1994
4      APPLICATION NUMBER: U.S. 08/292,827
5      FILING DATE: 23 August, 1994
6      APPLICATION NUMBER: U.S. 08/141,248
7      FILING DATE: 22 October, 1993
8      APPLICATION NUMBER: U.S. 08/009,389
9      FILING DATE: 23 February, 1993
10     APPLICATION NUMBER: U.S. 08/017,127
11     FILING DATE: 12 February, 1993
12     APPLICATION NUMBER: U.S. 07/993,161
13     FILING DATE: 21 August, 1992
14     APPLICATION NUMBER: U.S. 07/83,044
15     FILING DATE: 11 February, 1992
16     APPLICATION NUMBER: U.S. 07/749,451
17     FILING DATE: 23 August, 1991
18     ATTORNEY/AGENT INFORMATION:
19     NAME: Heber, Sheldon O.
20     REGISTRATION NUMBER: 38,179
21     REFERENCE/DOCKET NUMBER: 213/004
22     TELECOMMUNICATION INFORMATION:
23     TELEPHONE: (213) 489-1600
24     TELEFAX: (213) 955-0440
25     TELE: 67-3510
26     INFORMATION FOR SEQ ID NO: 1:
27     SEQUENCE CHARACTERISTICS:
28     LENGTH: 5275 base pairs
29     TYPE: nucleic acid
30     STRANDEDNESS: single
31     TOPOLOGY: linear
32     MOLECULE TYPE: cDNA to mRNA
33     FEATURE:
34     NAME/KEY: CDS
35     LOCATION: 515..3769
36     OTHER INFORMATION:
37     US-08-480-751-1

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RESULT 9  
 US-08-943-986-1  
 ; Sequence 1, Application US/08943986  
 ; Patent No. 5962314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edward M. Brown  
 ; APPLICANT: Steven C. Hebert



APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,986  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,565  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 39,179  
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TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 515..3769  
OTHER INFORMATION:  
US-08-943-986-1

Query Match 6.1%; Score 157.2; DB 4; Length 5275;  
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Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

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 QY 1786 tctcacaagcctgttgtgagtcagcttgggtaggcgtgtctctcctatgtctgtc 1845  
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 QY 2026 cacttgggcccacaacatgtgtgcggaatatctgcatatgtcagctccacaggttccatt 2085  
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 QY 2146 ctcccccaactgtgattcttgaagtgcagaggtcaactcgttggcttctgtgyc 2205  
 Db 2785 GGAGGACGAGATATCTTCACTGACGAGGGGTGCTGCTATGAGCGCTGGCTTCTCT 2844  
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 Db 2845 GATCGGCTACCTGCTGTGTGGCGGCACTGCTTCTTGTGCGCTTCAAGTCCGGAA 2904  
 QY 2266 actgcggagaaactataacgaagccaaatgttcaacctcagcctgtctccactcgt 2325

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 QY 2446 atgtcagtgatctctgcgcgtccagaaactcaacacagaaacattcagcctccat 2505  
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RESULT 10  
 US-08-353-784-1  
 ; Sequence 1, Application US/08353784  
 ; Patent No. 6011068  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edward F. Nemeth, Edward M.  
 ; APPLICANT: Brown, Steven C. Hebert,  
 ; APPLICANT: Bradford C. Van Wageningen, Manuel  
 ; APPLICANT: F. Balandrin, Forrest H. Fuller,  
 ; APPLICANT: Eric G. Delmar, and Scott T. Moe  
 ; TITLE OF INVENTION: MOLECULES  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: First Interstate World Center  
 ; STREET: Suite 4700  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: FASTSEQ  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/353,784  
 ; FILING DATE: 9 December, 1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; PRIOR APPLICATION DATA: including application  
 ; PRIOR APPLICATION NUMBER: PCT/US/94/12117  
 ; FILING DATE: 21 October, 1994  
 ; APPLICATION NUMBER: U.S. 08/292,827  
 ; FILING DATE: 23 August, 1994  
 ; APPLICATION NUMBER: U.S. 08/141,248  
 ; FILING DATE: 22 October, 1993  
 ; APPLICATION NUMBER: U.S. 08/009,389  
 ; FILING DATE: 23 February, 1993  
 ; APPLICATION NUMBER: U.S. 08/017,127  
 ; FILING DATE: 12 February, 1993  
 ; APPLICATION NUMBER: U.S. 07/993,161  
 ; FILING DATE: 21 August, 1992  
 ; APPLICATION NUMBER: U.S. 07/834,044  
 ; FILING DATE: 11 February, 1992  
 ; APPLICATION NUMBER: U.S. 07/749,451  
 ; FILING DATE: 23 August, 1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Heber, Sheldon O.  
 ; REGISTRATION NUMBER: 38,179  
 ; REFERENCE/DOCKET NUMBER: 209/069











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QY 1841 ggttccttgtagctggaggttcagccctacagcttcctcggaagcccaagtgccc 1900
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QY 1961 acatccgctccctcccaacggtcatcatcttcaagttcttaccaggaacccactc 2020
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Db 2608 CACCGCAAGTGTGGGGCTCAACCTCCACTTCTCTGTGTTTCTCTGACCTTATG 2667
QY 2081 catttgctctctctcctcagcttgctcgaatgtggaaccccaagcccaaggaagtac 2140
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Db 2668 CAGATTGTCTGTGTGATCTGGCTTACACGGCGCCCGCTCAAGCTACCGCAACGAG 2727
QY 2141 cagcgcttcccccatctggtgatctcttgagtgacagaaggtcaactctgtgggcttc 2200
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Db 2728 GACCTGGAGATGAGATCATCTTATCAGTGTGACGACGAGGGCTCCCTCATGGCCCTGGC 2787
QY 2201 gtgagcttcgacacaaacatctccctctcagctcagcactctgtcagctacactgg 2260
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QY 2261 aaggaactgcggagaaactaatacgaagcaaatgtgtcacttcagcctcctctccac 2320
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Db 2848 CGGAGCTGCGGAGAACTTCATGAAGCCAGATTCATCATCTTACACATGCTCATCTTTC 2907
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Db 2908 TTCTATCTGTGATCTCTCTTCTTATCCAGCTATGCCAGCCTATGCGCAAGTGTGTCT 2967
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Db 2968 GCCGTAGAGTGTATGCTCATCTCTGCGCAGCCAGCTTTGGCTTGGCTGCTCATCTTCTTC 3027
QY 2441 cctaaatgctacgtgattctctcgcgtccgctcgaactcaacacacacaga 2487
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Db 3028 AACAGATCTACATCATCTTCTTCAAGCCATCCCGCAACCATGCA 3074

RESULT 12
US-08-484-565-2
: Sequence 2, Application US/08484565
: Patent No. 5763569
: GENERAL INFORMATION:
: APPLICANT: Edward M. Brown
: APPLICANT: Steven C. Hedert
: APPLICANT: James E. Garrett, Jr.
: TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: First Interstate World Center
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: FASTSEQ
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/484,565
: FILING DATE: 7 June, 1995

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: CLASSIFICATION: 435
: PRIOR APPLICATION DATA: including application
: PRIOR APPLICATION DATA: described below: 9
: APPLICATION NUMBER: 08/353,784
: FILING DATE: 9 December, 1994
: APPLICATION NUMBER: PCT/US/94/12117
: FILING DATE: 21 October, 1994
: APPLICATION NUMBER: U.S. 08/292,827
: FILING DATE: 23 August, 1994
: APPLICATION NUMBER: U.S. 08/141,248
: FILING DATE: 22 October, 1993
: APPLICATION NUMBER: U.S. 08/009,389
: FILING DATE: 23 February, 1993
: APPLICATION NUMBER: U.S. 08/017,127
: FILING DATE: 12 February, 1993
: APPLICATION NUMBER: U.S. 07/934,161
: FILING DATE: 21 August, 1992
: APPLICATION NUMBER: U.S. 07/834,044
: FILING DATE: 11 February, 1992
: APPLICATION NUMBER: U.S. 07/749,451
: FILING DATE: 23 August, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Heber, Sheldon O.
: REGISTRATION NUMBER: 38,179
: REFERENCE/DOCKET NUMBER: 213/006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5006 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: MOLECULE TYPE: linear
: TOPOLOGY: linear
: Molecule type: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 436..3699
: OTHER INFORMATION:
: US-08-484-565-2

Query Match 5.9%; Score 152.6; DB 2; Length 5006;
Best Local Similarity 48.4%; Pred. No. 1.6e-33;
Matches 487; Conservative 0; Mismatches 514; Indels 6; Gaps 2;

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QY 2081 catgtgtctctgtctcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2140
Db 2668 CAAATGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2127
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Db 3028 AACAAATCTACATCATCTCTTCAAGCCATCCCGCAACCATCGA 3074

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## RESULT 13

US-08-480-751-2  
Sequence 2, Application US/08480751

Patent No. 5858684  
GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: Forrest H. Fuller  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA

ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,751

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? FILING DATE: 7 June, 1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? PRIOR APPLICATION DATA: Including application
? PRIOR APPLICATION DATA: described below: 9
? APPLICATION NUMBER: 08/353,784
? FILING DATE: 9 December, 1994
? APPLICATION NUMBER: PCT/US/94/12117
? FILING DATE: 21 October, 1994
? APPLICATION NUMBER: U.S. 08/292,827
? FILING DATE: 23 August, 1994
? APPLICATION NUMBER: U.S. 08/141,248
? FILING DATE: 22 October, 1993
? APPLICATION NUMBER: U.S. 08/009,389
? FILING DATE: 23 February, 1993
? APPLICATION NUMBER: U.S. 08/017,127
? FILING DATE: 12 February, 1993
? APPLICATION NUMBER: U.S. 07/934,161
? FILING DATE: 21 August, 1992
? APPLICATION NUMBER: U.S. 07/834,044
? FILING DATE: 11 February, 1992
? APPLICATION NUMBER: U.S. 07/749,451
? FILING DATE: 23 August, 1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Heber, Sheldon O.
? REGISTRATION NUMBER: 38,179
? REFERENCE/DOCKET NUMBER: 213/004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5006 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 436..3699
? OTHER INFORMATION:
? US-08-480-751-2

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Query Match 5.9%; Score 152.6; DB 3; Length 5006;  
Best Local Similarity 48.4%; Pred. No. 1.6e-33;  
Matches 487; Conservative 0; Mismatches 514; Indels 6; Gaps 2;

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QY 1484 cagtgccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1543
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QY 1721 ctattagcagctaaacagctattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1780
Db 2311 CTCACCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2370
QY 1781 tgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1840
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OY 1841 gttctcttgtagctgagttgcaaccccttaacagtttcttcttggaagcaagagttgcc 1900
Db 2431 TTCTCCCTGCTGCTGCTGCTCTTCTTCCACCTCCCTGTTTATGGSAGAGCCCAAGACTGC 2490
OY 1901 gctgtcttgctgcgtcacagccctcttctctctgagtttgccatttctctctctgctctg 1950
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Db 2551 CTGTGTGAANAACCAACCTGTCTCTCTGTTGTTGAAG--CCAAATATCCACACAGCTTC 2607
OY 2021 taccacacttgggcccacaacacatctgtctgcggaatactgtcatgttaagtttcaaggtc 2080
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OY 2081 catctgtctccctctgtctcgaatgtgactgcaatgtgacccccaagcccaagaggtac 2140
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OY 2441 cctaaatgcacagatctctctctgcgtccagacctaacaacaagca 2487
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RESULT 14
US-08-943-986-2
: Sequence 2, Application US/08943986
: Patent No. 5962314
: GENERAL INFORMATION:
: APPLICANT: Edward M. Brown
: APPLICANT: Steven C. Hebert
: APPLICANT: James E. Garrett, Jr.
: TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
: NUMBER OF INVENTIONS: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: First Interstate World Center
: STREET: Suite 4700
: STREET: 633 West Fifth Street
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: FASTSEQ
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/943,986
: FILING DATE: 03-OCT-1997

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1 CLASSIFICATION: 530
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/484,565
4 FILING DATE: 7-June-1995
5 APPLICATION NUMBER: 08/353,784
6 FILING DATE: 9 December, 1994
7 APPLICATION NUMBER: PCT/US/94/12117
8 FILING DATE: 21 October, 1994
9 APPLICATION NUMBER: U.S. 08/292,827
10 FILING DATE: 23 August, 1994
11 APPLICATION NUMBER: U.S. 08/141,248
12 FILING DATE: 22 October, 1993
13 APPLICATION NUMBER: U.S. 08/009,389
14 FILING DATE: 23 February, 1993
15 APPLICATION NUMBER: U.S. 08/017,127
16 FILING DATE: 12 February, 1993
17 APPLICATION NUMBER: U.S. 07/9934,161
18 FILING DATE: 21 August, 1992
19 APPLICATION NUMBER: U.S. 07/834,044
20 FILING DATE: 11 February, 1992
21 APPLICATION NUMBER: U.S. 07/749,451
22 FILING DATE: 23 August, 1991
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Heber, Sheldon O.
25 REGISTRATION NUMBER: 38,179
26 REFERENCE/DOCKET NUMBER: 213/006
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (213) 489-1600
29 TELEFAX: (213) 955-0440
30 TELEX: 67-3510
31 INFORMATION FOR SEQ ID NO: 2:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 5006 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA to mRNA
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 436..3699
41 OTHER INFORMATION:
42 US-08-943-986-2
43
44 Query Match 5.9%; Score 152.6; DB 4; Length 5006;
45 Best Local Similarity 48.4%; Pred. No. 1.5e-33;
46 Matches 487; Conservative 0; Mismatches 514; Indels 6; Gaps 2
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48 Oy 1484 caggtagctgtgtcagtggtacccaggaagctctcgaaggagaccacacaggtgtcat- 1543
49 |||||
50 Db 2071 CAGGTGCCCTTCTCCAAATGTCGACGCCGAGACATGCTCTGCGAGCCAGMAAGGATCAT 2130
51 |||||
52 Oy 1543 --gggttccacacatggtgtcttcgagfagcatgcccttgaaagctgggaacattctaac 1600
53 |||||
54 Db 2131 GAGGGGAGACCCACTGCTGCTTTAGGTGTGGAGTGTCTGTATGGGAGATATAGTGAT 2190
55 |||||
56 Oy 1501 acgaatgagcttcaacagctccagcagctgtggaacagaagaatggccccctgaagggagc 1660
57 |||||
58 Db 2131 GAGAAAGATGCCAGTGCCTGTAAACAAGTCCCAAGATGACTTGTGCTCCATATGAAACCC 2250
59 |||||
60 Oy 1661 tcagctgtcttcacagcagcagctggaagttcttggggcgcatgaaacccatctcttggtg 1720
61 |||||
62 Db 2251 ACCCTCTGCAATGCCAAAGAGATGCAAGATTTCTGTGTGACGAGACCCCTTTGGATCGCA 2310
63 |||||
64 Oy 1721 ctatagcagctcaaaagcgtatcgctgtcgtcgtgaattggagcgcgtggcctgtgttgc 1780
65 |||||
66 Db 2311 CTCACCTCTTTGCGGTCTGGGCAATTTCTCGACACGCTTTGTGCTGGGTGTGTATC 2370
67 |||||
68 Oy 1781 tggcgtcttcacagcagcgtgtgtgagtgacgttgagggtgagctgtgtctctcatgtcg 1840
69 |||||
70 Db 2371 AAGTTCGCCAACAACCCATTGTCAAGGCCACCAACCGAGAGACTTCTCTACTCCTCTC 2430
71 |||||
72 Oy 1841 ggtctcttgtagtctggagagttgcagcctctcaagcttcttcgggaagccacagtgccc 1900

```



[illegible]

15  
US-08-353-784-2  
Sequence 2, Application US/08353784  
Patent No. 6011068  
GENERAL INFORMATION:  
APPLICANT: Edward F. Nemeth, Edward M.  
APPLICANT: Brown, Steven C. Hebert,  
APPLICANT: Bradford C. Van Wageningen, Manuel  
APPLICANT: F. Balandrin, Forrest H. Fuller,  
APPLICANT: Eric G. Delmar, and Scott T. Moe  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
MOLECULES  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSED  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,784

```

1 FILING DATE: 9 December, 1994
2 CLASSIFICATION: 514
3
4 PRIOR APPLICATION DATA: including application
5 PRIOR APPLICATION DATA: described below: 8
6 APPLICATION NUMBER: PCT/US/94/12117
7 FILING DATE: 21 October, 1994
8 APPLICATION NUMBER: U.S. 08/292,827
9 FILING DATE: 23 August, 1994
10 APPLICATION NUMBER: U.S. 08/141,248
11 FILING DATE: 22 October, 1993
12 APPLICATION NUMBER: U.S. 08/009,389
13 FILING DATE: 23 February, 1993
14 APPLICATION NUMBER: U.S. 08/017,127
15 FILING DATE: 12 February, 1993
16 APPLICATION NUMBER: U.S. 07/934,161
17 FILING DATE: 21 August, 1992
18 APPLICATION NUMBER: U.S. 07/834,044
19 FILING DATE: 11 February, 1992
20 APPLICATION NUMBER: U.S. 07/749,451
21 FILING DATE: 23 August, 1991
22
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Heber, Sheldon O.
25 REGISTRATION NUMBER: 38,179
26 REFERENCE/DOCKET NUMBER: 209/069
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (213) 489-1600
29 TELEFAX: (213) 955-0440
30 TELEX: 67-3510
31
32 INFORMATION FOR SEQ ID NO: 2:
33
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 5006 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: cDNA to mRNA
40 FEATURE:
41 NAME/KEY: CDS
42 LOCATION: 436..3699
43 OTHER INFORMATION:
44
45 US-08-353-784-2

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Query Match	Similarity	5.9%	Score 152.6	DB 5	Length 5006
Best Local	Similarity	48.4%	Pred. No. 1.6e-33		
Matches 487	Conservative	0	Mismatches 514	Indels	Gaps
OY	1484	caggtcctgtgttcagtgatgttcaacaggagactgtcttcgaaggacacacaggtgtgtcat-	1543		
Db	2071	CAGGTGCCCTTCTCCAACTGCAGCGCGAGACTCCCTGGCGAGGCCAGCAAGAAAGATCATT	2130		
OY	1543	--gggttcccaacacactgtcgtcttcgaagtgcabgcctgtgaaagtgggaacatttcctaac	1600		
Db	2131	GAGGGGGAGACCCACTGCTGCTTTGAGTGTGTGGAGTGCCTCGATGGGAGATATAGTAT	2190		
OY	1601	acgagtggagcttcaacactgtccagcctcgtgtgaaacaagaagaatggccccctgaagggagc	1660		
Db	2191	GAGACAGATGCCAGTGCCTGTAAACAAGTCCCGATGATCTTGCTGCATATAGAACCCAC	2250		
OY	1661	tcaagctctctctcaacgcacacgttgaagtctcttgagttgcacgaacccactccttggtg	1720		
Db	2251	ACCTCTCGATTGCCAAGAGAGATCGAGTTCTGTGTGTGACCGAGCCCTTTGGATCGCA	2310		
OY	1721	ctattagaagctaaacagcctatctgtctgtcgtcgtatgtgaaactgtgcactgttctgc	1780		
Db	2311	CTCACCCCTTTTGGCGTGTGTGGGATTTTCCGACAGACCTTTGTGTGTGGTGTGTTTATC	2370		
OY	1781	tggcgtctctcaacagcctgtgttgtagtcaagcttgggtgtgaagctgtgtctctcaabctg	1840		
Db	2371	AGTTTCGGAACACACACCATTTGTCAAGGCCACCAACCGAGAGCTCTCCATCTCCCTC	2430		
OY	1841	ggctccttgtagtgcgtgggaagtgcagcctctcaagactcttctgggaagccacagtgcc	1900		











GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 18:57:59 : Search time 185.6 Seconds

(without alignments)  
3476.338 Million cell updates/sec

Title: US-09-361-652-5

Perfect score: 2579

Sequence: 1 ttggcgcagatgcttctc.....ggcgcctgcgcactactctga 2579

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125056042 residues

Database : N\_Geneseq\_36:\*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	166.2	6.4	3809	1	T61382	Parathyroid calcinu
2	166.2	6.4	3809	1	T95859	Human parathyroid
3	166.2	6.4	3809	1	V26964	Human parathyroid
4	166.2	6.4	3809	1	V82485	Human parathyroid
5	157.2	6.1	5275	1	T95857	Bovine parathyroid
6	157.2	6.1	5275	1	V25962	Bovine parathyroid
7	157.2	6.1	5275	1	V82483	Bovine parathyroid
8	152.6	5.9	5006	1	T61381	Parathyroid calcinu
9	152.6	5.9	5006	1	T95858	Human parathyroid
10	152.6	5.9	5006	1	V26963	Human parathyroid
11	152.6	5.9	5006	1	V82484	Human parathyroid
12	151	5.8	4000	1	T86186	Nucleotide sequenc
13	150.8	5.8	4131	1	T89290	Dogfish shark kidn
14	138.2	5.4	4131	1	T95860	Rat kidney cell ca
15	138.2	5.4	4131	1	V25965	Rat kidney calcium
16	138.2	5.4	4131	1	V82486	Rat parathyroid ca
17	127	4.9	3384	1	T86185	Nucleotide sequenc
18	125.4	4.9	2148	1	Q73222	BoPCar 1, bovine p
19	82.2	3.2	3919	1	Q80418	Human mglur3 DNA.
20	82.2	3.2	3410	1	T03887	Human mglur3 DNA.
21	73.8	2.9	2732	1	X05810	Mouse pheromone re
22	73.8	2.9	2962	1	X05811	Mouse pheromone re
23	72.6	2.8	2907	1	X05803	Mouse pheromone re
24	72.6	2.8	2409	1	X05842	Mouse pheromone re
25	71.4	2.8	2561	1	X05808	Mouse pheromone re
26	70.8	2.7	2619	1	T16710	Metabotropic gluta
27	70.8	2.7	2519	1	T29408	Human metabotropic
28	70.8	2.7	2821	1	X05813	Mouse pheromone re
29	70.8	2.7	2773	1	X05813	Mouse pheromone re
30	69.2	2.7	3080	1	X05801	Mouse pheromone re
31	69.2	2.7	2550	1	X05840	Mouse pheromone re
32	65.8	2.6	1889	1	X05806	Mouse pheromone re
33	65.8	2.6	1889	1	X05845	Mouse pheromone re
34	65.6	2.5	2394	1	X05863	Rat pheromone rece
35	65.6	2.5	3359	1	X05824	Rat pheromone rece
36	65.2	2.5	3108	1	X05814	Mouse pheromone re
37	65.2	2.5	2412	1	X05853	Mouse pheromone re
38	64.8	2.5	2085	1	X05864	Rat pheromone rece
39	64.8	2.5	3012	1	X05825	Rat pheromone rece

## ALIGNMENTS

40	64.4	2.5	2304	1	X05857	Rat pheromone rece
41	64.4	2.5	3584	1	X05818	Rat pheromone rece
42	64.2	2.5	2961	1	X05802	Mouse pheromone re
43	64.2	2.5	1889	1	X05807	Mouse pheromone re
44	64.2	2.5	2424	1	X05841	Mouse pheromone re
45	64.2	2.5	1889	1	X05846	Mouse pheromone re

## RESULT 1

T61382  
ID T61382 standard; cDNA to mRNA; 3809 BP.

AC T61382; 22-APR-1997 (first entry)

DE Parathyroid calcium receptor coding sequence clone pHPuCAR4.0.

KW Calcium receptor; human parathyroid gland adenoma tumour; pHPuCAR1;

KW primary hyperparathyroidism; Xenopus oocyte; alternative splicing;

KW calcium-activated chloride current; agonist; NPS R-467; NPS R-568;

KW variant; untranslated region; alternative polyadenylation; probe;

KW alternative transcription initiation; pHPuCAR5.2; pHPuCAR4.0;

KW human Car gene; isoform; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 373..3609

FT /\*tag= a /product= Calcium receptor

FT /note= "Pages 94-95 are missing from the specification,

sequence information was obtained from the EPO"

FT W09612697-A2.

PD 02-MAY-1996.

PF 23-OCT-1995; U13704.

PR 21-OCT-1994; WO-U12117.

PA 08-DEC-1994; US-353784.

PI (NPS-) NPS PHARM INC.

PI Balandin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;

DR WPI: 96-23050/23.

DR P-PSDB: W11889.

PT New di:arylalkyl amine cpds. useful for modulating inorganic ion

PT receptor activities - esp. for modulating effect of extracellular

PT calcium on cell surface calcium receptors, useful for treating e.g.

PT hyperparathyroidism, Paget's disease or osteoporosis

PS Example 1, Page 93-100/231pp. English.

CC The sequences given in T61381-82 encode functional calcium receptors.

CC These sequences were isolated from human parathyroid gland adenoma

CC tumour using pHPuCAR1 as a hybridisation probe. mRNA was isolated from

CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism

CC and two clones of approx. 5 and 4 kb were identified. These cDNAs were

CC injected into Xenopus oocytes which were assayed for the presence of

CC functional calcium receptors. Both clone types gave rise to functional

CC chloride currents upon addition of appropriate calcium receptor agonists,

CC e.g. NPS R-467 and NPS R-568. Sequence analysis of the two cDNA clones

CC indicated the existence of at least two sequence variants differing in

CC the 3' untranslated region and which may result from alternative

CC polyadenylation. Sequence variation also exists in the 5' end of the

CC inserts. These sequence differences may have arisen due to alternative

CC transcription initiation and/or splicing. Three additional sites of

CC sequence variation occur within the coding regions of cDNA clones

CC pHPuCAR5.2 and pHPuCAR4.0 demonstrating that they encode distinct

CC proteins. Sequence analysis of the human Car gene indicates that the

CC additional 30 bp in clone pHPuCAR5.2 as compared to pHPuCAR4.0, results

CC from alternative mRNA splicing. Thus alternative splicing is predicted

CC to insert 12 additional amino acids into the Car protein encoded by

CC pHPuCAR5.2 between residues 536 and 537 of the protein encoded by

CC pHPuCAR4.0. In addition pHPuCAR4.0 encodes Gln at position 925 and Gly

CC at position 990, whereas pHPuCAR5.2 encodes Arg at both equivalent

CC positions. The human Car gene encodes for Gln and Arg respectively at

CC these positions. These two receptor isoforms may be functionally and/or

CC pharmacologically distinct.

SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;



Query Match 6.4%; Score 166.2; DB 1; Length 3809;  
 Best Local Similarity 46.3%; Pred. No. 1.6e-33;  
 Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

QY 206 tctgacagcttcaacggcagctatcaaccttccaagcagctggttcaacgttga 265  
 DB 550 TGTATGAGTATATTTCCGCGTTTCGCTGTACAGGCTATGATATTTGCCATAGAG 609  
 QY 266 gagataaacacctccacagctctgttcccaacacccctgggtgtatgaactatgac 325  
 DB 610 GAGATTAACACGCCACGCCCTTCTCCCACTTGACGCTGGGATACAGATATTTGAC 669  
 QY 326 gtgtctcagagcttccaaatgtct---atggcacccttggaggtgcccacagca--- 379  
 DB 670 ACTTGCAACACCGTTTCTAAGGCTTGAAGCCACCGTGAATTTGTTGCTCAAAACAAA 729  
 QY 379 --aggagcaggccacatagatagacagagatcttcgcaacacacccctccaaggtgtg 436  
 DB 730 ATTGATCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACAAATTCCTTACGATT 789  
 QY 437 gcaactatggcgctgatacactgacacagctgtcaacactgtgccttgccttgaagcct 496  
 DB 790 GCTGTGGTGGAGTCACTGGCTCAGCGCTCTCCACGGCAAGTGGCAAACTGCTGGGCTC 849  
 QY 497 ttctcgtacccctgtcagctatagacagcagcagctgtatcctcagtgaggagcgaag 556  
 DB 850 TTCTACATTCGCCAGTCAAGTATGCTCTCCACAGACACTCCCTCAGCAACAAACAAACAA 909  
 QY 557 ttccgctctctgtgcacacacacccacagacatgaacaggtggaatcatatgtcgg 616  
 DB 910 TTCAAGCTTTCTCCCAACCATCCCAATGATGAGCACCGGCACTGCCCTTACGCGAC 969  
 QY 617 ctgctgagagagctcggctgagctgtgatactcgtctgttgcagctgtgtgactaagg 676  
 DB 970 ATCATCAGATATTTCCCTGCACTGGGTGGCCAAATTCGAGCTGATGACACTATGAGG 1029  
 QY 677 cagctggcgtacacagcgttggaggagctgtgcacacccacagcagctgtcgtccttc 736  
 DB 1030 CGGCGGGGAGTTGAAATTCGAGAGGAAGCTGAGAAAGGAGATCTGATGAGACTTC 1089  
 QY 737 aaggagctgtgtcctctcccgccagcaggcgggtgacccaagatgcagcagatgtcgt 796  
 DB 1090 AGTGA-----ACTCATCTCTCCACTACTCTGATGAGAGAGATGACAGATGCTGTAGAG 1143  
 QY 797 cgtctgctcgaagcagacacccgtgtgtgtcttcttcaacggcagcctgtgcgtga 856  
 DB 1144 GTGATTTAAAATTCACGGCCAAAGTATCGTGGTTTCTCCAGTGCGCCAGATCTTGAG 1203  
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 DB 1204 CCCCTCATCAAGGAGATTTGCCGGCAATATCACGGGCAAGATCTGGCTGCCAGGAG 1263  
 QY 917 gactggcactcctccacgtacatacacaatgtgcggagatccaaggaatgtggagcgtg 976  
 DB 1264 GCCTGGGCGAGCTCTCCATGATGCGCATGCTCAGTACTTCACTGATGCTGGGGGCGAC 1323  
 QY 977 ctgggggtgtgcacatccagcagagacagctcctgtgagagaggtt----- 1024  
 DB 1324 ATTGGATTCGCTCTGAAGGCTGGGACATCCAGGCTTCCGGGAATTCCTGAAAGAGTTC 1383  
 QY 1024 -----tgaagagctctatgtccagcagtgatgt----- 1052  
 DB 1384 CATCCAGAGAGTGTGCAAAATGTTTGGCAAGAGTTTGGGAAGAAACATTTAAC 1443  
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 DB 1444 TGCACCTCCAGAGAGGTGCAAAAGACCTTTACTGTGACACACTTCTTAGAGGTTCAC 1503  
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 DB 1504 GAAGAAAGTGGCAGAGGTTTAGCAACAGCTCGACAGCCTTCGAGCCCTCTGTACAGGG 1563

QY 1112 tgtcacgttccagacatgtgaacatgcccagacttggagccttccatcagcgtgc 1171  
 DB 1564 GATGAGAAATCATGAGAGTGTGAGACCCCTTACATGATATACAGCATTTAGAGATATCC 1623  
 QY 1172 taacaagtatataagctgtgtatgtctgtgtgcccagggcctccaagctcctgtgagt 1231  
 DB 1624 TACAAATGTACTTACAGAGTCTACTCCATGTCCAGCGCTTGGCAAAATATATATACCTGC 1683  
 QY 1232 acctgtggagcctgt-----tgcagagggcccaggtcacc 1267  
 DB 1684 TTACTGTGGAGAGAGGCTCTTACCAATGCTCCTGTGCAACATCAAGAAAGTTGAGCG 1743  
 QY 1268 tggcagcttcttcaagagatctcaaggtgaattcttcttacaataaga---agactgta 1324  
 DB 1744 TGGCAGGTCTGAAGACACTTACGGCATCTTAACATTACAAACAAATGTGGGGAGCAGGTG 1803  
 QY 1325 gcaatgatgtacaaaggggagccctcaggtatataagacatcgtcctgtggacttgaat 1384  
 DB 1804 ACCTTGATGATGTGTGTGCTGAGGAGAACTATTCATCAACTGACACTCTCC 1863  
 QY 1385 ggaacctgaatggaaccttggagctgtgtgtgtcct-----cactgtct 1429  
 DB 1864 CAGAGGATGTGCTCCATCGTGTTAAGGAAGTGGGATATTACAAGCTTATGCAAGAA 1923  
 QY 1430 ccaattcatatagacataaataagacaaaatccagtgagcagcggagaaacalcagtg 1489  
 DB 1924 GGAAGAAAGACTTCTTCAACGAGAGGAAATCTGTGAGGTGGTCTCCAGGAGGTG 1983  
 QY 1490 cctgtgtcagtggtgtacagagagctgtctcgaaggcaccacaggtgtgtcat---gggt 1546  
 DB 1984 CCTTCTCCAACTGCAAGCCAGCTGCTGGCAGGAGACCGAAGAGGATCAATTGAGGG 2043  
 QY 1547 tccacacacagctcgtctcgtgagatgcccgtggaagctgtgagacatttcccaacagagt 1606  
 DB 2044 GAGCCCACTGCTGCTTTAGAGTGTGTGAGATGCTCTGATGAGGAGATATGATGAGACA 2103  
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 DB 2104 GATGCGAGTCTCTGTAAACAGTCCCAAGATGACTTGTGCTGCTCAATGAGAACACACTCC 2163  
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 DB 2164 TGCATTGCCAAGAGATTCAGATTCTGTGCTGAGCAGGAGCCCTTGGAGTCGACATCAC 2223  
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 QY 1787 cttaacacgctgt 1846  
 DB 2284 CGCAACACACCCATTGCAAGGCGCACCAACCGAGACTCTCTTACCTCTCTCTCC 2343  
 QY 1847 ttgt 1906  
 DB 2344 CTGCTGTGCTGTCTTCCACACTCTCTGTCTTCAATGGGGAGGCCCAAGAGCTGAGAGTGC 2403  
 QY 1907 ttgt 1966  
 DB 2404 CGCTGTGGCAGCGCGGCTTGTGGCATCAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2463  
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 DB 2521 AAGTGTGGGGGTCAACCTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
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 DB 2581 GTATCTGT 2640  
 QY 2147 ttcccccactgt 2206



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Db 2641 GAGAGATGATCATCTTCAATCAGCTGCGACAGAGGCTCCCTCATGGCCCTGGGCTTCTG 2700
QY 2207 ttgcacaaacactctctctccalcacagaccttctgtcgcagcttaacctggtaaggaa 2266
Db 2701 ATCGGCTACACCTGCTGCTGGCTGCATCTGCTTCTTTCTTCAAGTCCCGAAG 2760
QY 2267 ctgcacgaagaactatacagaagaatgttacccttcagctgcctgcctccactcgtc 2266
Db 2761 CTGCCGAGACACTTCATGAAGCCAGTTTATACCTTCAGCATGCTCATCTTCTTCATC 2820
QY 2327 tccctgagctcctcttcacacatgctcagacatlaacaggagcagctaccacccgagtc 2386
Db 2821 GCTCGATCTCCTTCAATCCAGCCCTATGCCAGCAGCTATGCCAAGTTGCTCTGCCGTA 2880
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Db 2881 GAGGTATTGCCATCTCGAGGAGCAGCTTGGCTTGGCTGCGATCTTCTTCAACAAG 2940
QY 2447 tgcctagctatctctgcgcgtccagacactcaacaacagaa 2487
Db 2941 ATCTNATCATCTCTTCAAGGCATCCCGACACCATGCA 2981

RESULT 2
ID 195859
T95859 standard; cDNA to mRNA; 3809 BP.
AC T95859:
DT 08-MAY-1998 (first entry)
DE Human parathyroid cell calcium receptor 4.0 (HuPCar 4.0) cDNA.
KW Human parathyroid cell calcium receptor 4.0; HuPCar 4.0;
KW calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 373..3809
FT /tag= a
FT /product= parathyroid_cell_calcium_receptor_4.0
PN US568938-A.
PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM) BRIGHAM & WOMEN'S HOSPITAL.
PA (NESP) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
PI WPI; 98-008040/01.
DR P-PDB; W38274.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PT Claim 15; Columns 125-134; 174pp; English.
CC The present sequence encodes human parathyroid cell calcium
CC receptor 4.0 (HuPCar 4.0).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T;
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Query Match 6.4%; Score 166.2; DB 1; Length 3809;
Best Local Similarity 46.3%; Pred. No. 1.6e-33;
Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;
```

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QY 206 tctgacagcttcaacggccatgctatacacccttcaccaagccatgggtcaacggttag 265
Db 550 TGTATAGGATATTAATTCCTGGGTTCGCTGTTACAGGCTATGATTTCCCATAGAG 609
QY 266 gagataaacaactccacagctctgtctccacaatacacccttgggagtgaactgtatgac 325
Db 610 GAGATTAACAGCAGCCACCCCTCTCTCCCACTTGACGCTGGGATACAGATATTGAC 669
QY 326 gttgtctcagagctctccaatgtc--atgccaccctgaaggtgcccgcacaga---- 379
Db 670 ACTTGCAACACGCTTCTTAAGGCTTGAAGCCACACCCCTAGTTGTTGCTCTCAAAAACAA 729
QY 379 --agggacggccaccataagatgacgaagaagctcttcgaacacacccccaagtgtg 436
Db 730 ATTGATTTCTTGAACCTTATAGATTCTGCAACTGCTCAGACACGACATTCCTCTACGATT 789
QY 437 gcactcatgggacctgataaacctgacacgctgtacacacgtgcctgtctgaagccct 496
Db 790 GCGTGTGTGGAGCAACTGGCTCAGGCCGCTCCACGGCAGTGGCAAAATTCGTGGGGCTC 849
QY 497 ttctgaatgccctctggctcagctatgaagcagacgttatcctcagttggagcgcgaag 556
Db 850 TTCTACATTCGCCAAGGTCAAGTATGCTCTCCAGAGACTCCTCAGCAACAAGATCAA 909
QY 557 ttcccgctctcttctgggcacccatcccccagcgttaagctacagagtggaagtcatagtg 616
Db 910 TTCAAGTCTTCTCTCGAAGCATCCCAATGATGAGCACACGACCACTCCATGGCAGAC 969
QY 617 cgcctcagaagctcgcgcgtgggtcgtgacatcgcctcgttggcagctatgttactacg 676
Db 970 ATCATGAGATATTTCGCTCGAAGCTGAGTGGGACACATTCGACGCTGATCAGCATATGG 1029
QY 677 cagctgggcgtacagggcgtggaagagcctggcaccctcaacggggatctgcctgccttc 736
Db 1030 CGGCGGGGATTGAGAAATTCGAGAGAACTGAGAAAGGATATCTGCATCGACTTC 1089
QY 737 aaggacgtgtgtcctctccgcgccagggggtgagcccaagatcagagcatgtagtgc 795
Db 1090 AGTGA-----ACTCATCTCCAGTACTCTGATGAGGAAAGATCCAGATGTGGTAGAG 1143
QY 797 cgtctgcgcagccagacacacgctggtcgtgtgtctctcaccagggacctggtcga 856
Db 1144 GTGATTCAAATTCAGAGGCCAAAGTCATCGTGGTTTCTCCAGTGGCCCAATCTTGAG 1203
QY 857 gttctctcaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 916
Db 1204 CCCCTCATCAAGAGATTTGTCGGCGCAATATCACGGGAGATCTGGCTGGCCAGCGAG 1263
QY 917 gactggggcactctccacgtacatacacaatgtgcctcgagataccagggcatgtgagcgtg 976
Db 1264 GCTTGCGCCAGCTCTCTCCGTGATCCCAAGCCCTCAGTACTTCACGCTGGTTGGCGGACCC 1323
QY 977 ctgggggtggccatccagagagacaagtccctggccctgaagagatt----- 1024
Db 1324 ATTGATTTGGCTCTAAGGCTGGGCAATCCAGGCTTCCGGGAATTCCTGAAGAAGTTC 1383
QY 1024 -----tgaagatctatgtccagcagttgta----- 1052
Db 1384 CATCCAGGAACTGTGTCACAAATGTTTGCCAGAGATTTTGGGAAGAAACATTTAAC 1443
QY 1052 -----gtgtctccagaaacttgcagaagaggtctgtgtgcgactaac 1096
Db 1444 TCCCACTTCAGAAAGGTGCAAAAGACCTTACCTGTGGAGACCTCTTGAGAGGTAC 1503
QY 1097 -----cagcttgcagggag 1111
Db 1504 GAAGAAAGTGGGACAGGTTTAGCAACAGCTGAGACGCTTCGACCCCTCTGTACAGGG 1563
QY 1112 tctcagcttccagacatgacacatgacacatgacacatgacacatgacacatgacacatg 1171
Db 1564 GATGAGAACATCAGCAGGTGTGTCAGAGCCCTTATCATAGATTTACAGCCATTTACGATATCC 1623
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OY	1172	taaatggtatagagcctgtgtatgctgtgagccacagcgctccacagctctcgtggaagt	1231
Db	1654	TACAAATGTGTCTTAACGAGTACTCATTCATTGCCAGCCTTGCAAGATATATATACCTGC	1683
OY	1232	acctctggaccctg-----tgccagagccagctctacccc	1267
Db	1684	TTACTGGGAGAGGGCTCTTCCAAATAGGCTCGTGTGACAGACATCAAGAAATTTGAGGG	1744
OY	1268	tgagcgtctcttcacgagatctacaagtgaaattccctctacataaga--agactgta	1324
Db	1744	TGGCAGGTCCTGAAGACACTACGGCACTATACTTACAAACAAATATGGGGAGCAGAGTG	1803
OY	1325	gcattcgatgacaaggagagaccctcgtgtattatagacatacgccggagcaggaat	1383
Db	1804	ACCTTTGATGTGCTGTGTGACCTGTGTGGAGACTTATTCATCATCAATCGGCACCTTCC	1863
OY	1385	ggacctgaaatgaaactcttgagtgatcattgcttcgcct-----cactgtct	1429
Db	1864	CCAGAGATGGCTCTCATTCGTGTTTAAAGAGTGGGGATTATCAACTATATCCAAAG	1922
OY	1430	ccagttcatctagacataaataaagaacaaaaaccagtgcaacgggaaagaacaatacagtg	1489
Db	1924	GGAGAAAGACTCTTCATCAACAGAGGAAATAATCCTGTGGAGTGGTTTCCAGGAGAGTG	1983
OY	1490	ccgtgtcaagtgcttaccaagagctgtctcgaaggcacacaagtgctat---aggt	1546
Db	1984	CCCTTCTCAACTCAACCCGAGACTGCTGTGGCAGGACCAAGAAAGGATCTTGAAGGG	2043
OY	1547	tccacacactgtccttcctcagtgcatccctcgtgaaagctggagaaactctcaacagagt	1606
Db	2044	GAGCCACACTCCTCTTGTAGTGTGTGAGATGTCTCGATGGGAGATATGTCATAGACA	2103
OY	1607	gaacttcaacactctgcagccttgtgaaacgaagaatlyggcccgtgaaggagactcaagc	1666
Db	2104	GATGCCAGTGGCTGTATAAGATGCCCGCAGATGACTTGTGGTCAATGAGAACACACACTCC	2163
OY	1667	tgctcttcaacgcaacgctggaggtctcttgagtgacagaaccatccttggtglatata	1726
Db	2164	TGCAATTGCCAAGAGATGAGATTCGTCTGTGACGAGACCCTTGGATGCCACTCAAC	2223
OY	1727	gcacgtaacaacgctatctgtcgtcgtcgtcgtatctgaaagctgcgtctgttcctgcgagt	1786
Db	2224	CTCTTTGCCGTGTCTTCCAACTCCCTGTTCATGTGGGAGACCCCAAGACATGACGTGC	2283
OY	1787	cttcaacagcctgttgtgagtgcaagctggggatgaagctgtgcttccatcagctgggttc	1846
Db	2284	CGCAACACACCCATTGTCTCAAGGGCACCAACCGAGAGCTCTCTACCTCCTCTTCTTC	2343
OY	1847	ttgttagctggaggtgtgcaagccctcaagcttcttggaagcccaagctgcgcgcgtgc	1906
Db	2344	CTGCTGTGCTTCTTCCAACTCCCTGTTCATGTGGGAGACCCCAAGACATGACGTGC	2403
OY	1907	ttgtctgctcaagccccctctctctctcgtgggttgccattctctctcgtctgcaatc	1966
Db	2404	CGCCTGGCCAGCGCGCCTTTGGCAATCAGTTGTGTCTGTCAATCATGATCCTGGTG	2463
OY	1967	cgcctcttcaacatgycatcalcatcttcaagtttcttcaacaagttaaccaatcttcaac	2026
Db	2464	AAAACCAACCGTGTGCTCTCGGTGTGAG---GCCAAGATCCCAACAGCTTCCACGCG	2520
OY	2027	acttgggcccaaaaaccatgtgtccggaatatctcgtcatgtgaagctcaaggtccatttg	2086
Db	2521	AAGTGTGGGGGCTCAACCTGAGATTCTGTGCTGTTCCTCTGCACTTCATGTGAGATT	2580
OY	2087	ttctcctgtctcaatgtgctgtgcaatgtgtaacccacggccacaagggaagtaacaggc	2146
Db	2581	GTCATCTGTGTGATCTGTGCTTACACCGCGCCCTCCACAAGTACCGCAACGAGAGTG	2640
OY	2147	ttcccccactgtgtatctcttgatgtcacaaagtaactcgtgtgcttcgttggtc	2206
Db	2641	GAGGATGAGATCACTTCATCACTACGTGCAAGAGAGGTCCCTCATGGCCTGGGCTTCTG	2700
OY	2207	ttcgacacaacatcctctctccatcagaacacctgtgtcagcthaacctggtlaagaa	2266

DB	Accession	Position	Sequence	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length
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D	b	550	TGTATCAGGTAATAATTCCGGTGTTCCTGGTTACAGGCCTATGATATTGCCATAGAG	609
O	y	266	gagataaaacatccacaagctctgcctcccaacatalaccctggsgtatgaactgtagac	325
D	b	610	GAGATAAACGACGCCACCCTCTTCCCAACTTACCCCTGGGATACAGATATTTGAC	669
O	y	326	gtgtcctcagaagctctccaagtct--atgccacctgaagggtgcccgcccagca---	379
D	b	670	ACTTCACACACCGTTTCTTAAGCCCTTGAAGCCCATCCCTAGTTTGTGCTCAAACAA	729
O	y	379	--agggaacagccaccttaagaatgacagaagattctgcgaaccacctcccccaagtgag	436
D	b	730	ATTGATTTCTTGAACCTTGATAGATTCTGCACACTGCTCAGAGCACATTCCTCTACGATT	789
O	y	437	gcaaccatttggccctgatatacaacttgaccaagctgltcaccaagcttcgccctggaacct	496
D	b	790	GCTGTGTGGTAGACAAGTGGCTCAGCGCTCTCCACGGCAGTGGCAATGTCTGGSGGCTC	849
O	y	497	tctctgatgccccttggtcagctaataggcgagcagcgctgataccctcagttggaaaagcgcaa	556
D	b	850	TTCTCATATCCCACAGTCAAGTATAGGCTCTCCACAGACACTCCTCAGCAACAAAGATCAA	909
O	y	557	tcccgctcctctctgcgcgcccatlccccagaataagtlaccaggtggaaatcataagtcgag	616
D	b	910	TTCAAGTCTTTCCTCCGAACCATCCCAATGATGAGCACACAGCCACTGCCATGGCAGAC	969
O	y	617	ctgcgcgaagagcttcgcgctgggtctgatatctgcctcgtctgcacagctatgtgtacacgg	676
D	b	970	ATCATCGAATATTCCGCTGGAACTGGTGGGCACATTCGACACTATATACGACTATGGG	1029
O	y	677	cagctcgcgcgtacaaagcgcttggaagagctcgcgcacatcccaagggcaatctgcctgcctc	736
D	b	1030	CGCGCGAGATTGAGAATTCGAGAGGAAGTGAAGAAAGGATATCTGCATCGACTTC	1089
O	y	737	aaggaagtgagtgctctctcctcgcgcccaagcgcggtgacccaagaatgacgcgcatagtatcg	796
D	b	1090	AQTGA-----ACTCATCTCCAGTACTCTGATGAGAGAGAGATCCAGCATGTGGTAGAG	1143
O	y	797	cgctcgcctcgcgcgaagacacccggtgctcgttgtctctctcaaccggaacctggtctga	856
D	b	1144	GTGATTTCAAAATTCACGGCCAAAGTCATGTGTGTTTTCTCCAGTGGCCCAAGATCTTTGAG	1203
O	y	857	gtgtctcctaagctcgtgtgtgtctgcgccaaccgtacgtgcgaagtgtgtatgcgctccgaa	916
D	b	1204	CCCCATCAAGAGATGTCCGGCGGCATATCACGGGCAAGATCTGGCTGGCCACAGAG	1263
O	y	917	gactcgcgcacatccacgtatcatcaccaatgtgcgcggatcccaaggcatctggagacggtg	976
D	b	1264	GCCTGGGCGAGTCTCTCCCTCGATCGCATGCCATGCTACTTCCACGTGGTTGGCGGCACC	1323
O	y	977	ctcgggggtggtccatccagaagaagaagctccctgcgtctgaagagctt-----	1024
D	b	1324	ATTGATTTGCTCTGAAGGCTGGGCGATGCCAGGCTTCGGGAATTTCTGAAGAAAGTTC	1383
O	y	1024	-----tgaaggtctctatgtcceaagcagtgatg-----	1052
D	b	1384	CATCCAGGAAGTCTGTCCACATGTGTTGCCAAGAGATTTTGGGAAGAAACATTATAC	1443
O	y	1052	-----ggtctcccaagaacttgcccagaaggggtcctgtgtgcgcactaac	1096
D	b	1444	TGCCACCTCCAGAAGAGTGTCAAAAGACCTTTACTGTGGACACTTTCTGAGAGGTGAC	1503
O	y	1097	-----cagctgtgcagggag	1111
D	b	1504	GAGAAAGTGGCGACAGTTTGAACAAGCTCGACAGCCTTCGACGCCCTCTGTATACAGG	1563
O	y	1112	gtctacgctcttaacgacatgacacatgcccgaagcttgagacctctccatgagcgtccg	1171
D	b	1564	GATGAGAACATCAGAGTGTCCAGAGACCCTTATCATATGATTTACACGCAATTACGGAATTC	1623
O	y	1172	tacaaatgtatgagagctgtgtatgctgtgcgccacgcgctccacacagctcctcggagatg	1231



OY	2267	ctccggaggaactaatacgaagcaaatgtgtcacctcagctgcctccacactcgta	2326
Db	2761	CTCGCGGAGAACTTCATGGAAGCCAAATTATCATCCTTCAGCATGCTCATCTTCTTCAATC	2820
OY	2327	tccctgatacgtcttcttcaccatgltccagaattaccagggcagactaccocgagtc	2386
Db	2821	GTCGGAATCTCTTCATTTCCAGCCTATGACAGACCATATGGAAGTTGATCTGTGCCGTA	2880
OY	2387	aatgtcgtcgagagggctcggccacactctgaigtggcggtctcagcgctatttcctcctaa	2446
Db	2881	GAGGAGATTCGCAATCCGAGCAGCCAGCTTTGGCTTGCTGGCGTCATCTTTCAACAAG	2940
OY	2447	tgctacgtgatctctcgcgcgcgcgaactacaaca	2487
Db	2941	ATCTCATCATCATCTCTTCAGCCATCCCGGACACCATGCA	2981
RESULT	4		
V82485			
ID	V82485	standard; cDNA to mRNA; 3809 BP.	
AC	V82485:		
DE	19-MAR-1999	(first entry)	
KW	Human parathyroid calcium receptor pHPaCR 4.0 encoding cDNA.		
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;		
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;		
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;		
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;		
OS	depression; anxiety; ss.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	373..3609	
FT		/*tag= a	
PN	US5858684-A.		
PD	12-JAN-1999.		
PF	07-JUN-1995; US-480751.		
PR	07-JUN-1995; US-480751.		
PR	23-AUG-1991; US-749451.		
PR	11-FEB-1992; US-834044.		
PR	21-AUG-1992; US-934161.		
PR	12-FEB-1993; US-017127.		
PR	23-FEB-1993; US-009389.		
PR	22-OCT-1993; US-141248.		
PR	19-AUG-1994; US-292827.		
PR	21-OCT-1994; WO-012117.		
PR	08-DEC-1994; US-353784.		
PA	(BGMH ) BRIGHAM & WOMEN'S HOSPITAL.		
PI	(NPSP-) NPS PHARM INC.		
PI	Balandrin MF, Brown EM, Del Mar EG, Garrett JE,		
PI	Hebert SC, Nemeth EF, Van Wagenen BC;		
DR	WPI: 99-119871/10.		
DR	P-PSDB: M89565.		
PT	Screening for calcium receptor-active compounds - by recombinant		
PT	expression of nucleic acid encoding calcium receptor and determining		
PT	the effect of compounds on calcium receptor activity		
PS	Claim 1; Fig 49; 176pp: English.		
CC	A method has been developed of screening for a compound able to affect		
CC	one or more activities of a calcium receptor (CR) comprises: (A)		
CC	contacting a recombinant cell with a test compound, where the		
CC	recombinant cell comprises a recombinant nucleic acid expressing the CR,		
CC	provided that the cell does not have functional CR expression from		
CC	endogenous nucleic acid; (B) determining the ability of the test		
CC	compound to affect one or more activities of the calcium receptor; and		
CC	(C) comparing the ability with the abilities of the test compound to		
CC	affect the one or more CR activities in a cell not comprising the		
CC	parathyroid nucleic acid. The present sequence encodes human		
CC	parathyroid CR, designated a pHPaCR 4.0. The nucleic acid sequence of		
CC	pHPaCR 4.0 can be used as part of the recombinant nucleic acid in the		
CC	method described above. The compounds identified can be used to treat		
CC	diseases or disorders characterised by abnormal calcium homeostasis, e.g		
CC	hyperparathyroidism, osteoporosis and other bone and mineral-related		
CC	disorders. They can also be used for the treatment of diseases and		

CC disorders associated with disrupted Ca2+ responses, e.g. seizures,  
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
CC diseases such as Alzheimer's disease, Huntington's disease and  
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
50 Sequence 3809 BP: 910 A; 1071 C; 979 G; 849 T;

Query Match	6.48;	Score 166.2;	DB 1;	Length 3809;
Best Local Similarity	46.38;	Pred. No. 1.6e-33;		
Matches 1130;	Conservative	0;	Mismatches 1143;	Indels 168; Caps 11

QY	206	tcctaaagcttaagcgcaatgagctctctaaaccccttccaagcaagatcggtttacacgtttg	265
Db	550	TGTAATCAGGATTAATTTCCGTGGGTTTCCTGGTTACAGGCTATGATATTTTGGCATAG	609
QY	266	gagaataacaacatcccaagctctgtcttcccaacatcaccccttgggttlaagaaactlatagc	325
Db	610	GAGATAAAGACAGCCAGCCCTTCTTCCAACTTGAGCGTGGATTACAGATATTGGAC	669
QY	326	gtgtgtcctcagagctctctccaatgtct---atgcacccttgaagggtgtcccgccagca---	379
Db	670	ACTTGCACACCGTTTCTTAAGGCGCTTGAAGGACACCGACTGAGTTTGTGTCCAAACAAA	729
QY	379	--aaggacagcgccacatagatagcaagagaatcttcgaaccaccctctccaaggtgtg	436
Db	730	ATTGATTTCTTTGAACCTTGATGATTTCTTCAACTGCTCAGACACATTTCCCTTACGATT	789
QY	437	gcactcaattgagcctgataacaacttgcacacgctgtccaccactgtccctctgtagccct	496
Db	790	GCATGGTGGGAGCAACTGGCTTCAGGCGCTCCAGGGCAGTGGCAATCTCTGGGGCTC	849
QY	497	ttctctgctcccttgcataagcatalgaagcgagcagtgatctcactagtgaggaaqcgcaag	556
Db	850	TTTACACTTCCCGAGTCAAGTATGCGCTCTCAGACAGACTCTCAGCAAGAAATCAA	909
QY	557	ttcccgctcctcttgcagcaatccccagcgtatgaatccaggttgaaagtatatgtgcg	616
Db	910	TTTCAAGCTTTCTTCGGAACCATCCCAATGATGAGCAACAGGCGACTGCGATGGAGAC	969
QY	617	ctgtgtcagaagctctgagctgggtctgtgactcgtctgttgagctatgtgtactgaag	676
Db	970	ATCATGACGATATTTCCGCTGGAACTGGGTGGGCAAAATTGCAAGCTGATGAGACTATGG	1029
QY	677	caagctggcgctaacaggcgcgttgaaggaagctgtgcactccacgcgggcatctgtctgcctc	736
Db	1030	CGGCGGGGATTGAGAAATTCGAGAGGAAGCTGAGGAAGGATATTCGATCGACTTC	1089
QY	737	aagaagctgtgtcctctctccgcccagcggtgtgaacccaagatgacgcgcatgtctg	796
Db	1090	AGTGA-----ACTCATCTTCCAGTACTCTGTATGAGGAAGAAATCACACATGTGTAG	1143
QY	797	cgctgtcctcagcagaagacacacgctgtgtcgtgtctctctcaacgcgcacctgtgcgtga	856
Db	1144	GTAATTAATAATTCCACGGCCAAAGTCATCTGTGTTTCTCCAGTGGCCAGATCTTGAG	1203
QY	857	gtgtcttctcaggtctgtgtgtctgtgcaccaactgcacttgcgcaagtgtgatacgctccga	916
Db	1204	CCCTCATTAAGAGATTTCTCGGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGGAG	1263
QY	917	gacttgggcactctccacgtatcaccaccaagtgtgccggagatccaggaacttgggaacgtg	976
Db	1264	GCGTGGCGCAGCTCTCCCTGTATCGGCATGCTCTCACTTCCACAGTGTGGCGGCAACC	1323
QY	977	ctggtgggtgtgcctcagcagagagaacagtcccttgccttgaagggatt-----	1024
Db	1324	ATTGGAATTCCTCTGAAGGCTGGCGAGATCCACAGGCTTCCGGGAATTTCTGAAGAGGTC	1383
QY	1024	-----tgaaagctcctatgtccagcagtgatg-----	1052
Db	1384	CATCCCAAGGAGTCTGTCCACATGTTTTTGGCCAAAGGATTTTGGGAAGAAACATTTAAC	1443
QY	1052	-----ggtgtctccagaacttgcacagaaggttctctgtgtgcgactaac	1096



1444 TGGCACCTCCAGAGGCTGCAAAAAGGACCTTACCTGTGGACACTTTCAGAGGTAC 1503  
1097 -----cagcgttgaggag 1111  
1504 GAAGAAAGTGGCGACAGTTTAGCACAGCTCGACAGCCTTCGACCCCTCTGTACAGGG 1563  
1112 tgcacgcttcacagacatgaaatgccgagcttgagcccttcctcatgagcgcgc 1171  
1564 GATGAGAACTACGACAGTGTGAGACCCCTTAGATAGATTACAGCGATTACGGATTCC 1623  
1172 tacaatgtatagagcgtgtatgtctgtgcccacggcctcaacagcctctggagat 1231  
1624 TACAATGTACTAGTACGAGCTACTCCATTGCCACGCCCTTGCAAGATATATATACCTGC 1683  
1232 accttggagacctg-----tgccagaggccagcttacc 1267  
1684 TTACCTGGAGAGGGCTTTCACCAATGGCTCTGTCCACAGATCAAGAAAGTTGAGCGG 1743  
1268 tggcagcttcctcagcagatcacaaagtgaatttcctctacaaga--agactgta 1324  
1744 TGGCAGGTCTTGAGGACCTACGGCATCTTAACCTTACAAACATATGGGGGACAGGTG 1803  
1325 gcaatgatacaaggaggaccctcagttatatagacatcagccttgagctggat 1384  
1804 ACCTTGATGATGTGTGATGCTGTGGGAGACTATTCATCATCACTGGACACTCTCC 1863  
1385 ggcacggaaatggaccttgagctatgtgttcgcct-----cactgtct 1429  
1864 CCAGAGATGGCTCCATCGTGTAAAGAGTGGGTATACAAAGTCTATGCCAAG 1923  
1430 ccagttatctagaataaataagacaaatccagtgcacaggaagaacaatcagtg 1489  
1924 GGAGAAAGATCTTCTACACAGAGAGAAATCTGTGAGATGGCTCTCCACGAGAGTG 1983  
1490 cctgtgtcagtggttacagggacgtctcgaaggcgaccacaggttgatcat---gggt 1546  
1984 CCTTCTCCACTGACGCCAGCAGACTGCTGTGGAGGACCGAAGAGGATCATTTGAGGGG 2043  
1547 tccacacacgctgcttgatgagctcgtggaagcttgagacatctccacaacgaat 1606  
2044 GAGCCCACTGCTGCTTTGAGTGTGAGTGTCTGATGGGAGTATAGATGAGACA 2103  
1607 gacgttacacacgtgcagcccttgagacagaagaatggccccctggaggagatcagcc 1666  
2104 GATGCCAGTCTCTGTAACAGATGCCGAGATGACTTCTGTGCTCAATGGAACACACTCC 2163  
1667 tgccttcacgacacgttgagctcttgagggtgagatgaaccatctcttggtgctatta 1726  
2164 TGCATTGCCAAGAGATCGAGTTCTGTCTGACGAGCGCCTTTGGATCGCACTACCC 2223  
1727 ggcagctaacacgtatgctgcgtgcgtgcgtatctggagacgtcgtgcgttgccctggcgt 1786  
2224 CTCTTGGCTGTGGGCAATTTCTGTACAGCCTTTGTGTGGGTGTGTTATCAAAATTTC 2283  
1787 ctccacagcgtctgtgaggtcagcgtggaggtcgtgcttcctccagcgtgggttc 1846  
2284 CGCAACACACCATTTGTCAAGGCCACCAACGAGAGCTCTCTCACTCTCTCTTCTCC 2343  
1847 ttgtagatggaggttgacgctcttaacgctcttcggagagcccaaggtgacgcggtgc 1906  
2344 CTGCTCTGCTGCTTTCACACTCCCTGTCTCATCGGAGGCCCGCAGACTGGAGCTGC 2403  
1907 ttgcttgtagagccctcttctctcgggttgccatcttctctcctcgtcgtacatc 1966  
2404 CGCTTCGGCGAGCGGCTTTGGCATAGCTTGTGTCTGCACTCTCATCATCACTCTGGTG 2463  
1967 cgtctctccaaatggtatcatcatctcaaatcttctacaagagaccacatcttacaac 2026  
2464 AAACCAACCGTCTCTCCGCGGTTTGAG---GCCAAGATCCCCACACACTTCCACCGC 2520  
2027 acttgggcccacaaacatggtgcgcgaataatggtcatgttcagcttccacggttccatg 2086

2521 AAGTGTGGGGGCTCAACCTGACTTCCTGCTGTTTCTCTGACACTTCATGACGATTT 2580  
2087 ttctctgtctcagcgtggcttgcaatgtgacccccacgcgccacaggagatccagcgc 2146  
2581 GTGATCTGTGTATGTGGCTTACACCGCGCCCCCTCAAGCTACCGCAACGAGGAGCTG 2640  
2147 ttcccccactctgtgattctctgagtgacagagtaactcgttggtcttcctggtgct 2206  
2641 GAGATGAGATCATCTTTCATCAGGTGCGACAGAGGCTCCCTCATGGCCCTGGGCTTCG 2700  
2207 ttgcacacacacatcctctctccatcagaaccttgctctgcaagctacctggtaaggaa 2266  
2701 ATCGGCTACACCTCGCTGGCTGCCATCTGCTTCTTCTTCTTCAAGTCCCGGAAG 2760  
2267 ctgcgggagacatatacgaagcaaatgtgtactcttagcctgtgtctccacttcgta 2326  
2761 CTGCGGAGAACTTCATGAGCAAGTTCATCACTTCAAGCATGCTCATCTTCTCATC 2820  
2327 tccgtatcgccttcttccacatgctccagcatttaccagggcagcttaccacccggtc 2386  
2821 GTCTGGATCTCCTTATTCATCCAGCTTATGCCAGCAGCTATGCGCAAGTTGTCTGTGCCGTA 2880  
2387 aatgtctggcagaggtctggccactctgaatggtgcggtctcaagcgctattctccctaa 2446  
2881 GAGGTGATTCCATCTCTGGAGCGCAGCTTTGGCTGTGCGTGCACTTCTTCAACAAG 2540  
2447 tgcctagtgattctctgtcgcgtccagactccaacaacaga 2487  
2941 ATCTACATCATTTCTTCAAGCCATCCCGCAACCATCGA 2981

## RESULT 5

T95857 standard; cDNA to mRNA; 5275 BP.

T95857;

08-MAY-1998 (first entry)

DE Bovine parathyroid cell calcium receptor 1 (BOPcar 1) cDNA.

KW Bovine parathyroid cell calcium receptor 1; BOPcar 1;

KM Calcium homeostasis; hyperparathyroidism; osteoporosis; ss.

OS Bos sp.

FH Key

FT Location/Qualifiers

FT CDS

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PT DNA encoding calcium receptor polypeptide(s) - useful for  
PT Therapeutic purposes, e.g. hyperparathyroidism and osteoporosis  
PS Claim 1: Columns 107-116; 174p; English.  
CC The present sequence encodes bovine parathyroid cell calcium  
CC receptor 1 (BOPcar 1).  
CC The specification includes details of molecules that can modulate  
CC one or more inorganic ion receptor activities, and antibodies and  
CC antibody fragments targeted to inorganic ion receptor proteins. The  
CC proteins, nucleic acids and antibodies may be used to treat  
CC disorders by modulating one or more inorganic ion receptor  
CC activities, preferably disorders of calcium homeostasis, e.g.







ID	Accession	Gene	Species	Length (bp)	Location/Qualifiers
Db	2725	TGTCATCTGTGCCATTTGCTCTCAATACAGGCCGCCCCCTCGAGCTACCCGACACAGAGCT	Human	2784	
Qy	2146	cttcccccatcttgatgattcttgagtgacagagagtaactctgtggtcttcgtgtgc	Human	2205	
Db	2785	GGAGGACGAGATCATCTTCATCACTGCGACAGAGGGGTGCGCTATGAGCGCTGGGCTTCCT	Human	2844	
Qy	2206	tttcgcacacaaatcctctctcttcacacagacacctgtgtctgacgtacattggtgaagga	Human	2265	
Db	2845	GATCGGCTACACCTCGCTTGCTGGCGCGGCATCTGCTTCTTCTTGCCCTTCAGTCCCGGAA	Human	2904	
Qy	2286	acttcgcgaagacataacaaagccaaagtgtcaccttcacgtctctctccacttgct	Human	2325	
Db	2905	GCTGCGAGAGACTTCATATGAGCAAGTTCATCACTTCATCAGATGCTCATCTTTCAT	Human	2964	
Qy	2336	atcccgatctgccttcttcacatgctcagacattaccagaggaagtaaccacgcgt	Human	2385	
Db	2965	CGCTGGATCTCTTTCATCTCCCGCGCTACGCGACACACTACGGCAATTTGCTCTGCGCT	Human	3024	
Qy	2386	caatgtctgcagcagagcttcgaccactcgtatggcggacttcagcgctattctccctaa	Human	2445	
Db	3025	GGAGGTGATCCGCCATCTCGCGCGGCACACTTGGCTTGCTGACCTGATCTTTCACAA	Human	3084	
Qy	2446	atgtcagtgatgtctgcgcgtccagagaccacaacaacagaaaccttcagcctcat	Human	2505	
Db	3085	GGCTACACTCATCTCTTCAAGCTTCTCCGGAACACCATGAGAGAGTCCGCTGACGAC	Human	3144	
Qy	2506	ccagagactaac 2517	Human		
Db	3145	CGCGGACACGCC 3156	Human		
RESULT	6				
ID	V26962	standard: cDNA to mRNA; 5275 BP.			
AC	V26962:				
DT	01-SEP-1998	(first entry)			
DE	Bovine parathyroid calcium receptor 1 gene 5kb fragment.				
KW	ss: calcium ion concentration; parathyroid hormone; homeostasis;				
KW	kidney; calcium receptor; detection.				
OS	Bos sp.				
FT	Key	Location/Qualifiers			
FT	CDS	515..3772			
FT		/*lag= a			
FT		/product= "bopCar 1 5kb fragment"			
PN	US5763569-A.				
PD	09-JUN-1998				
PF	07-JUN-1995	484565.			
PR	07-JUN-1995	US-484565.			
PR	23-AUG-1991	US-749451.			
PR	11-FEB-1992	US-834044.			
PR	21-AUG-1992	US-934161.			
PR	12-FEB-1993	US-017127.			
PR	23-FEB-1993	US-009388.			
PR	22-OCT-1993	US-141248.			
PR	19-AUG-1994	US-292827.			
PR	21-OCT-1994	WO-012117.			
PR	08-DEC-1994	US-353784.			
PA	(BGHM.) BRIGHAM & WOMEN'S HOSPITAL.				
PA	(NPSP.) NPS PHARM INC.				
PI	Brown EM, Garreht JE, Hebert SC:				
DR	WPI: 98-347412/30.				
DR	P-PSDB: W54844.				
PT	Calcium receptor poly:peptide(s) - useful for drug screening or				
PT	antibody production				
PS	Example 25; Fig 47; 174pp; English.				
CC	The bovine parathyroid calcium receptor gene encodes a 1085 amino acid				
CC	protein. The tissue from which this receptor and receptors from human				
CC	parathyroid and rat kidney are derived, respond to changes, and control				
CC	changes, in calcium ion concentration, e.g. parathyroid hormone regulates				
CC	Ca2+ homeostasis in blood and extracellular fluid, and kidney function				
CC	alters through changes in Ca2+ levels in juxtaglomerular and proximal				
CC	tubule cells in the kidney. The purified receptors that modulate calcium				
CC	recombinantly) can be used to screen for compounds that modulate calcium				

CC receptor activity, especially those that can be used to treat diseases  
CC associated with the receptors in these tissues. They can also be used  
CC to raise antibodies or use in detection assays.  
SQ Sequence 5275 bp; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match 6.18; Score 157.2; DB 1; Length 5275

best local similarity 40.0%; P-vec. NO. 3.8e-31;  
Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

OY	205	gtctgaagcttcaagcgcatatgcatataacctctccaagccatgcggtttacacgtttga	264
Db	694	GTGATACGGATATATTTCGAGGAGATTTCGGCTGTGTACAGGTATATGATTTTGGCATAGA	753
OY	265	ggagataaacacatccacagctctgcttcccaacatccacccctcggtatgaactatga	324
Db	754	GGAAATTAACAGCAGCTCCACCCCTTCTTCCCAACATGACCCCTGGGATACAGATTTTGA	813
OY	325	cgatgtg--ctcaagatcttccaatgctatgtccaaccttgaggtgtgcccgcacgaag	381
Db	814	CACCTGTAAACCCGCTCTCTAAACCTTTGGAGGACACCCGAGTTTGTGGCCACAAACA	873
OY	382	gaacggc-----cacttaagaatgcagagagatctctccaacacactctctcaagtgtc	435
Db	874	AATTGACCTTTGAAACCTTATGATGTTCTGCAACTGCTCAGACACATCCCTCTACCAT	933
OY	436	ggaactcatgtggcctatatacactgaccacgctgtccacactgctgcctcgctctgaacc	495
Db	934	CGCAGTGTGGGAGCTACTGGCTCGGGCATCTTCACAGCATGTGGCCAACTCTGTGGGCT	993
OY	496	tctctatgccccctgtgtcagctatgagcgagacgagcgtatccctcagtgaggaaagcga	555
Db	994	CTTCTACATCCCCAGGTGAGTATGCTGCTCTCCACAGACACTCTCAGCAACAAATCA	1053
OY	556	gttcccgctctcttctgtgcgacacatccccagcgataaagtccacagtggaagttcagtgcg	615
Db	1054	AATTGAAGTCTTCTCTCCGACCATATCCCATGATGATGAAACACAGGCGACGGCATGTGCTGA	1113
OY	616	gtctgtcagaagcttggcgtgggtctcggatctcgctcgtgtgacgtatggtgaactagcg	675
Db	1114	CATATGAGTACTTCCGCTGGAACTGGGTGGGACATTTGCACTGACGATGACTATAGG	1173
OY	676	gcaagcttgagcgtatacagcgctgtgagagagctgtgcacctccacaggggacatctgtcgctt	735
Db	1174	CCGGCCACGAGGATCGAAGAGTTTGGAAAGAGAGTGAGAGAGGACATCTGCATGACTT	1233
OY	735	caagagacgtgggtgcctctctccgcccagcgoggtgagcccaagatgcagcgcgatgatct	795
Db	1234	CAGGGA-----GCTCATCTCCCAATACCTGTGATGAGAAAGATCCAGACAGTGTGTCGA	1287
OY	796	gcgtctgtgcctcgagccagagaccacgltgtcgtgtgtctctcttaacggtgaactgtcgcg	855
Db	1288	GGTGATCCAGATTCACCGCCAAATTCATATGCGTTCCTCCACGGCGCCAGACCTGGA	1347
OY	856	agtgctctcaaggtcgt	915
Db	1348	ACCCTCATTAAGASAGATCGTCCGGCCCAATTCACAGSCAAGATCTGGCTGGCAGCGA	1407
OY	916	agactgtggcatctccagctatataccaatgctgtccggatccagggcatctggagcgt	975
Db	1408	GGCCTGGGGCAGCTCTCCCTGATTCGTCGCCGAGATTCATCCATGTGTGTGGAGGCAC	1467
OY	976	gctgtgggtgtgcatctcagcagagagaaagtccctggcctggaagaggtt-----	1024
Db	1468	CATTGGGTTTGGTTGAACCTGGGACATCCAGAGCTTCGGGAATTCCTGCAGAAAT	1537
OY	1024	-----tgaaggtccctatgtccagcgagttatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1086
Db	1528	CCACCCACGGAAGTCTCTCCACATATGTTTGGCCAAAGAGATTTTGGGAAGAAACATTAA	1587
OY	1067	tgcaccaaggggtctctgt	1124
Db	1588	CTGGCACTCTCAAGAGGGTCTCTAAAGGCCATTACCGGTGAGACACTCTCTGAGAGTCA	1647







CC one or more activities of a calcium receptor (CR) comprises: (A)  
CC contacting a recombinant cell with a test compound, where the  
CC recombinant cell comprises a recombinant nucleic acid expressing the CR,  
CC provided that the cell does not have functional CR expression from  
CC endogenous nucleic acid; (B) determining the ability of the test  
CC compound to affect one or more activities of the calcium receptor; and  
CC (C) comparing the ability with the ability of the test compound to  
CC affect the one or more CR activities in a cell not comprising the  
CC recombinant nucleic acid. The present sequence encodes bovine  
CC parathyroid CR, designated a BopCAR 1. The nucleic acid sequence of  
CC BopCAR 1 can be used as part of the recombinant nucleic acid in the  
CC method described above. The compounds identified can be used to treat  
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.  
CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
CC disorders. They can also be used for the treatment of diseases and  
CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures,  
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
CC diseases such as Alzheimer's disease, Huntington's disease and  
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
CC Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match 6.1%; Score 157.2; DB 1; Length 5275;

Best Local Similarity 46.0%; Pred. No. 3.8e-31;

Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

QY 205 gctcagagctcgaagccatgctatcacccttccaagccatggtaccggtga 264  
DB 694 GGTGTACGATTAATTCGAGATTTTCGTGTTACAGATGATGATTTGCAATAGA 753  
QY 265 ggaataaacaacccacagctctctccacacacaccccggtgtgaactataga 324  
DB 754 GGAATTAACAGCACTCCAGCCCTTCTTCCACATGACCCCTGGATACAGATATTGCA 813  
QY 325 cgtgtg----ctagaagcttccaaatgctatgcccacccctgaagcgccgccaagaag 381  
DB 814 CACTGTAAACACCTGCTCTAAAGCCTTGAGGCCACCCGTGATTTTGCGCCACAAACA 873  
QY 382 gacaaagc-----caactaagaatcagaagaatcttcgcaacacactcccaagtggt 435  
DB 874 AATTACCTCTTGAACCTTGATGATGATTCGAACTGCTCAGAGCAATCCCTCTACCAT 933  
QY 436 ggaactatctggccctgatacactgaccacgctgtaacacactgctcctctgaagccc 495  
DB 934 CGCACTGATGGAGCTACTGCTCGGCATCTCCACAGACAGTGGCAACCTGCTGGGCT 993  
QY 496 ttctctgctgcccctgctcagctatgagcgagcgctgatacctcgaatgggaagcgcaa 555  
DB 994 CTTCTACATCCCCAGTACAGTATGCTCTCCACAGACACTGCTCAGCAACAAATCA 1053  
QY 556 gtcccgctcctctctgcaacacatcccaagcgaataagtaacgaagtgaagtaatgctg 615  
DB 1054 ATTCAAGTCTTCTCCACCATACCCAAATGATGAAACCCAGCGCCACTGACTGGA 1113  
QY 616 gctgctgagaagcttcggctgctgctgctgctgctgctgctgctgctgctgctgctg 675  
DB 1114 CATATCAGTACTTCCCTGGAATGGGTGGGCAATTCGAGCTGACGATGACTATGG 1173  
QY 676 gcaagctggcgctacagcgctggaagagctgcccacacacacacacacacacacacac 735  
DB 1174 CCGGCGAGGATCGAGAGATTTCAGAGAGAAAGCTGAGAGAGAGACATCTGATGACTT 1233  
QY 736 caaggaagctgctcctcctcccgccagcggtgtaaccaagatgcaagcgcatgctct 795  
DB 1234 CAGCA-----GCTCATCTCCCAATACTGATGAGAAAAAGATCCAGAGTGTGGA 1287  
QY 796 ggccttgctcgagccaggaacccgtgctgctgctgctgctgctgctgctgctgctgct 855  
DB 1288 GGTGATCCAGATTCACCGCCAAAGTATGCTCTTCTTCACAGGCGCCACGAGACTGGA 1347  
QY 856 agtgctctcaggtctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 915  
DB 915 agtgctctcaggtctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg

DB 1348 ACCCTCATCAAGATGTCGCGGCAATATACAGSCAGAGATGCTGCTGGCCAGCA 1407  
QY 916 agactgggcatcttcaagtaatacaccatgctccggatccagggccttggagagt 975  
DB 1408 GGCCTGGGCGACCTTCTTCCTGATGCTATGCCGAGTATTTCCATGTGTGGGAGC 1467  
QY 976 gctggggtgcccacacagacagcagcagcagcagcagcagcagcagcagcagcagc 1024  
DB 1468 CATGGGTTGGTTGAAAGCTGGGCACATCCAGGCTTCGGGGATTTCTGCAGAAAGT 1527  
QY 1024 -----tgaagatcctatgtccagagcagatgctgctccagaact 1066  
DB 1528 CCACCCAGGAAGTGTGTCACAAATGTTTGCCAAAGAGATTGGAGAAACATTAA 1587  
QY 1067 tggcagaagggctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 1124  
DB 1588 CTGCCACCTGCAAGAGGCTGTAAAGGCCATTACCGGTGAGACACTTCTGAGAGGTCA 1647  
QY 1125 ggaactgaacatgcccagccttgagcctctccatgagcgtg----- 1170  
DB 1648 CGAAGAGAGGTGCCAGGTTAAGCAACATCCACTCCCTTCGACCTGTGTGACTGG 1707  
QY 1170 ----- 1170  
DB 1708 GGAGAGAAATCAGCAGTGTGAGACTCTTACATGATTAACATTTAGGATATC 1767  
QY 1171 ctacaatgtatgaagcctgtatgctgtgcccagcctccagcctcctggagtg 1230  
DB 1768 CTACACGCTACTATGAGCGCTACTACTGCTCATGCTCATACAAAGATATATACCTG 1827  
QY 1231 taaccttgga-----cctgtgcagagggccagcctacc 1266  
DB 1828 CATACCTGGAGAGGGCTCTTACCACAGGTTCTCGCCCAATATCAAGAGTTGAAGC 1887  
QY 1267 ctggagctcttccagcagatctaaagtgaaatllccttatacatala---gaagactgt 1323  
DB 1888 TTGGCAGGTCTGAAACACCGCGCGACCTTAATTTACAGCAATATGGGGAGCAAGT 1947  
QY 1324 agcatcgaatgaagagggagacactctaggtatattatgaatcatcgctgagtgtaa 1383  
DB 1948 AACTTTCATGAAATGAGAGACTGGAGGAGACATATTCATCATCACTGGACCTCTC 2007  
QY 1384 tggacctgaatggacacttgagcctgctgctgctgctgctgctgctgctgctgctgct 1428  
DB 2008 CCGAAGAGACGGCTCATAGTGTTTAAGGAAGTTGGAATTACATGCTTATGCCAAGAA 2067  
QY 1429 tccagttatctagaacataaataagacaaaatccagtgagcagcaggaagaacatcag 1488  
DB 2068 AGGACAGAGACTCTTCAATCATGATGAAATAATTCGTGAGTGGATTCGAAGGAGGT 2127  
QY 1489 ggcgtgtcagttgtgtacagggactgtctcgaaggcacaaggttgatcat---ggg 1545  
DB 2128 GCTTTCTCAACTGCACTGCACTGAGACTGCTCGAGGGACCGAGAAAGAAATCATGAGGG 2187  
QY 1546 ttcccacacacgctgctcctgagctgctgctgctgctgctgctgctgctgctgctgct 1605  
DB 2188 GGAGCCCACTGCTGCTTGTGAGTGTGGAATGTCCTGATGAGGAGTCAACGAGAGAC 2247  
QY 1606 tgaagcttaccaccttgccagccttctggaacagaagaatggccctggagggagctcagc 1665  
DB 2248 AGATCAAGTGGCTGTGATGATGAGGCTGATGAGTCTGTGATGAGAACACACACTTC 2307  
QY 1665 ctgctctcgaagcagcgtgaggtctctgggtgtggaatgaaccacatcctctgtgtcat 1725  
DB 2308 CTGATTCGCCAAGAGATCGAGTTCGTCTGTGAGACCGAGCCCTTCGGGATCGCACTAC 2367  
QY 1726 agcagctaaacagcctatgctgctgctgctgctgctgctgctgctgctgctgctgct 1785  
DB 2368 GCTCTTCTGTGCTGGGCAATTTCTCTACAGCTTCTGCTGAGGCTCTTCTCATCAAT 2427  
QY 1786 tcttcaacagccttctgtgagctcagctgggggtgaggtgcttctcactcagctggtctc 1845  
DB 2428 CCGAACAAGCCCATGCTCAAGGCGACCAACCGGAGCTCTCTATGCTCTTCTCTCTC 2487



QY	1846	cttgtagatgtaggaggttgcaagccctctacacagctctctcgggaagcccaagctgcccgggtg	1905
Db	2488	cttgccttgcctgcttcttccacgcttccctgcttcttcttcaatcgaggagaccccaagactgcagctg	2547
QY	1906	cttgcctgcctcgaagcccccctcttctctcgggttttgccatttctctcctcctgcttgcacat	1965
Db	2548	ccgctgcctgcgcacccggccttcttggaatcacacttctgctctgcacttctgcacttctcctgct	2607
QY	1966	ccgctcctctcgaatggtctcaatcttccaaagtttcttaccaaagttacccaactcttacc	2025
Db	2608	GAATAAC---CAATGGGATCTCTCTGTTGTAGGCCAAAGATTCCACACAGCTTCCACCG	2664
QY	2026	caattgggcccacaacacatggtgcggaatatctgcattctgtcgaagctccacagctccatt	2085
Db	2665	GAAGTGGGGGGGCTCAACTGCAGTTCGCGTTCGTCGTCCTCTGTGACCTTGATGACAT	2724
QY	2086	gttccctctgtctcaagtcgtgcttgcacatgtgagcccaagcccaagggagttaccagcg	2145
Db	2725	TGTATCTGTGCCATTTGGTCAATACAGGCCCCCTCGACTACCGGACACAGACT	2784
QY	2146	cttcccccatctgtgtacttcttgatgtagcagagagttcaactctgtggcttccgtgtgc	2205
Db	2785	GGAGAGAGAGATCATCTTTCATCACCTGCCACGAGGGCTGGCTCATAGGGCTTGGCTTCT	2844
QY	2206	tttcgcacacaacatccctctctctccatcagcaccttctgtcgaagctactgtggtaaaga	2265
Db	2845	GATGGCTACACCTGCTTGGCTGCGGCAGCATCTCTTCTTCCTGAGCTCAAGTCCCGGAA	2904
QY	2266	actgcgaggaacatcaagaagaacccaatgtgtcacacttcagcctgcgtccctccactgt	2325
Db	2905	GCTGCCAGAGAACTTCATATAAGCCAAAGTTTCATCACCTTCAGCATGCTCATCTTTTAT	2964
QY	2326	atccctgacgccttcttctccacatgtgtccagcatltaaccaagggaagctaacaccgcggt	2385
Db	2965	CGTCTGATCTCTTTCATCCCGCCCTACGCGACACACATCTACGGAAGTGGTCTGCGCGT	3024
QY	2386	caatgtctctgcagggggtgtgcacctctcgtatgtgvcgcttcacgvcgtatcttctccaa	2445
Db	3025	GGAGGTATGCGCATCTCTGCGCGCGACGCTTGGCTTGTGGCCTGTATCTTTTACAA	3084
QY	2446	atgtcagtgattatctctgcgcgtccagaaactcaacacacagaaactttcagcctccat	2505
Db	3085	GGTCTACATCATCTCTTTCAAAGCTTCCGGAAACACATTCAGAGAGTTCGCTGCAGAC	3144
QY	2506	ccaggactaac	2517
Db	3145	CGCGGCACACGC	3156

RESULT	8	
ID	T61381	
AC	T61381 standard; CDNA to mRNA; 5006 BP.	
DT	22-APR-1997 (first entry)	
KW	Calcium receptor; human parathyroid gland adenoma tumour; p30PCaR1.2.	
KW	primary hyperparathyroidism; Xenopus oocyte; alternative splicing;	
KW	calcium-activated chloride current; agonist; NPS R-467; NPS R-568;	
KW	variant; untranslated region; alternative polyadenylation; probe;	
KW	alternative transcription initiation; p30PCaR5.2; p30PCaR4.0;	
OS	human Car gene; isoform; ss.	
FT	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	436..3702	
FT	cds	
FT	/*tag= a	
FT	/product= Calcium receptor	
PN	W09612697-A2.	
PD	02-MAY-1996.	
PF	23-OCT-1995; U13704.	
PR	21-OCT-1994; W0-U12117.	
PR	08-DEC-1994; U5-355784.	
PA	(NPS)- NPS PHARM INC.	

PI Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagonen BC;  
WR: 96-23050/23.  
DR P-FSDS: W11888.  
PT New d:arylalkyl amine cpds. useful for modulating inorganic ion  
PT receptor activities - esp. for modulating effect of extracellular  
PT calcium on cell surface calcium receptors, useful for treating e.g.  
PT hyperparathyroidism, Paget's disease or osteoporosis  
PS Example 1: Page 85-93; 23pp: English.  
CC The sequences given in T61381-82 encode functional calcium receptors.  
CC These sequences were isolated from human parathyroid gland adenoma  
CC tumour using pHPcPar4 as a hybridisation probe. mRNA was isolated from  
CC a 39 year old caucasian male diagnosed with primary hyperparathyroidism  
CC and two clones of approx. 5 and 4 kb were identified. These cDNA's were  
CC injected into Xenopus oocytes which were assayed for the presence of  
CC functional calcium receptors. Both clone types gave rise to functional  
CC calcium receptors as assessed by the stimulation of calcium-activated  
CC chloride currents upon addition of appropriate calcium receptor agonists  
CC e.g. NPS R-467 and NPS R-568. Sequence analysis of the two cDNA clones  
CC indicated the existence of at least two sequence variants differing in  
CC the 3' untranslated region and which may result from alternative  
CC polyadenylation. Sequence variation also exists in the 5' end of the  
CC inserts. These sequence differences may have arisen due to alternative  
CC transcription initiation and/or splicing. Three additional sites of  
CC sequence variation occur within the coding regions of cDNA clones  
CC pHPcPar5.2 and pHPcPar4.0 demonstrating that they encode distinct  
CC proteins. Sequence analysis of the human Car gene indicates that the  
CC additional 30 bp in clone pHPcPar5.2 as compared to pHPcPar4.0, results  
CC from alternative mRNA splicing. This alternative splicing is predicted  
CC to insert 10 additional amino acids into the Car protein encoded by  
CC pHPcPar5.2 between residues 536 and 537 of the protein encoded by  
CC pHPcPar4.0. In addition pHPcPar4.0 encodes Gln at position 925 and Gly  
CC at position 990. Whereas pHPcPar5.2 encodes Arg at both equivalent  
CC positions. The human Car gene encodes for Gln and Arg respectively at  
CC these positions. These two receptor isoforms may be functionally and/or  
CC pharmacologically distinct.  
SQ Sequence 5006 BP; 1228 A; 1376 C; 1220 G; 1182 T;

[illegible]



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QY 1961 acaatccgctccctcccaactggtacatcatctcaagttttctacacaaggtaccacattc 2020
Db 2551 CTGGTGAACCAACACCGTCTCTCTCGTGTTGAAG---CCAAGATCCCAACCACTTTC 2607
QY 2021 taccacacttggcccaaaaacacatggtgcgggaatactgcattgttcagctccacagtc 2080
Db 2608 CACCCCAAGTGTGGGGGTCAACCTGCAGTTCCTGCTGTTTCTCTGCACCTTCATG 2667
QY 2081 cattgtctctctgtctcagctggtctgcaatgtgaccccaagcccaagggagttac 2140
Db 2668 CAGATTGTCATCTGTGTATCTGGCTCTACACGCCGCCCTCAAGCTACCGCAACCAAG 2727
QY 2141 cagcgctcccccacatctgtagttctctgagtgacagagatcaactctgtgggtcccg 2200
Db 2728 GAGCTGGAGAGATGACATCTCTTCACTACGTCGCAAGAGGCTCCTCATGGCCCTGGGC 2787
QY 2201 gtggtcttcgcacacaacatccctctccatcagacacttgtctgcagctaacctgggt 2260
Db 2788 TTCCTGATCGGCTACACCTGCTGCTGGCTGCCATCTGCTTCTTTGCTTCAAGTCC 2847
QY 2261 aagggaactgcgggaagaactataaagaagcaaatgtgtcaacttaagctgtctccac 2320
Db 2848 CGGAAGCTGCCGGAACACTTCAATGAAGCAAGTTTCATCAGCTTGCATCTTC 2907
QY 2321 ttctgtatccctggtatcgcttctctccacatgctcagagattaccagggagagctaacctacc 2380
Db 2908 TTCATCTGTCGATCTCTCTTCACTTCCAGCTTATGCCAGCACTATGGCAAGTTGTCTT 2967
QY 2381 gcggtcaactgtctgcagaggtgcgtccactctgaatggtgcgtctcagcggtattctctc 2440
Db 2968 GCGGTAGAGGTGATTCCTCTCTCTGAGCCAGCTTGTGCTGCTGGCGTGCATCTTCTTC 3027
QY 2441 cctaaatgtcagtgatctctctgcgcgtccagaactccaacaacagaga 2487
Db 3028 AACAAGATCTACATCTTCTTCAAGCCATCCCGACACCATCGA 3074

RESULT 9
T95858
ID T95858 standard; cDNA to mRNA; 5006 BP.
AC T95858.
DT 08-MAY-1998 (first entry)
DE Human parathyroid cell calcium receptor 5.2 (HupCar 5.2) cDNA.
KW Human parathyroid cell calcium receptor 5.2; HUPCAR 5.2;
KW Calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 436..3702
FT /tag= a
FT /product= parathyroid-cell-calcium_receptor_5.2
PN US6688938.A.
PD 18-NOV-1997.
PE 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (Bghm ) BRIGHAM & WOMEN'S HOSPITAL.
PA (NNSP-) NPS PHARM INC.
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;
PI WPI; 98-008040/01.
DR P-BSDB; M38273.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 15: Columns 117-126; 174pp; English.
CC The present sequence encodes human parathyroid cell calcium

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CC receptor 5.2 (HupCar 5.2).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 5006 BP; 1227 A; 1378 C; 1219 G; 1182 T;

Query Match 5.9%; Score 152.6; DB 1; Length 5006;
Best Local Similarity 48.4%; Pred. No. 5,8e-30;
Matches 487; Conservative 0; Mismatches 514; Indels 6; Gaps 2;

QY 1484 caggtgacctgtcagtgatgacagagagctgtctgaaggacacacaggtgtcat- 1543
Db 2072 CAGGTGCCCTTCTCCACATGCAAGCGAGACTGCTGCGAGGACCAAGAAAGGATCAT 2130
QY 1543 --gggtccacacactgtcgtctcagtgatgacccctgtgaagctggagacattctaac 1600
Db 2131 GAGGGGAGCCCACTGCTGCTTGTAGTGTGTGAGTGTCTGTAGGGGAGTATAGTAT 2190
QY 1601 acgaatgaacttcaaacactgcgcagcctgtggaacagaagaatggccctgaagggaagc 1660
Db 2191 GAGACAGATGCCAGTGCCTGTAAAGTCCCAAGTGAATGACTTGTGCTTCAATAGAACAC 2250
QY 1661 tcaagctgtcttcaogaacagctgagttcttgggtgtgcatgaacacatctcttgggtg 1720
Db 2251 ACCCTGATGATGCCAAGAGATGCAATGTTCTGTGTGAGACGAGCCCTTGTGATGCA 2310
QY 1721 ctattacagcttaaacgtatattgtcgtcgtcgtcgtatgtgacgtcgtgctgttggc 1780
Db 2311 CTACCCCTTTGGCCGTGTGTGGGCAATTTCTGACACCCCTTGTGCTGGGTGTGTTATC 2370
QY 1781 tggctcttcaacacccctgtgtgagtgacgtctgssgtgaagctgtctctcctcagtg 1840
Db 2371 AAGTTCGGAACACACCACTTGTCAAGGCAACCAACGAGACTCTCTCACTCTCTC 2430
QY 1841 gattccttgtagctgggaagtgtcagcctctacagcctcttcgggaagccaggtgcgc 1900
Db 2431 TTCTCCTGCTCTGCTGTCTTCCAGCTCCCTGTCTTCATCTGAGGAGCCCAAGACTGG 2490
QY 1901 ggttccttgcctgcagagccctcttctctcgtgttgcatttctctccgtctcg 1960
Db 2491 ACGTCCGCCCTGCGCAGCGGCTTTGGATCAGACTCTGTGCTGTGCACTCAAGCATC 2550
QY 1961 acaatccgctccctccaaatgtgtacatctcaagctcttaccagaagttaccacatctc 2020
Db 2551 CTGGTGAACCAACACCGTCTCTCTCGTGTTGAAG---CCAAGATCCCAACCACTTTC 2607
QY 2021 taccacacttggcccaaaaacacatggtgcgggaatactgcattgttcagctccacagtc 2080
Db 2608 CACCCCAAGTGTGGGGGTCAACCTGCAGTTCCTGCTGTTTCTCTGCACCTTCATG 2667
QY 2081 cattgtctctctgtctcagctggtctgcaatgtgaccccaagcccaagggagttac 2140
Db 2668 CAGATTGTCATCTGTGTATCTGGCTCTACACGCCGCCCTCAAGCTACCGCAACCAAG 2727
QY 2141 cagcgctcccccacatctgtagttctctgagtgacagagatcaactctgtgggtcccg 2200
Db 2728 GAGCTGGAGAGATGACATCTCTTCACTACGTCGCAAGAGGCTCCTCATGGCCCTGGGC 2787
QY 2201 gtggtcttcgcacacaacatccctctccatcagacacttgtctgcagctaacctgggt 2260
Db 2788 TTCCTGATCGGCTACACCTGCTGCTGGCTGCCATCTGCTTCTTTGCTTCAAGTCC 2847
QY 2261 aagggaactgcgggaagaactataaagaagcaaatgtgtcaacttaagctgtctccac 2320
Db 2848 CGGAAGCTGCCGGAACACTTCAATGAAGCAAGTTTCATCAGCTTGCATCTTC 2907
QY 2321 ttctgtatccctggtatcgcttctctccacatgctcagagattaccagggagagctaacctacc 2380

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FT CDS 436. .3702  
ET /+tag= a  
FN US585684-A.  
FD 12-JAN-1999.  
PF 07-JUN-1995; 480751.  
PR 07-JUN-1995; US-480751.  
PR 23-AUG-1991; US-749451.  
PR 11-FEB-1992; US-834044.  
PR 21-AUG-1992; US-934161.  
PR 12-FEB-1993; US-01127.  
PR 23-FEB-1993; US-009389.  
PR 22-OCT-1993; US-141248.  
PR 19-AUG-1994; US-292827.  
PR 21-OCT-1994; WO-U12117.  
PR 08-DEC-1994; US-353784.  
PR (BGHM.) BRIGHAM & WOMENS HOSPITAL.  
PA (NPSF-) NPS PHARM INC.  
PI Balandrin MF, Brown EM, Dei Mar EG, Garrett JE,  
PI Hebert SC, Nemeth EF, Van Wageningen BC;  
PI WPI: 99-119871/10.  
DR P-PSDB: W89564.  
PT Screening for calcium receptor-active compounds - by recombinant  
PT expression of nucleic acid encoding calcium receptor and determining  
PT the effect of compounds on calcium receptor activity  
PS Claim 1; Fig 48; 176pp: English.  
CC A method has been developed of screening for a compound able to affect  
CC one or more activities of a calcium receptor (CR) comprises: (A)  
CC contacting a recombinant cell with a test compound, where the  
CC recombinant cell complises a recombinant nucleic acid expressing the CR,  
CC provided that the cell does not have functional CR expression from  
CC endogenous nucleic acid; (B) determining the ability of the test  
CC compound to affect one or more activities of the calcium receptor; and  
CC (C) comparing the ability with the ability of the test compound to  
CC affect the one or more CR activities in a cell not comprising the  
CC recombinant nucleic acid. The present sequence encodes human  
CC parathyroid CR, designated a pHPaCR 5.2. The nucleic acid sequence of  
CC pHPaCR 5.2 can be used as part of the recombinant nucleic acid in the  
CC method described above. The compounds identified can be used to treat  
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g  
CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
CC disorders. The compounds can also be used for the treatment of diseases and  
CC disorders associated with disrupted Ca2+ responses, e.g. seizures,  
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
CC diseases such as Alzheimer's disease, Huntington's disease and  
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
SQ Sequence 5006 Bp; 1228 A; 1376 C; 1220 G; 1182 T;

Query Match	Similarity	Score	DB 1	Length
Best Local	48.4%	Pred. No. 5,8e-30;		
Matches	487	Conservative	0	Mismatches 514; Indels 6; Gaps 2
Oy	1484	caggtgcctcgtgtcagttggtacccaaggaactgtctcgaagaggacacacagttgtgtcat-	1543	
Db	2071	CAGGTGCCCTTCTCCAACTGCAGCCAGACTGCTCGCAGGGACACGAAAGGATCATTT	2130	
Oy	1543	--gggttcccaacacatgcctgccttcagagtcatagcctctggaactctggacattctccac	1600	
Db	2131	GAGGGGGACCCACTGCTGCTCTTTTGAAGTGTGTGAAGTGTCTGATGAGGAGTTAATGAT	2190	
Oy	1601	acgaattgagcttcaacacttgcagcctcttggacaagaagaatggccctcagggggaagc	1660	
Db	2191	GAGACAGATGACAGTGCCTCTGTAAACAAGTCCCGAGATGACTTTCGTGCTCAATGAGAACAC	2250	
Oy	1661	tcaagctcgttctcagaacacggtggagttctcttgggttggcatbaaacacatctcttgggt	1720	
Db	2251	ACCTCTGATTTGCCAAGAGATCGAGTTTCTGTCTGTGACGAGACCCCTTTGGGATCGCA	2310	
Oy	1721	ctattagcagctaaacagctatctgctcgtctgtcatctgggaactcctgacctgtttgcc	1780	
Db	2311	CTCACCCCTCTTTCGCGGTGTGGCATTTCCTTACACAGCCTTTGTGTGGATGTGTATTC	2370	

QY	1781	tgagctcttaacacgcctgttggaggtgaagctggaggtgaagctgctcttcattcagctg	1840		
Db	2371	AAGTTCGCAACACACCCATTGCAAGGCGACCAACCCAGAGCTCTCTACCTCTCTCT	2430		
QY	1841	gattccctctgtagctggagagtgtagaacctcttaagctctcttcgggaagccacagtgccc	1900		
Db	2411	TTCTCCCTGCTCTGCTGCTTCTTCTCCACCTCCCTGTTCTTCTTCAATCGGAGGACCCACAGACTGG	2490		
QY	1901	gcgtctctgtctgcgtacagccctcttctctcgggttggttcacattctctctcctgtctg	1960		
Db	2491	ACGTGCGCGCTGCGCGACCGCGGCTTGGCATCAGCTCTGCTCTGATCTCATGTGATC	2550		
QY	1951	acaatccgctctctccaactatggtcatcatcttcaagttttctacaagaagtaccacattc	2020		
Db	2551	CTGGTGAACCAACACCGTGTCTCTCTCTGTTGTAGG---CCAAGATCCCCACACAGCTTT	2607		
QY	2021	taccacacttgggccccaaacccatggtctgggaataatctcatctgtcacctccacagctc	2080		
Db	2608	CACCGCAAGTGTGGGGGCTCAACCTGCGAGTTCCTGCTGTTTCTCTGACCTTCATG	2667		
QY	2081	catttgtctctctgtctcagctggcttggcaatgttgacccacagccacagagagttac	2140		
Db	2668	CAGATGTCTATCTGTGTGATCTGTGGCTCTACACCGCGCCGCCCTCAAGCTACCGCAACAG	2727		
QY	2141	cagcgctctcccccacatctgtgatactcttaggtgcacagcagtgtaactctgctggctctg	2200		
Db	2728	GAGCTGGAGGATAGATCATCTTCAATCAAGTCCGACGAGGAGGCTCTCATAGGCGCTGGGC	2787		
QY	2201	gtgctcttgcaacaaatctctctctccatcagcaccttgtctctgagctaacctgggt	2260		
Db	2788	TTCTGTATCGGCTACACCTGCGCTGGGCTGCAATCTCTTCTTTGGCTTTCAAGTCC	2847		
QY	2261	aagaaacttcggagaaactataagaaagccaatgtgtcaccttcacagctgctctccac	2320		
Db	2848	CGGAAGTGTGCGGAGAACTTCAATGAAGGCAAGTTCACTACCTTCAGCATGCTCATCTTC	2907		
QY	2321	tctgatactgtatgcgtctctcttaacatgltccagcatttaccagggagactaacacc	2380		
Db	2908	TTTCATCGTCTGGAATCTCTTCAATTCGAGCGCTATGCCACACCTATGGCAAGTTGTCTCT	2967		
QY	2381	gcggtcaatgtctggtcagaaggctcggccaaactctgaatggcggtctcagagctattctctc	2440		
Db	2968	GCGCTAGAGGTGATGCCATCTCTGGGAGGCAAGCTTTGGCTTGGCGGTGATCTCTTCT	3027		
QY	2441	ccataatgcatactgattctctgcgcgtccagacacacacacacaga	2487		
Db	3028	AACAAGATCTACATCATCTCTTTCAAGGATCTCCGCAACACACATCGA	3074		
RESULT 12					
ID	T86166	T86166 standard; DNA: 4000 BP.			
AC	T86166;	02-DEC-1997			
DT	02-DEC-1997	(first entry)			
DE	Nucleotide sequence of pCAR/RI.				
KM	Chimeric receptor: extracellular domain; seven transmembrane domain;				
KW	intracellular cytoplasmic tail domain; metabotropic glutamate receptor				
KM	MGR; calcium receptor; CR; mGluR; G protein-coupled receptor;				
OS	neurological disease; ss.				
OS	Chimeric - Homo sapiens.				
FI	Key	Location/Qualifiers			
FT	cds	41..3700			
FT	/*tag= a				
FT	/product= pCAR/RI				
PN	W09705252-A2.				
PD	13-FEB-1997.				
PR	25-JUL-1996; U12336.				
PR	26-JUL-1995; US-001526.				
PA	(NPSF-) NPS PHARM INC.				
PI	Fuller FH, Hammett LG, Krapcho KJ.				
DR	WPI: 97-145690/13.				
PT	P-SDS; W25763.				
Chimeric receptors comprising metabotropic glutamate receptor and					



PT calcium receptor - used for screening for neurologically active  
 PT compounds  
 Example 3: Fig 3: 177bp; English.  
 CC This sequence encodes a chimeric receptor. The chimeric receptor  
 CC comprises an extracellular domain, a seven transmembrane domain, and  
 CC an intracellular cytoplasmic tail domain, and a sequence of at least  
 CC 6 contiguous amino acids is homologous to a sequence of a metabotropic  
 CC glutamate receptor (mGR), and a sequence of at least 6 contiguous amino  
 CC acids is homologous to a sequence of a calcium receptor (CR). The  
 CC chimeric receptor may be used for screening for compounds that bind to  
 CC or modulate the activity of mGR or CR and for determining the site-of-  
 CC action of a CR active compound. The compounds can be used in the  
 CC treatment of neurological diseases and disorders. They can also be  
 CC used as diagnostic agents. Chimeric receptors such as this, allow the  
 CC coupling of certain functional aspects of an mGR with certain functional  
 CC aspects of a CR. They allow for more efficient high-throughput screening  
 CC of compounds.  
 SQ Sequence 4000 BP; 955 A; 1128 C; 1010 G; 907 T;

Query Match 5.9%; Score 151; DB 1; Length 4000;  
 Best Local Similarity 51.6%; Pred. No. 1.4e-29;  
 Matches 427; Conservative 0; Mismatches 385; Indels 15; Gaps 3;

QY 206 tctgaacagctcaacggcagctatccaccccttccaaagcagtgccggtcagcgttga 265  
 DB 218 TGTATCAGGTATATTCCTCGGGTTTCGCTGTACAGCATATGATTTGCGATAGAG 277  
 QY 266 gaataaacaaccccaacagcttgcctccaaactccacccctgggtgtatgaactatgac 325  
 DB 278 GAGATTAACAGCACGCCAGCCCTTCTCCCACTGACGGGTGATAGAGATATTTGAC 337  
 QY 326 gtgtcagcagcttccaaatgtct--atgcacccctggaggtgcccgcacga---- 379  
 DB 338 ACTTGCACACCGCTTTTAAGGCTTGAAGCCACCTGATTTTGTGCTCAAAACAAA 397  
 QY 379 --agggacagccacagtagagagagatcttcgaacacacccctcccaagtggtg 436  
 DB 398 ATTGATCTTTGACCTTGATGATTTGCAACCTGCAAGCTCAACATTCCTCTACGATT 457  
 QY 437 gcaactcttgagctgtatacactgacacagctgtacacactgtgctccgtcagacct 496  
 DB 458 GCTGTGGTGGAGACTGCTCAGGGCTCTCCACGGCACTGGCAAAATGCTGGGGCTC 517  
 QY 497 ttctcagtccttcgacagctatgagagcagcgttgatccctcagtgaggacagcgaag 556  
 DB 518 TTTCACATTCGCCAGTCACTATAGCTCTCCACAGACTCCTCACACACACAAAGATCAA 577  
 QY 557 ttcccgctccttctgacacacaccccaagcagataagcagagtggaagtcagtgcg 616  
 DB 578 TTCAAGCTTTCTCCGACACCATCCCAATGATGACGACAGCCATGCCATGCGACAG 637  
 QY 617 ctgcgacagagcttgagctgtgctgctgctgctgctgctgctgctgctgctgctgctg 676  
 DB 638 ATCATCAGATTTTCCCTCGAAGTGGTGGGCAAAATTCAGCTGATGACGACTATGGG 697  
 QY 677 caagctggcttacaagcgcgtgagagagctgacaccccaagcagcagctcgtcgtccctc 736  
 DB 698 CGCCCGGGGATTAGAAATTCGAGAGAGAGCTGAGGAAAGGAGATATCTGCATGCAATTC 757  
 QY 737 aaggaagctgtgctcctcctcccaagcagcgtgagcacaagagatgacagcagtgatgctg 796  
 DB 758 AGTGA-----ACTCATCTCTCCAGTACTCTGATGAGGAAAGACACAGCATGTGTAGAG 811  
 QY 797 cgtcgtcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 856  
 DB 812 GTGATTCAAATTTCCAGCGCAAGTATCATGTGTTTTCACATGCGCCACAGATCTTTGAG 871  
 QY 857 gtgtcttcagctgt 916  
 DB 872 CCCTCATCAAGAGATTTGTCGCGGCAATATCAGGCAAGATCTGCTGCGCCAGAG 931  
 QY 917 gactgggcacatccacgatacaacaaatgtgcccgagatcccaaggcattgggaagtg 976

DB 932 GCCTGGGCCAGCTCTCCCTGATCGCCATGCTCACTACTCCAGCTGATGGGCGACC 991  
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RESULT 13  
 ID T89290 standard; cDNA: 4131 BP.  
 AC T89290;  
 DT 27-MAR-1998 (first entry)  
 DE Dogfish shark kidney calcium receptor related protein cDNA.  
 KW Calcium receptor related protein; Car-RP; dogfish shark; SKCAR-RP;  
 KW polyclonal-sensing receptor; aquaculture; fish farming;  
 KW salinity tolerance; ss.  
 OS Squallus acanthias.  
 FH Key Location/Qualifiers  
 FT CDS 439..3519  
 FT /tag= a  
 FT /tag= b  
 FT polyA\_site 4076..4113  
 FT W09735977-A1.  
 PN 02-OCT-1997.  
 PF 27-MAR-1997; U05031.  
 PR 27-MAR-1996; PR-622738.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 PI Brown E, Harris HW, Hebert S;  
 DI WPI; 97-489640/45.  
 DR P-PDB; W32059.  
 PT New Isolated Aquatic polyvalent cation-sensing receptor - used to  
 PT develop products for increasing or decreasing the salinity tolerance  
 PT of fish for use in aquaculture  
 PS Claim 2: Fig 4A-F; 57pp; English.  
 CC This cDNA clone codes for dogfish shark kidney calcium receptor  
 CC related protein (SKCAR-RP, see W32059), an aquatic polyvalent  
 CC cation-sensing receptor (PVCAR). It was isolated from a shark  
 CC kidney cDNA library using a rat kidney calcium receptor cDNA as  
 CC probe. Also claimed are: a probe comprising the 4131 bp SKCAR-RP  
 CC sequence; an isolated PVCAR present in the plasma membranes of  
 CC aquatic species, especially on the apical membrane of epithelial  
 CC cells of elasmobranch fish, particularly from cells found in the  
 CC collecting duct or late distal tubule in the kidney, intestine,  
 CC gill, rectal gland, gonad or brain; an antibody that specifically  
 CC binds to a PVCAR; and a method of screening for aquatic PVCAR  
 CC agonists and antagonists. Modulation of the expression of the  
 CC aquatic PVCAR activates or inhibits aquatic PVCAR mediated ion  
 CC transport and endocrine changes that permit fish to adapt to fresh  
 CC or salt water. The method facilitates the aquaculture of marine  
 CC fish and can provide for the development of marine fish that are  
 CC easily adaptable to fresh water aquaculture.  
 SQ Sequence 4131 BP; 1028 A; 1161 C; 1019 G; 923 T;

Query Match 5.8%; Score 150.8; DB 1; Length 4131;  
 Best Local Similarity 47.5%; Pred. No. 1.6e-29;  
 Matches 514; Conservative 0; Mismatches 562; Indels 6; Gaps 2;

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 QY 1499 gtgtgacacagcagctgtcgaaggcagcagcagcttgatc--gggtccacacac 1555  
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 DB 2140 TCGTCTTTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 2199  
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D8	ACCTGCTGCTGCTGCCATCTGCTTCTTTTGCTTAAAGTCCAGGAAGTACCAAG	2910
D7	2276 aactataacgaagccaatggtgtaacctcagaagctgtccctccactcgtataccatgacatc	2335
D6	2971 AACTTCAACGAAGGACCAAGTTCACTTACCTCAGCATCTCATCTTCTTATCGTGGATC	3030
D5	2336 gcttctctcaccaagtcacgaatttaccaaggagcttacctaccgcyggtcaatgctgc	2395
D4	3031 TCTCTTCATTTCCAGGCTTATGCCAGACACCTACGGCAAGATTGTCTGCGGTGAGGTGATC	3090
D3	2396 gcaagagcctgcgaactctgaatgagggagcttcaagcggctatcttccctccaaatgcatcgt	2455
D2	3091 GCCATTATGGCAGGCACGCTTTGGTTACTGATGCTGCATCTTTTACACAAGGTCTACACTT	3150
D1	2456 attctctgcgctccagaactcaacaacacagaacacttcaagccttcacatc	2506
D0	3151 ATCTCTTTCAGGCTTCTCCGGAAACACCATTTGAGGAAGTCCGCTCCAGGACC	3201











AUTHORS Hoon, M.A., Adler, E., Lindemeier, J., Batley, J.F., Ryba, N.J. and Zaker, C.S.  
 TITLE Putative mammalian taste receptors: a class of taste-specific GPCRS with distinct topographic selectivity  
 JOURNAL Cell 96 (4), 541-551 (1999)  
 MEDLINE 99159821  
 REFERENCE 2 (bases 1 to 2520)  
 AUTHORS Hoon, M.A., Adler, E., Lindemeier, J., Batley, J.F., Ryba, N.J.P. and Zaker, C.S.  
 TITLE Direct Submision  
 JOURNAL Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center Drive MSC 1188, Bethesda, MD 20892-1188, USA  
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 BASE COUNT 479 a 749 c 676 g 616 t  
 ORIGIN  
 Query Match 83.5%; Score 2153.6; DB 12; Length 2520;  
 Best Local Similarity 91.1%; Pred. No. 0;  
 Matches 2301; Conservative 0; Mismatches 219; Indels 6; Gaps 1;

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 QY 491 agccctttctgagccctgtcagactataggagcagacgltgactcctgtggaag 550  
 Db 475 GGTCTTCTCTGATGCGCCCGGTCACTATGAGGACAGAGCGTGTACTAGTGGCAAG 534  
 QY 551 cgaagatcccgctctctcttgccaccatcccaagcagatgaagtgagatcata 610  
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 QY 611 gtccgctgctgagagcttcgagctggtgtgactgctcgtttgagcagctatgtgac 670  
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DEFINITION Rattus norvegicus putative taste receptor TR2 mRNA, partial cds.
ACCESSION AF127390
VERSION AF127390.1 GI:4337087
KEYWORDS .
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
AUTHORS Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 2529)
Hoon,X.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J. and
Zuker,C.S.
TITLE Putative mammalian taste receptors: a class of taste-specific GPCRs
with distinct topographic selectivity
JOURNAL Cell 96 (4), 541-551 (1999)
MEDLINE 99159821
REFERENCE 2 (bases 1 to 2529)
AUTHORS Hoon,M.A., Adler,E., Lindemeier,J., Battey,J.F., Ryba,N.J.P. and
Zuker,C.S.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-1999) Taste and Smell Unit, NIDCR, 10 Center
Drive MSC 1188, Bethesda, MD 20892-1188, USA
FEATURES
source location/Qualifiers
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Db	333	CCAAACAATATCCACCTTGGGCTCTACTTCTGGCAAGAGACG---ACGACCTCTGGCCCA	379
QY	399	tgcagaagatcttcgcaaccaactccctccaaagtgtgtgcaactcttggccttgataaa	458
Db	380	TCCTCAAGAGATCAAGCCAGTACATGTCCCCAGCTGTGGTGTCTCATTTGGCCCCGACAACT	439
QY	459	ctgaccacgctgctcaacctgtcctccgtcgtcgaagccctttctgatagcccctgtgaagt	518
Db	440	CTGACTCCGGCCATTCACGGTGTCCAACTCTCTCATTTCTCTCATCCCAAGATACAT	499
QY	519	atgaaagcagacaggtgtactcctcagttggaagcgaagtccgcctccctcttgscacaca	578
Db	500	ACAGGCGCATCTCCACACAGCTGCGGGACAAACGGCATTCTCCCTAGCATGCAACGACAG	559
QY	579	tcocccagataaagtaaccagagtgtgaagtcatagtgcgctgtcgtcgaagcttcggtg	638
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QY	1038	tccaagcagatgavvggtgtcctccagaacttgcacsaagggtctcgtgtgctgcgaactaac	1097
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Db	1214	GACTCTCTGGGCTGTAAACGGGGTCCCTGTGCACCAACAAAGGTTCAACCGTGTGACGCTAC	1273
QY	1278	tccaagcagatctacaagggtgaattctcctctacataagaagaagctgtagactcgaatgaca	1337
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QY	1338	agggggaccctctaggttatattatgaacatcatcgcttggaactggaatgaaactgtatgga	1397
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QY	1398	cctttgaggtcaattggtttctgcctcaactgtctccagttcaatctagacataaataagaaca	1457
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QY	1458	aaatccaggtgcagcggaaagaacaactcaagtggtgcgtgtgtcagtggtgtacaaagagctgtc	1517
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QY	1518	tcgaaggcacacacaggtgtgtcaattggtttcccaacacgtcgtcttgatggaagtgcctt	1577
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Db	1571	GTATGCGAAGCACTTACTCTCAACCGCTACAGCATGATGATTTAAGTGTCTGTCTGCCGG	1630
QY	1635	cagaagaatgggcccccttaggggaagctcaagcctgtcttccacgaacgctggaagcttcttg	1694
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QY	1875	gcttcttgggaagacacacaggtgcccgcgtgtgttgctgtggtgaagcccttctctctgcg	1934
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QY	1935	ggttttgcaatttctctctctctgtcctgaacatccgctctcttccaaactgtgtcatcatctta	1994
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QY	1995	agttcttcaacaaagtlacccaactcttcaacaaacttggagcccaaaacatggtgtccgaa	2054
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QY	2055	tattgcatactgcagctccacagctcaatttgcctcgtctc---caagtggtctgcaa	2111
Db	2051	TCTTGTGGCCTTATCAACGGCATCAAGTGTGCGCTGTGTGGCAACATGTGGCCA	2110
QY	2112	tgtgaacccacagcgccacacaaagagtaacagcgcttcccacatcgtgtatcttgaagt	2171
Db	2111	CCACCATCAACCCCATTTGGCCGGACCGACCCGAGATGACCCCAACATCATGATCTCTGCT	2170
QY	2172	gcaacagagtgcaactctgtgggtcctccgtgtgtgtgttgcacaacaacatccctcttca	2231
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Oy	2472	aactaacacacagacacacttcagccttcacatccaggacacagagagcc	2523
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DEFINITION	human STS CHLC.GC115G02.P16729 clone GC115G02.		STS
ACCESSION	G09859		15-AUG-1995
VERSION	G09859.1	GI:941708	
KEYWORDS	STS sequence; primer; sequence tagged site.		
SOURCE	human vector:pUC1 host-E.coli dut-ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.		
ORGANISM	Homo sapiens		
	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Carnarina; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 270)		
AUTHORS	Murray,J., Sheffield,V., Weber,J.L., Duyk,G. and Buelow,K.H.		
TITLE	Cooperative Human Linkage Center		
JOURNAL	Unpublished (1995)		
COMMENT	Synonyms: GC115G02, CHLC.GC115G02.T16713		
	Contact: Dr. Jeffrey C. Murray		
	The University of Iowa		
	Department of Pediatrics, Iowa City, IA 52242, USA		
	Tel: (319) 356-3508		
	Fax: (319) 356-3347		
	Email: jeff-murray@uiowa.edu		
	Primer A: CTCACACAGGGTGCTCTAG		
	Primer B: TGGTGTGTTTGCGCTTTC		
	STS size: 124		
	PCR Profile:		
	denature: 30 seconds at 94 degrees C		
	annealing: 75 seconds at 55 degrees C		
	extension: 15 seconds at 72 degrees C		
	PCR cycles: 27		
	extension: 6 minutes at 72 degrees C		
	Protocol:		
	Template: 30ng genomic DNA		
	Primer: each 1.5 pmole		
	dNTPs: each 200 uM		
	Taq Polymerase: 0.3 units		
	Total Vol: 10 ul		
	Buffer:		
	MgCl2: 1.5mM		
	KCl: 50mM		
	Tris: 10mM		
	pH: 8.3.		
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	Best Local Similarity	79.9%, Pred. No. 1.5e-30;	
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Db	270	GGGAAGAGAGATGGGGACACTGAGGGAAGCCAGACCTGCTTCCCGGACGTGTGGTTT	211
Oy	1691	ttggggttgcatgaaccacatcctctgtgtgcatataggacgctaaacagctatgtgctg	1750

Db	210	TTGGCTTTCGGAGAGACACACCTCTTGCGTGGCTGCTGCGACGCTAACACGCTGCTGCTGCTG	151
QY	1751	ctgcgtgattgggaactgctgctgttggcctgagctcctcaagcctgtgtgaaagttca	1810
Db	150	CTGCTGCTTGGAGACAGCTGGCTGCTGCTGCTGGACACTGACACACCCCTGTGGTGAAGTCA	91
QY	1811	gctggggggaagcctgtgtctctcctatgctgggtctccctgtgtagcttgggaaggttgcagccctc	1870
Db	90	GGAGGGGGGCGCGCTGGCTTCTTATAGCTGGGCTCCCTGGCAGCAGATAGTGGACGCTTC	31
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Db	30	TATGGCTTCTTGGGGAAACCCACAAAGGCC	2
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LOCUS	AR012624	3809 bp	DNA
DEFINITION	Sequence 3 from patent US 5763569.		
ACCESSION	AR012624		PAT
VERSION	AR012624.1	GI:3970614	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3809)		
AUTHORS	Brown, F.M., Hebert, S.C. and Garre, J.E. Jr.		
TITLE	Calcium receptor-active molecules		
JOURNAL	Patent: US 5763569-A 3 09-20UN-1998;		
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source	1..3809		
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Best Local Similarity	46.3%;	Pred. No. 4.9e-27;	Length 3809;
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QY	266	gagataaacacatccacagcctctgcttcccaacatcacccctgggtatgaactgtatgac	325
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QY	326	gtgtgctcaagatcttccaatgtct--atgcacacctgaagggtgcccggccagca---	379
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QY	437	gcaacatctggggccctgataaacatctacaagcctgtcaccaatctgcccctgttgaagccct	496
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QY	497	ttctcgaagcccttgtaagtctc--taagcgaagcagcgtgatactctatgtggaagcgcgaag	556
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QY	557	tcccgctctctcttgccgacacatccccaagcagataagtaacaaagtggaaagtaagtgccg	616
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QY	617	ctgcgaagagccttcgagctgagctcgtgatactcgtcttggaagctatggtgtacagcg	676
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TITLE Method of screening calcium receptor-active molecules  
JOURNAL Patent: US 5858684-A 3 12-JAN-1999;  
FEATURES Location/Qualifiers  
source 1. 3809  
/organism="unknown"  
BASE COUNT 910 a 1071 c 979 g 849 t  
ORIGIN

Query Match 6.48: Score 166.2; DB: 5; Length 3809;  
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Matches 1130; Conservative 0; Mismatches 1143; Indels 168; Gaps 11;

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REFERENCE	Unclassified.			
1 (bases 1 to 3809)				
AUTHORS	Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.			
TITLE	Calcium receptor-active molecules			
JOURNAL	Patent: US 5688938-A 3 18-NOV-1997;			
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Best Local Similarity	46.3%	Pred. No. 4.9e-27		
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AUTHORS	Garrett,J.E., Capuano,I.V., Hammerland,L.G., Hung,B.C., Brown,E.M., Hebert,S.C., Nemeht,E.F. and Fuller,F.		
TITLE	Molecular cloning and functional expression of human parathyroid calcium receptor cDNAs		
JOURNAL	J. Biol. Chem. 270 (21), 12919-12925 (1995)		
MEDLINE	95279439		
REFERENCE	2 (bases 1 to 3783)		
AUTHORS	Garrett,J.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-FEB-1995) James E. Garrett, Molecular Biology, NPS Pharmaceuticals, Inc., 420 Chipeta Way, Salt Lake City, UT 84108, USA		
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 KEYWORDS S83176.1 GI:1836093  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 3234)  
 AUTHORS Freichel,M., Zink-Lorenz,A., Holloschi,A., Hafner,M., Flocke, V. and Raue,F.  
 TITLE Expression of a calcium-sensing receptor in a human medullary thyroid carcinoma cell line and its contribution to calcium secretion  
 JOURNAL Endocrinology 137 (9), 3842-3848 (1996)  
 MEDLINE 96343808  
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI g1dbsg 179653] from the original journal article. This sequence comes from Fig. 6.  
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DEFINITION	H. sapiens PCAR1 gene.		
ACCESSION	X81086		
VERSION	X81086.1 GI:599819		
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SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3234)		
TITLE	Pearce, S.H.S.		
JOURNAL	Direct Submission		
REMARK	Submitted (16-AUG-1994) S.H.S. Pearce, MRC Molecular Medicine Group, Collier Bldg, Royal Postgrad Med School, London W12 0NN, UK		
REFERENCE	2 (bases 1 to 3234)		

REFERENCE	AUTHORS	JOURNAL	COMMENT
3 (bases 1 to 3234)	Pearce, S.H.S. and Thakker, R.V.	Unpublished	
TITLE	Pearce, S.H.S.	Direct Submission	
JOURNAL	Submitted (05-DEC-1994)	Group, Collier Bldg, Royal Postgrad Med School, London W12 0NN, UK	
On Dec 7, 1994	this sequence version replaced g1:556648.		
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RESULT	11			
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LOCUS	AF110179	4319 bp	mRNA	ROD
				02-MAY-1999



DEFINITION Mus musculus calcium-sensing receptor (CaSR) mRNA, alternatively spliced, complete cds.

ACCESSION AF110179

VERSION AF110179.1 GI:4731164

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

AUTHORS Oda,Y., Tu,C.-L., Mauro,T. and Bikle,D.

TITLE The calcium-sensing receptor and its alternatively-spliced form in murine epidermal differentiation

JOURNAL Unpublished

REFERENCE Oda,Y., Tu,C.-L., Mauro,T. and Bikle,D.

AUTHORS Oda,Y., Tu,C.-L., Mauro,T. and Bikle,D.

TITLE Direct Submission

JOURNAL Submitted (10-NOV-1998) 190 Dermatology, VA Medical Center - San Francisco, 4150 Clement Street, San Francisco, CA 94121, USA

FEATURES

source

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BASE COUNT 1046 a 1235 c 1058 g 980 t

ORIGIN

Query Match 6.3%; Score 162; DB 12; Length 4319;

Best Local Similarity 46.0%; Pred. No. 4.2e-26;

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DEFINITION Ca(2+)-sensing receptor [cattle, parathyroid gland, mRNA, 5249 nt].
ACCESSION 567307
VERSION 567307.1 GI:453108
KEYWORDS
SOURCE
ORGANISM Bos taurus parathyroid gland.
Bos taurus
Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
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Bovinae; Bos.
REFERENCE 1 (bases 1 to 5249)
AUTHORS Brown,E.M., Gamba,G., Riccardi,D., Lombardi,M., Butters,R.,
Klor,O., Sun,A., Hediger,M.A., Lippert,J. and Hebert,S.C.
TITLE Cloning and characterization of an extracellular Ca(2+)-sensing
receptor from bovine parathyroid
JOURNAL Nature 365 (6455), 575-580 (1993)
MEDLINE 94077182
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gtdbseq 140593] from the original journal article.
This sequence comes from Fig. 2.
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Best Local Similarity 46.0%; Pred. No. 4,7e-25;
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VERSION 175051.1 GI:3011192
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 5275)
AUTHORS Brown,E.M., Fuller,F.H., Hebert,S.C. and Garrett,J.E. Jr.
TITLE Calcium receptor-active molecules
JOURNAL Patent: US 5588938-A 1 18-NOV-1997;
FEATURES
source 1..5275
BASE COUNT 1277 a 1475 c 1316 g 1207 t
ORIGIN

Query Match 6.1%; Score 157.2; DB 5; Length 5275;
Best Local Similarity 46.0%; Pred. No. 4,7e-25;
Matches 1136; Conservative 0; Mismatches 1168; Indels 168; Gaps 11;

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Qy	1786	tcttcaacagcctgtgtgtgaggttcagcgtggggtaagcgtgtctctctcaatgctggttc	1845
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2000, 18:09:40 ; Search time 97.56 seconds  
(without alignments)  
2862.981 Million cell updates/sec

Title: US-09-361-652-6  
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Scoring table: IDENTITY\_NUC

Searched: 214294 seqs, 59861208 residues

Database : Issued\_Patents\_NA:\*

Word size : 0

Number of hits that pass the threshold : 428568

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	143.2	6.1	5275	3	US-08-480-751-1	Sequence 1, Appl1
4	143.2	6.1	5275	4	US-08-943-986-1	Sequence 1, Appl1
5	143.2	6.1	5275	5	US-08-353-784-1	Sequence 1, Appl1
6	138.4	5.9	3809	1	US-08-485-588-3	Sequence 3, Appl1
7	138.4	5.9	3809	2	US-08-484-565-3	Sequence 3, Appl1
8	138.4	5.9	3809	3	US-08-480-751-3	Sequence 3, Appl1
9	138.4	5.9	3809	4	US-08-943-986-3	Sequence 3, Appl1
10	138.4	5.9	3809	5	US-08-353-784-3	Sequence 3, Appl1
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37	51.6	2.2	4300	2	US-08-463-642-1	Sequence 1, Appl1
38	51.6	2.2	4300	2	US-08-455-602-1	Sequence 1, Appl1
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40	51.6	2.2	4300	6	PCT-US91-09422-16	Sequence 16, Appl1
41	51.6	2.2	5236	1	US-08-072-574-1	Sequence 1, Appl1
42	50.2	2.2	3330	1	US-08-072-574-7	Sequence 7, Appl1
43	46.2	2.0	4085	1	US-08-072-574-9	Sequence 9, Appl1
44	46.2	2.0	4181	1	US-08-072-574-9	Sequence 9, Appl1
45	46.2	2.0	2997	6	PCT-US94-14989-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1  
US-08-485-588-1  
Sequence 1, Application US/09485588  
Patent No. 5688938  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: Forrest H. Fuller  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,588  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/005



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5275 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 515..3769  
OTHER INFORMATION:  
US-08-485-588-1

Query Match 6.1%; Score 143.2; DB 1; Length 5275;  
Best Local Similarity 47.3%; Pred. No. 5.5e-28;  
Matches 501; Conservative 0; Mismatches 553; Indels 6; Gaps 2;

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RESULT 2  
US-08-484-565-1  
Sequence 1, Application US/08484565  
Patent No. 5763569  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: James E. Garfield, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSO  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,565  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:







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APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 515..3769
OTHER INFORMATION:
US-08-480-751-1

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Query Match      6.1%; Score 143.2; DB 3; Length 5275;
Best Local Similarity 47.3%; Pred. No. 5.5e-28;
Matches 501; Conservative 0; Mismatches 553; Indels 6; Gaps 2;

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DB 3035 GCCATCTGCGCGGCGCACTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3094
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QY 2250 atcctctgcccagcactcaacacagcacagcagcacttcc 2289
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DB 3095 ATCTCTTCAAGCTTCCCGGAACACATGAGAGAGTGTG 3134
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```

# RESULT

```

US-08-943-986-1
; Sequence 1, Application US/08943986
; Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCULUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
City: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127

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APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-485-568-3

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Query Match          5.9%: Score 138.4: DB 1: Length 3809:
Best Local Similarity 47.0%: Pred. No. 8.4e-27:
Matches 498: Conservative 0: Mismatches 556: Indels 6: Gaps 2:

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DB 1933 CTCTTATCAACAGAGAGAGAAATCCTGTGAGTGGTTCTCCAGGAGAGTGCCTTCTCC 1992

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QY 1350 tgcctcttgaatgtgtccctgtgagcgtgagaccttcctcaacaagaagcagctctac 1409
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DB 2113 GCCTGTAAACAAGTGCACAGATGCTTGTGTCATGAGAACACACACCTCTGCAATGGCC 2172

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QY 1830 caaacacccggtgtcgtgcttcttggatgatcagcctcagcgccacgctctcttctgt 1889
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DB 2530 GGGCTCAACCTGACATCTCTGTGTTTCTCTGTGACCTTTCATGACATTTGTCTGT 2589
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QY 1890 ctacttgcctgtgtgtgtgagccaccacgtcctcaggaataaccagccttcccccat 1949
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QY 1950 ctgtgtatgcttgaatgacagaagaacacccctcctgtgctc--catactgtcctctcac 2009
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DB 2710 ACCTGCTGCTGTGCTGCTCATCTGCTTCTTCTTGTGCTTCAAGTCCCGAAGCTGCGGAG 2769
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QY 2070 aactacaagagcccaaatgtgtcaccttcagcctcctcctcaactcgtgtcctgagtc 2129
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DB 2770 AACTCAATGAAAGCCAACTTATCATACCTTCAAGCATGCTCATCTTCTTCTGTGATC 2829
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QY 2130 gctctcttcaacacagcgcagcgttctagaacggcaaatcctcgtcgtgagcacaatgatg 2189
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DB 2830 TCTTTCATTTCCAGCTTATGACGACCTATGCAAGTGTGCTGTGCGGTGAGAGTGAAT 2889
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QY 2190 gctgagcgtgagcagccttgaagcagcgcgtcctggtgtgtatcttgcctcaagtgtcagtg 2249
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DB 2890 GCCATCTGCGACCGCAGCTTGTGCTTGTGCTGCGGTGCACTTCTTTCACAAAGATCTACATC 2949
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QY 2250 atcctctgcgcgccagacctcacaagcacaagacaccttcc 2289
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DB 2950 ATTCCTTCAAGCCATTCGCCGACACATCGAGGAGGTGTC 2989
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RESULT
US-08-484-565-3
Sequence 3, Application US/08484565
Patent No. 5763569
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: Including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784

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CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3505
OTHER INFORMATION:
US-08-480-751-3

Query Match          5.9%; Score 138.4; DB 3; Length 3809;
Best Local Similarity 47.0%; Pred. No. 8.4e-27;
Matches 498; Conservative 0; Mismatches 556; Indels 6; Gaps 2

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Oy      1650   gtagtggcagccctatagtcttc::ttgggaaacccaaggccctgcgtgct-vgtaagc    1709
Db      2353   TGCTTCHCAGCTCCCTGTTCTCTCATCGGGGAGGCCAACAGATCGAAGCGGCGCCTGC    2412
Oy      1710   caggccctcttgcccttggtttcacactcttcctcg::cctggcc::caadgttcgcatac    1769
Db      2413   CAGCGGCGCTTTTGGAACAACACTCTGCTCTGCATCTCATGTGATCCTGTGTAANAACAA    2472
Oy      1770   caactaa::catcatc::caag::tttcaccacaagga::aac::taaccttacaccaagccgggct    1829
Db      2473   CGTGTCTCTCTGTTTAGG---CCAAGAATCCCACCAGCTTTCACACGCAATGGGTGG    2529
Oy      1830   caaaccacagtgctgcgcgctglttgatgatcagctcagcgcccagaactgatalcgt    1889
Db      2530   GGGGTCAACTGGAGATTCCTGCTGCTGTTTTCCTGTGACCTTCATGCAATGTGTACTGT    2589
Oy      1850   ctacttgctgtgtgtgtgtgtgaccaccaatgcctgtctaggaataccaaagcctccccat    1949
Db      2590   GTGATCTGGCTCTACACCGCGCCCCCTCAAGCTACCGCACACAGAGCTGGAGGATGAG    2649
Oy      1950   ctggtgtagtgccttagtgtcacagaagaaccaactccctgcgcttaactagcctccctaac    2009
Db      2650   ATCACTTTCATCAGTCCACAGAGGCTCCCTCATGCGCTTGCGCTTCTTGATTCGGCTAC    2709
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Oy      2070   aactacaagaaggccaaa::tgtgtacccttcagccgtcct::taacteg::tgc::tgaatc    2129
Db      2770   AACCTCAATGAAGGACCAAGTTCATCACCTTCAGCATCTCTTCTTATCCTCTGGATC    2839
Oy      2130   gccctcttcaccaagcgccagcgcgtctagcgcggaatctacctgcgcggccaaatatg    2189
Db      2930   TCTCTTATCCAGCTATGCCACGACCTAAGCMAATTTGCTCTGCCGTAGAGGTGATT    2889
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Db      2890   GCCATCCCTGGAGGCGACACTTTGGCTGTGCTGGCTGATCTTCTTCAACAAGATCTACATC    2949
Oy      2250   atcctctgcgcgccagaactccaacagaacagagacctcc    2289
Db      2950   ATTCTTCAAGCCATCCCGCAACACATCGAGAGAGTGC    2989

RESULT          9
US-08-943-986-3
Sequence 36, Application US/08943986
Patent No. 5952314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
City: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ

```



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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373..3606
OTHER INFORMATION:
US-08-943-986-3

Query Match          5.98; Score 138.4; DB 4; Length 3809;
Best Local Similarity 47.08; Pred. No. 8.4e-27;
Matches 498; Conservative 0; Mismatches 556; Indels 6; Gaps 2;

QY 1233 ctaacataatgagacaaatccagtcgacggaagaacacccagctgacgaagctc 1292
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DB 1993 AACTGACGCGGAGACTCTGTGCGAGGAGACAGAAAGGATCATGAGGGGAGCCACC 2052
QY 1350 tgtgtcttgaagtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1409
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DB 2053 TGCTGCTTGAAGTGTGTGGAGTGTCCATGATGGGAGATAGTGTGAGAGATGCCAGT 2112
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DB 2113 GCCTGTAAACAAGTCCAGATGACTTGTGTCATATAGAACACACACTCTGCAATGCC 2172
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DB 2173 AAGGAGATCGAGTTTGTGTGTGAGCGAGGCCCTTGGATCGCACTCACCCCTTTGCC 2232
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DB 2293 CCATTTTCAAGGCAATCAACCGAGACTTCTTACTCTCTCTCTCTCTCTCTCTCTCTGC 2352
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DB 2353 TGCTTTCAGCTCCCTGTTCTTCTATCGGGAGCCCGAGACATGAGAGTCCGCCCTGCGC 2412
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DB 2413 CAGCGGCTTTTGGACATCACTTCTGTCTCTCATCTCATCTCTGTGGGAAACCAAC 2472
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DB 2473 CGTGTCTCTGTGTGTGTAGG---CCAGATCCCAACACGCTTCCACCCCAAGTGTG 2529
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DB 2590 GTGATCTGGCTCTACACCGCGCCCTCAAGCTACCGCAACCGAGAGCTGAGATGAG 2649
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DB 2650 ATCATCTTCAACGCTGTGCAAGGCTCTCTCTATGAGCTGTGAGCTGTGAGCTGTG 2709
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DB 2890 GCCATCTGTGACAGCAGCTTGTGCTGTGCGCTGATCTTCTTCAACAAAGATCTATCT 2949
QY 2250 atccttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2289
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RESULT 10
US-08-953-784-3
; Sequence 3, Application US/08353784
; Patent No. 6011068
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen, Manuel
; APPLICANT: F. Baladrin, Forrest H. Fuller,
; APPLICANT: Eric G. DelMar, and Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
```











PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993

APPLICATION NUMBER: U.S. 08/017,127

FILING DATE: 12 February, 1993

APPLICATION NUMBER: U.S. 07/934,161

FILING DATE: 21 August, 1992

APPLICATION NUMBER: U.S. 07/934,044

FILING DATE: 11 February, 1992

APPLICATION NUMBER: U.S. 07/749,451

FILING DATE: 23 August, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 213/006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1500

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5006 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 436..3699

OTHER INFORMATION:

US-08-484-565-2

Query Match 5.7% Score 132.6; DB 2; Length 5006;

Best Local Similarity 50.4%; Pred. No. 3,1e-25;

Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agctcaatgagcgtgctacaccccttccagcgtatgagcgttgggttgaagagata 69

DB 619 AGGTATATTTCCGTGGGTTCCGTGTACAGGCTATGATATTGCCATGAGAGATA 678

QY 70 aacaaccacagcccgctgctccacacacacccctgsggtacacgctgtatgagtgt 129

DB 679 AACAGCAGCCAGCCCTTCTTCCCACTTGACGCTGGGATACAGSATATTGACACTTGC 738

QY 130 tctgactctgccaatg--tgtatgcaagcgtgagagtgtctctcc-----tgcca 177

DB 739 AACACGTTTCTAAGGCTTGGAAGCCACCTGAGTTTGTGTGCAAAACAAATTCAT 798

QY 178 gggcaacaacacatagagctccaagagagaccttccactatcccttaagtgctggca 237

DB 799 TCTTGAACCTTGATGAGTTCTGCACTGCTCAGAGCAATTCCTCTACCATTTGCTGTG 858

QY 238 gtgattggcgctgacagcaccacacgctgctgcaacacagcgcgcctgctgagcccttc 297

DB 859 GTGGAGACACTGGCTCAGCGGCTCTCCACGCGAGTGGCAATTCGTGGGCTCTTCTAC 918

QY 298 ctggtgcatatagactgctgagcagcagcagcgtcctcaagcgtgaagcggcaglatccc 357

DB 919 ATTCGCCAGGTGATGCTCTCTCCAGACAGCTCCACAGCAACAAGATCAATTCAG 978

QY 358 tcttctctgacacatcccaatgacaagtacccaagtggaagacaaatggtgtctgctg 417

DB 979 TCTTCTCCGACCAATCCCAATGATGAGCAGCAGCGCCACTGCTCATGGCAGACATCATC 1038

QY 418 cagaagctcggtgtgacatgacatctctgtgtgcccagctgacgactatggtgacgcta 477

DB 1039 GAGTATTTCGCTGAGACTGGGTGGCACAATTGCACCTATGACACTATGGCGGCGG 1098

QY 478 ggggtcagagcactggaagacacagccctgtcagggcactgtcatgtctttaaagac 537

DB 1099 GGGATTGAGAAATTCGAGAGGAGAGTGAAGAAAGGATCTCTCATGCACTTACGTGAA 1158

QY 538 atcagccctctctgcccaggtgtgagatgagagatgagtgcccatgagcgcacctg 597

DB 1159 CTCATCTCCAGTACTGTGATGAGAGAGA-----GATCCAGCATGTGTGAGAGTATT 1212

QY 598 gccacggccgggscacacgctgctgtgtgttttcccccggcagtggtgccaaggtgtt 657

DB 1213 CAATATTCACAGGCGCAAGTATGATGTTTCTCCAGTGCGCCAGATCTTGAGACCCCTC 1272

QY 658 ttcgagctcgtgtgtgtgacaaacctgacgtgcaaggtgtgtgtcgcctcagaagcctg 717

DB 1273 ATCAAGAGATTTGCCGCGCAATATCACGGCAAGATCTGGCTGGCCAGCAGGCGCTGG 1332

QY 718 gcccttccagcaccatcacctggtgtgtcccgagatccagccatggtggtgtgtgctg 777

DB 1333 GCCAGCTCTCTCCGTGATCGCATGCTCTCACTTCCACGTGTTGGCGGCACCATTTGA 1392

QY 778 gtggccatccagaagagggctgtccctggtcctgagcgtt 818

DB 1393 TTCGCTCTGAAGGCTGGCGAGATCCAGGCTTCGGGGAATT 1433

RESULT 13

US-08-480-751-2

Sequence 2, Application US/08480751

Patent No. 5858684

GENERAL INFORMATION:

APPLICANT: Edward F. Nemeth

APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert

APPLICANT: Forrest H. Fuller

APPLICANT: James E. Garrett, Jr.

TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

NUMBER OF INVENTION: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: First Interstate World Center

STREET: Suite 4700

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PASTSEO

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,751

FILING DATE: 7 June, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: described below: 9

APPLICATION NUMBER: 08/353,784

FILING DATE: 9 December, 1994

APPLICATION NUMBER: PCT/US/94/12117

FILING DATE: 21 October, 1994

APPLICATION NUMBER: U.S. 08/292,827

FILING DATE: 23 August, 1994

APPLICATION NUMBER: U.S. 08/141,248

FILING DATE: 22 October, 1993

APPLICATION NUMBER: U.S. 08/009,389

FILING DATE: 23 February, 1993



APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5006 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 436..3699  
OTHER INFORMATION:  
US-08-480-751-2

Query Match 5.7%; Score 132.6; DB 3; Length 5006;  
Best Local Similarity 50.4%; Pred. No. 3.1e-25;  
Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agctcaatgagcaggtacacaccccttcacagcgtatgagcgtgggtgagga 69  
DB 619 AGGTAATATTCGGGCTTGGCTGCTGCTACAGGCTATGATTTGCCATGAGGAGATA 678  
QY 70 aacaactcacagcctctgctgcccacacacacccctggggtacacagctgatgtgt 129  
DB 679 AACAGCAGCCAGCCCTCTTCCCAACTTGACGCTGGGATACAGATTTTGACACTTGC 738  
QY 130 tctgactctgccaatg---tgtatgcaagcgtgagagtgctcc-----tgcca 177  
DB 739 AACACCGTTTCTTAAGCGCTTGGAACCCACCTGAGTTTGTGTCTCAAAACAATATGAT 798  
QY 178 gggcaaacacacatagctcacaagagagaccccttcacacatccctcaggtgtgca 237  
DB 799 TCTTTGAACCTTGATGATGCTTCTGCAACTGCTCAGACACATTCCTCTACGATTGCTGTG 858  
QY 238 gtgattggcctgacagacacacacagctgtgctgacacacagccctctgagcccttc 297  
DB 859 GTGGAGCACTGCTGCTCAGGCTCTCCAGGCAAGTGGCAATCTCTGGGCTCTTCTAC 918  
QY 298 ctggtgatattagctatgctgagcagcagcagcagcgtcagcgtaagcggcaglatccc 357  
DB 919 ATTCCCGAGGTCAGTTAGCCCTCCCTCCAGCACTCTCAGCAACAAGAAATCAATTCAAG 978  
QY 358 tctttccggcagcaccatcccaatatacaagtaacagtggtggagacatggtgtgtgtg 417  
DB 979 TCTTTCTCCGAACCATCCCATATATGACACAGGCCACTGCCATGCGACACATCATC 1038  
QY 418 cagaagttcgggtgactgactcctctctggttggcagcagtgagcactatgagcagccta 477  
DB 1039 GAGTATTTCCGCTGTAATGCTGGTGGCACAAATTGCAAGCTGATGAGATATGGGGCGCG 1098  
QY 478 ggggtgagcagcagtgagaaacacagccctggtcagagcagcagcagcagcagcagc 537  
DB 1099 GGGATTGAGAAATTCGAGAGAGAACTGAGAAAGGATATCTGCATGACACTTCACTGAA 1158  
QY 538 atcaagccctctctgcccaggtggcgatgagagatgacatgctcctcagcagcagcagc 597  
DB 1159 CTCATCTCCCACTACTGATGAGGAGA-----GATCCAGCATGTGTAGAGGTGATT 1212

QY 598 gccacggccggggccacagctggtgtttttccacggcagcagtgccaggtgttt 657  
DB 1213 CAATATTCACAGGCGCAAGATCATGTGTTTCTCCAGATGGCCACGATCTTAGCCCTC 1272  
QY 658 ttgagtcctggtgtgtgacacacctgacgtgcaaggtgtgtgtgctcctgaagcctg 717  
DB 1273 ATCAAGGAGATTGTCCGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGGAGCCTCG 1332  
QY 718 gcccttcacagcaccatcacatcaggtgtgcccggatccagcagcattggatggtgtg 777  
DB 1333 GCCAGCTCTCTCCGATGAGGATGCTCAGTACTTCCACGTGTTGGCGCACCATTTGA 1392  
QY 778 gtggccatccagaagagggtgtccctggtgcccgtgaagcgtt 818  
DB 1393 TTCGCTCTGAAGGCTGGGAGATCCACAGGCTTCGGGATTT 1433

RESULT 14  
US-08-943-986-2  
Sequence 2, Application US/08943986  
Patent No. 5962314  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
City: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,986  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,565  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/006  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5006 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 435..3699  
OTHER INFORMATION:  
US-08-943-986-2

Query Match 5.7%; Score 132.6; DB 4; Length 5006;  
Best Local Similarity 50.4%; Pred. No. 3.1e-25;  
Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agcttcaatgagcatggtctaccctcttccaggctatgcygcttgaggatata 69  
DB 619 AGGTAATAATTCGTTGGGTTTCGCTGTTACAGGCTATGATATTGGCATAGAGAGATA 678  
QY 70 aacaactccagggccctgctgcacacatcacccctgggggtaccagctgtatgtgt 129  
DB 679 AACAGCAGCCGACGCCCTCTTCCCAACTTACGCTGGGATACAGATATTGGACACTTC 738  
QY 130 tctgactctgccaatg---tgatgccaagctgagagtgctctccc-----tgcca 177  
DB 739 AACACCGTTTCTTAAGGCTTGAAGCCACCCCTGAGTTTGTGCTCAAAACAAATTTGAT 798  
QY 178 gggcacaacacactatgagctccaaaggagacctctccacatctccctaaaggtgtgca 237  
DB 799 TCTTTGAACCTTGATGAGTTCTCAACTGCTCAGAGCACATTCCTCTACGATGCTGTG 858  
QY 238 gtgattgagcctgacaagcaccaacgctgctgcacacagccgctgcagagcccttc 297  
DB 859 GTGGAGACAACTGGCTCAGGCCGCTCTCACGGCAGTGGCAATTCGCTGGGGCTCTTTAC 918  
QY 298 ctggtgcatatagctatgctgcagcagcagcagctcagcgtgaaagcggcatatccc 357  
DB 919 ATTCCCGAGTCAAGTATGCTCTCCCTCCAGAGACTCCTCAGCAACAAATCAATTCAG 978  
QY 358 tcttctctgagcaccatcccccaatgacaatgaccaggtggaagcacaagtgtgctgtcgt 417  
DB 979 TCTTTCTCCGAACCACTCCCAATGATGAGCACACGACCACTGCTCATGGCAGACATCATC 1038  
QY 418 cagaagtctgggtgagcctgacatctctctgttgtagcagcagctgagcactatgagcacta 477  
DB 1039 GAGTATTTCGCTGGAACTGGGTGGGCAATTCACACTGATGACGACTATGGCGGCCG 1098  
QY 478 ggggtgtagcagcactggaacccagcgcctgtgcaaggagcactctgcatctgttcaagac 537  
DB 1099 GGGATTGAGAAATTCGAGAGAACTGAGGAAAGGATATCTGCACTGCACTTCAGTGAA 1158  
QY 538 atcatgcccctctctgcccaggtggtgcatgagaagatgagcctcattgcccacactg 597  
DB 1159 CTCATCTCCAGACTCTGTGATGAGGAGA-----GATCCAGCATGTGGTAGAGTGATT 1212  
QY 598 gcccagggccgggagccagcgtctgtgtttttccagccggcagctgtgccaaggtgtt 657  
DB 1213 CAAATTTCCACGGCCAAAGTATCGTGTTCCTCCAGTGGCCAGATCTTTGAGCCCCCTC 1272  
QY 658 ttctgagctcgtggtgtgctgacaacactgactgccaaggtgtgtgtcagctcagaagcctgtg 717  
DB 1273 ATCAAGAGAGATGTCCGGCGCAATATCACGGGCAAGATCTGGGTGGCCAGCAGAGCGCTGG 1332  
QY 718 gcccctctcagagacatcatctgggtgtcccggaatccagcagcattggtgagtggtgtggc 777  
DB 1333 GCCAGCTCTCCTGTGATGCCATGCTCATGACTTCCACGCTGTTGGCGGCGACCATTTGA 1392

QY 778 gtggccatccagaagaggtctgcccctggcctgaagcgtt 818  
DB 1393 TTCGCTCTGAAGGCTGGCGAGATCCAGAGGCTTCGGGGAATT 1433

RESULT 15  
US-08-687-289A-2  
Sequence 2, Application US/08687289A  
Patent No. 5981195  
GENERAL INFORMATION:  
APPLICANT: Fuller, Forrest H.  
APPLICANT: Knapcho, Karen J.  
APPLICANT: Hamerlund, Lance G.  
TITLE OF INVENTION: CHEMERIC RECEPTORS AND METHODS FOR  
IDENTIFYING COMPOUNDS ACTIVE AT  
TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND  
THE USE OF SUCH COMPOUNDS IN THE  
TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,289A  
FILING DATE: July 25, 1996  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,526  
FILING DATE: July 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 220/004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-687-289A-2

Query Match 5.7%; Score 132.6; DB 4; Length 4000;  
Best Local Similarity 50.4%; Pred. No. 2.8e-25;  
Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agcttcaatgagcatggtctaccctcttccaggctatgcygcttgaggatata 69  
DB 224 AGGTAATAATTCGTTGGGTTTCGCTGTTACAGGCTATGATATTGGCATAGAGAGATA 293  
QY 70 aacaactccagggccctgctgcacacatcacccctgggggtaccagctgtatgtgtgt 129  
DB 284 AACAGCAGCCGACGCCCTCTTCCCAACTTACGCTGGGATACAGATATTGGACACTTC 343  
QY 130 tctgactctgccaatg---tgatgccaagctgagagtgctctccc-----tgcca 177  
DB 344 AACACCGTTTCTTAAGGCTTGAAGCCACCCCTGAGTTTGTGCTCAAAACAAATTTGAT 403







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2000, 19:00:09 : Search time 185.6 Seconds  
(without alignments)  
3144.925 Million cell updates/sec

Title: US-09-361-652-6  
Perfect score: 2333  
Sequence: 1 agcgttgtagctcaatga.....ggcgcgtgcgcctccactga 2333

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database: N\_Geneseq\_36:\*

Word size: 0

Number of hits that pass the threshold: 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	143.2	6.1	5275	1	T95857	Bovine parathyroid
2	143.2	6.1	5275	1	V26962	Bovine parathyroid
3	143.2	6.1	5275	1	V82483	Bovine parathyroid
4	138.4	5.9	3809	1	T61382	Parathyroid calcitri
5	138.4	5.9	3809	1	T95859	Human parathyroid
6	138.4	5.9	3809	1	V26964	Human parathyroid
7	138.4	5.9	3809	1	V82485	Human parathyroid
8	132.6	5.7	5006	1	T61381	Parathyroid calcitri
9	132.6	5.7	4000	1	T86166	Nucleotide sequenc
10	132.6	5.7	5006	1	T95858	Human parathyroid
11	132.6	5.7	5006	1	V26963	Human parathyroid
12	132.6	5.7	5006	1	V82484	Human parathyroid
13	129	5.5	4131	1	T89290	Dogfish shark kidn
14	123.4	5.3	4131	1	T95860	Rat kidney calcium
15	123.4	5.3	4131	1	V26965	Rat kidney calcium
16	123.4	5.3	4131	1	V82485	Rat parathyroid ca
17	111	4.8	3384	1	T86165	Nucleotide sequenc
18	104.4	4.5	2148	1	Q33222	BopCar 1, bovine p
19	76.6	3.3	3584	1	X05857	Rat pheromone rece
20	76.6	3.3	3584	1	X05818	Rat pheromone rece
21	74	3.2	2618	1	T16710	Metabotropic gluta
22	74	3.2	2619	1	T29408	Human metabotropic
23	72	3.1	3919	1	O80418	Human mglur3 cDNA.
24	72	3.1	3410	1	T03887	Human mglur3 DNA.
25	71.8	3.1	3108	1	X05814	Mouse pheromone re
26	71.8	3.1	3589	1	X05815	Mouse pheromone re
27	71.8	3.1	2412	1	X05853	Mouse pheromone re
28	70.8	3.0	2961	1	T38322	Metabotropic gluta
29	70.8	3.0	1889	1	X05807	Mouse pheromone re
30	70.8	3.0	1889	1	X05846	Mouse pheromone re
31	69.6	3.0	2732	1	X05810	Mouse pheromone re
32	69.6	3.0	2962	1	X05811	Mouse pheromone re
33	67.4	2.9	1889	1	X05805	Mouse pheromone re
34	67.4	2.9	1889	1	X05845	Mouse pheromone re
35	66.6	2.9	2565	1	X05804	Mouse pheromone re
36	66.6	2.9	2566	1	X05843	Mouse pheromone re
37	65.6	2.8	2394	1	X05863	Rat pheromone rece
38	65.6	2.8	2085	1	X05864	Rat pheromone rece
39	65.6	2.8	3359	1	X05824	Rat pheromone rece

40	65.6	2.8	3012	1	X05825	Rat pheromone rece
41	64	2.7	1644	1	X05856	Rat pheromone rece
42	64	2.7	2811	1	X05817	Rat pheromone rece
43	63.8	2.7	3125	1	X05805	Mouse pheromone re
44	63.8	2.7	2159	1	X05844	Mouse pheromone re
45	61.8	2.6	3307	1	X05822	Rat pheromone rece

## ALIGNMENTS

RESULT 1  
T95857  
ID T95857 standard: cDNA to mRNA: 5275 BP.  
AC T95857  
DT 08-MAY-1998 (first entry)  
DE Bovine parathyroid cell calcium receptor 1 (BopCar 1) cDNA.  
KW Bovine parathyroid cell calcium receptor 1; BopCar 1;  
KW calcium homeostasis; hyperparathyroidism; osteoporosis; ss.  
CS Bos sp.  
FH Key location/Qualifiers  
FT 515..3772  
FT CDS /\*tag= a /product= parathyroid\_cell\_calcium\_receptor\_1

US688938-A.  
PM 18-NOV-1997.  
PD 07-JUN-1995; 485588.  
PF 07-JUN-1995; US-485588.  
PR 23-AUG-1991; US-749451.  
PR 11-FEB-1992; US-834044.  
PR 21-AUG-1992; US-934161.  
PR 12-FEB-1993; US-017127.  
PR 23-FEB-1993; US-009389.  
PR 22-OCT-1993; US-141248.  
PR 19-AUG-1994; US-292827.  
PR 21-OCT-1994; WO-012117.  
PR 08-DEC-1994; US-353784.  
PA (BGHM.) BRIGHAM & WOMEN'S HOSPITAL.  
PI (NPSF.) NPS PHARM INC.  
PI Brown EM, Fuller FH, Garrett JE, Hebert SC;  
DR WPI: 98-008040/01.  
P-PSDB: W38272.  
PT DNA encoding calcium receptor polypeptide(s) - useful for  
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis  
PS Claim 1, Columns 107-116, 174pp, English.  
CC The present sequence encodes bovine parathyroid cell calcium  
CC receptor 1 (BopCar 1).  
CC The specification includes details of molecules that can modulate  
CC one or more inorganic ion receptor activities, and antibodies and  
CC antibody fragments targeted to inorganic ion receptor proteins. The  
CC proteins, nucleic acids and antibodies may be used to treat  
CC disorders by modulating one or more inorganic ion receptor  
CC activities, preferably disorders of calcium homeostasis, e.g.  
CC hyperparathyroidism and osteoporosis.  
SQ Sequence 5275 BP: 1277 A; 1476 C; 1315 G; 1207 T;

Query Match 6.1%; Score 143.2; DB 1; Length 5275;  
Best Local Similarity 47.3%; Pred. No. 2.6e-26;  
Matches 501; Conservative 0; Mismatches 553; Indels 6; Gaps 2;

OY 1233 ctaaacataatgagaccacaaatccagtcgacgaggaagaacacacacagtccttaagctt 1292  
DB 2078 cttctcattcattgagaaataattctgtgagtgatgattctcaaggagtgctttcttc 2137  
OY 1293 gtgtgtccacgactgtcttgaagggac--cagcagtcgttaaggtttccatcac 1349  
DB 2138 AACCTCAGTCCAGAGTGGCTTGGCAGGAGCAGAAAGAAATCATTTAGAGGGGAGCCAC 2197  
OY 1350 tctgtccttgagtcgtgtccctg\*cgggc\*ggagacc\*ccccaacaaga\*cgagccttac 1409  
DB 2198 TGCTCCTTTGAGTGCTGTGGAATGCTGTGAGGAGTACACGACGAGACAGATGCAAGT 2257



QY	1410	agatgcgaagccttctgtgaacaaagaagtagtggacaccctgaagggaagccagagccctgtccgc	1469
QY	1410	agatgcgaagccttctgtgaacaaagaagtagtggacaccctgaagggaagccagagccctgtccgc <td>1469</td>	1469
Db	2238	GCCTGTGTAATAGTCCCTGATGAGTCTTGTGCTCAATATGAGAACACCACTTCTGCAATCCGC	2317
QY	1470	cgcactgtagtcttcttctgtgcttctgtgacacacactcttbggtgtgtctgtgcagctaac	1529
Db	2318	AAGGAGATCGAGTTTCTGTGTGTGAGCCGAGACCCTTGGGATGCGACTACAGCTCTTTTCT	2377
QY	1350	acgcgtctgtcgtcgtcgtcgtcgttggagactgtgcgttgccgttctgtcgtgcactagacac	1589
Db	2378	GTGCTGGGCAATTTTCTTCACAGCCCTTGCTGGGGGTCTTCAATCAAGTTCCGGCAACAG	2437
QY	1590	ccgtgtgtgtgaagtagaagsgggcgccgtgtgttctctatgtgtgtgtccctctgcaca	1649
Db	2438	CCCATCGTCAAGGGCCACCAACCGGAGAGCTCTCTATCTCTTCTTCTTCTCTCTCTGTC	2497
QY	1650	gtagtagtgcacgcctctatgctcttcttgggaaaccaagaagcgtgcgtgtctgtacgc	1709
Db	2498	TGCTTTCACAGCTCCCGTTTCTTATGCGGAGACCCAGAGACTGAGACGTGCGGCTTGCGC	2557
QY	1710	caagccctcttctgtcccttgtgttaccacatcttcgtctcgtcgtgcagttcgtcatctc	1769
Db	2558	CAGCGGCGCTTTGGACATCAGGCTTGCTGTCTGTGATCTGATCGATCCTGGTGAACCAAT	2617
QY	1770	caactaatcatcatctcctaagttctccacaagaagtaactaatcttaccagcgcctggctc	1829
Db	2618	CGGGTCTCCCTCGGGTTTGAAG--GCCAAGATTCCACACAGCTTCCACCGAAGGGGTGG	2674
QY	1830	caaaacccaggtgtgcgcgcgttctgtgtatgatcagctcagcgccagagctgttatcgt	1889
Db	2675	GGGCTCAACCTGCAGTTCTCTCTGTCTTCTGTGACCTTATGACATTTGTATCTGT	2739
QY	1890	ctaactgtgctgtgtgtgtgtgaaccccaactcgtcgtcagaagaaataccagcgtctcccat	1949
Db	2735	GCAATTTGGCTCATTATGACGGGCCCCCTCGAGCTACCGAACAACAGAGCTGAGAGAGAG	2794
QY	1950	ctgtgtatgcttgaagtgtcacagagacaactccctgtgtgtctatctagtccttccctaac	2009
Db	2795	ATCATCTTCATCACTACCTCCACAGAGGCTCGCTATGAGCGCTGGAGCTTCTGTATCGGCTAC	2854
QY	2010	aatgcccctccctccatcagtagtgccttctgtcgtcagtagtactcgtgtgaagaacttgcagag	2069
Db	2855	ACCTGCTTGTGCGCCGCGCATCTGCTTTTCTTGCCCTTCAAGTCCCGGAAGCTGCGAGAG	2919
QY	2070	aactacaacagcgcaaatgtgttaaccttaagcctgtccttcaacttgcgttcctgaatc	2129
Db	2915	AACCTCAATGAGCGCAAGTTGATACCTTGAGATGCTCATCTTCTTCAATGCTGTGATGC	2974
QY	2130	gccttcttccacacgcccagcgtctacagcgcgaagttaacctgctgtcggccaatgatg	2189
Db	2975	TCTTTCAATCCCCCGCTACGCGCAGACACTTACGGCAAGTTGTCTCTCCCTGAGAGGTGATC	3034
QY	2190	gctgtgtgtgagcagccgcagcagcaggttctgtgtgtgtatcttctgcctaagtgctagtg	2249
Db	3035	GCCATCTCGGGCGCACGCTTTGGTTGTGCTGCGCTGTATCTTCTTCAACAAAGGCTTAATC	3094
QY	2250	atcctctgcgcgccagacacttcaacaagacagacagcacttcc	2289
Db	3095	ATCCTCTTCAAGCCTTCCCGGAACACATGAGAGAGGTGC	3134
RESULT 2			
ID	V26962	standard: cDNA to mRNA; 5275 BP.	
AC	V26962		
DT	01-SEP-1998	(first entry)	
DE	Bovine parathyroid calcium receptor 1 gene 5kb fragment.		
KM	ss; calcium ion concentration; parathyroid hormone; homeostasis;		
KW	kidney; calcium receptor; detection.		
OS	Bos sp.		
PH	Key	Location/Qualifiers	
FT	CDS	515..3772	/*tag- a

FT US5763569-A. /product="BoPCar 1 5kb fragment"  
 EN 09-JUN-1998.  
 PD 07-JUN-1995; 484565.  
 PF 07-JUN-1995; US-484565.  
 PR 23-AUG-1991; US-749451.  
 PR 11-FEB-1992; US-834044.  
 PR 21-AUG-1992; US-934161.  
 PR 12-FEB-1993; US-017127.  
 PR 23-FEB-1993; US-009389.  
 PR 22-OCT-1993; US-141248.  
 PR 19-AUG-1994; US-292827.  
 PR 21-OCT-1994; WO-U12117.  
 PR 08-DEC-1994; US-353784.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPS) NPS PHARM INC.  
 PI Brown EM, Garrett JE, Hebert SC;  
 DR WPI; 98-347412/30.  
 DR P-PSDB; W54844.  
 PT Calcium receptor poly:peptide(s) - useful for drug screening or  
 PT antibody production  
 PS Example 25; Fig 47; 174pp; English.  
 CC The bovine parathyroid calcium receptor gene encodes a 1085 amino acid  
 CC protein. The tissue from which this receptor and receptors from human  
 CC parathyroid and rat kidney are derived, respond to changes, and control  
 CC changes, in calcium ion concentration, e.g. parathyroid hormone regulates  
 CC Ca2+ homeostasis in blood and extracellular fluid, and kidney function  
 CC alters through changes in Ca2+ levels in juxtaglomerular and proximal  
 CC tubule cells in the kidney. The purified receptors (produced  
 CC recombinantly) can be used to screen for compounds that modulate calcium  
 CC receptor activity, especially those that can be used to treat diseases  
 CC associated with the receptors in these tissues. They can also be used  
 CC to raise antibodies for use in detection assays.  
 SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match	6.1%	Score 143.2	DB 1	Length 5275
Best Local Similarity	47.38%	Pred. No. 2.6e+26		
Matches 501; Conservative	0	Mismatches 553		Indels 6; Gaps 2

OY	1233	ctaaacctaataatagaccacaatccaggtgcaacggaagaaccacaggtgctaagtct	1292
Db	2078	CTCTTCATCATGTATGAAAAAATTCGTGTGAGTGGATTCTCAAGGAGAGTGCTTTCTCC	2137
OY	1293	gtgtgtccacgcagctgtctcttaagggcaac--cagcgagtgttacggtttccatcac	1349
Db	2138	AACGCAAGTGGAGACTGCTCGCAGGAGACACGAAAGGAATCATTTAGGGGGAGCCACC	2197
OY	1350	tgctgctttgagtggttgccctctgtgggctctggagaccttctaacaagaagagactcac	1409
Db	2198	TGCTGCTTTAGAGTGTGGGAAATCTGTATGGGGAGTACAGGACAGACAAATGCAAGT	2257
OY	1410	agaatgcacgctctgtgaaacaagaagatgtggaccttgaggaagcagacactgttccgg	1469
Db	2258	GCTTGATGATAAGTGCCCTGATGACTCTTGTCATAAGAACACACTTCGTGATGCGC	2317
OY	1470	cgcacgtgtgtgttttttgctcttgctgtgagcacacctcttgggtgtctgtgcagctaac	1528
Db	2318	AAGGAGATCAGATTCTGTGTGTGGACCGAGCCCTTGCGGATGCACTACGCTTTTCT	2377
OY	1530	acgctgtgtgcgtcgtcgtcgtcttggagctgtcgtgcgtgttgccttgaccctagacac	1589
Db	2378	GTCGCTGGGCAATTTCTCTACAGCCTTCGTGCTGGGCGTCTTATATCAAGTCCGCAACCG	2433
OY	1590	ccgttggttgaaagtcagaagaggggcgcgcgtgtcttctatagtctggctcccttgcagca	1649
Db	2438	CCCATGCTCAAGGCAACACCAACGGGAGCTCTCTATCTCTCTCTCTCCCTGCTGTGC	2497
OY	1650	ggtgtggtcagcgcctctatgtcctcttttggggaaccacaagcctcgcgtgtctgtacgc	1709
Db	2498	TGCTTCTTCACGCTCCCTGTTCTTTCATCTGGGGAGACCCTCAAGACTGAGCGTCGGCTTGGC	2557
OY	1710	caagcgcctcttgcccttgaatttcacacatcttcgtctgcctgtacaagttgcctcatc	1769



Db	2558	CAAGCCGGCCCTTTGGCATACGCTTCGTGCTTCGATCTGTGCATCTGGTGAACAAACCAAT	2617
QY	1770	caactacatcatcatcttcaagttttcccaacaagttaccatcttaccacagcccggtc	1829
Db	2618	CGGTCCTCTCTGCTTTTGAG--GCCAAGATTCGCCACCACTTCACCGGAAGTGGTGG	2674
QY	1830	caaaaacacagtgctgcgcctgtgtgtgatagtacgtcagcggccagctgtatctgt	1889
Db	2675	GGGCTCAACCTGCAGATTCCTGCTGTGCTTCCTGCTGCACCTTCATCATATGTATCTGT	2734
QY	1890	ctaattgcttcggtgtgtgtgtgaaccccaattgcctcgtctagtgaataccagcgttcccat	1949
Db	2755	GCCATTTTGGCTCAATACAGCCGCCCTTCGAGCTTACCCCAACACAGACCTGAGAGACGAG	2794
QY	1950	ctgtgtagctgtgtagtgacagagacaacatccctggccttcatactgcttcctac	2009
Db	2795	ATCATCTTTCATACCTGCGCACAGAGGGCTGCTCATAGGCGTGGCTTCTTATGGGCTTC	2854
QY	2010	aatggcctccctcccatagtcgtccttgcgcagctacgtcactcgtgtaagagactgcacag	2069
Db	2855	ACCTGCTTGTGGCGGCCCATCTGCTTCTTCTTGCGCTTCAGTCCCGGAAGCTGCACAG	2914
QY	2070	aactacaacagagcccaattgtctaaccttcagcctgtccttcaacttctgtcctgagtc	2129
Db	2915	AACCTCAATGAGGCAACATTATCATCACTTCAGCATGCTCATCTTCTCATGTGCTGATC	2974
QY	2130	gctctcttcacacagcggcagcgtctlaacagagcaagtaccgcctcgcgccacacatgagt	2189
Db	2975	TCTTTATCCCGCCCTTACGCCAGCACTTACGGCAAGTGTGTTGCGGTGGAGGTATC	3034
QY	2190	gctggcctgaacagcagcctagcagcgagcttcggtgtgtattcttcctcaagtgtcagctg	2249
Db	3035	GCCATCTCGGGGGCGGAGTTTGGCTTGGCTTGGCTGCTATCTTCTTCACAAAGCTCTACATC	3094
QY	2250	atcctctgcgcgccagaccctcaacagacagacagcacttcc	2289
Db	3095	ATCCTCTTCAAGCCTTCCCGGAGACCATCGAGGAGGTGC	3134
RESULT	3		
V82483			
ID	V82483 standard: cDNA to mRNA: 5275 BP.		
AC	V82483:		
DT	19-MAR-1999 (first entry)		
DE	Bovine parathyroid calcium receptor BoPar 1 encoding cDNA.		
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis; calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy; spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest; neuronal distress; neurodegenerative disease; Alzheimer's disease; Huntington's disease; Parkinson's disease; dementia; muscle tension; depression; anxiety; ss.		
KW			
OS	Bos sp.		
FT	Key	Location/Qualifiers	
FT	CDS	515..3772	
PD	US5858684-A.	/*tag- a	
PD	12-JAN-1999.		
PF	07-JUN-1995: 480751.		
PR	07-JUN-1995: US-480751.		
PR	23-AUG-1991: US-749451.		
PR	11-FEB-1992: US-834044.		
PR	21-AUG-1992: US-934161.		
PR	12-FEB-1993: US-017127.		
PR	23-FEB-1993: US-009389.		
PR	22-OCT-1993: US-141248.		
PR	19-AUG-1994: US-292827.		
PR	21-OCT-1994: WO-012117.		
PR	08-DEC-1994: US-353784.		
PA	(BGM) BRIGHAM & WOMEN'S HOSPITAL.		
PA	(NPS-) NPS PHARM INC.		
PA	Balandrin MF, Brown EM, Del Mar EG, Garrett JE,		
PA	Hebert SC, Nemeth EF, Van Wadenburg.		

DR WPI: 99-11981/1/10.  
DR P-PSDB: W89563.  
PI Screening for calcium receptor-active compounds - by recombinant  
PI expression of nucleic acid encoding calcium receptor and determining  
PI the effect of compounds on calcium receptor activity  
PS Claim 1: Fig 47; 17pp; English.  
CC A method has been developed of screening for a compound able to affect  
CC one or more activities of a calcium receptor (CR) comprises: (A)  
CC contacting a recombinant cell with a test compound, where the  
CC recombinant cell comprises a recombinant nucleic acid expressing the CR,  
CC provided that the cell does not have functional CR expression from  
CC endogenous nucleic acid; (B) determining the ability of the test  
CC compound to affect one or more activities of the calcium receptor; and  
CC (C) comparing the ability with the ability of the test compound to  
CC affect the one or more CR activities in a cell not comprising the  
CC recombinant nucleic acid. The present sequence encodes bovine  
CC parathyroid CR, designated a Bopar 1. The nucleic acid sequence of  
CC Bopar 1 can be used as part of the recombinant nucleic acid in the  
CC method described above. The compounds identified can be used to treat  
CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.  
CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
CC disorders. They can also be used for the treatment of diseases and  
CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g. seizures, and  
CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
CC diseases such as Alzheimer's disease, Huntington's disease and  
CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
SQ Sequence 5275 BP; 1277 A; 1475 C; 1316 G; 1207 T;

Query Match	5.1%	Score 143.2	DB 1	Length 5275
Best Local Similarity	47.3%	Pred. No. 2.6e-26		
Matches 501, Conservative	0	Mismatches 553	Indels 6	Gaps 2

[illegible]



Accession	Gene	Species	Chromosome	Start	End	Strand	Length	Source	Comment
U01830	caasac	Caenorhabditis elegans	II	11830	11889	+	60	GenBank	1889
D02675	gagc	Caenorhabditis elegans	II	2675	2734	+	59	GenBank	2734
U01890	ctaact	Caenorhabditis elegans	II	1890	1949	+	60	GenBank	1949
D02735	gcat	Caenorhabditis elegans	II	2735	2794	+	59	GenBank	2794
U01950	ctgtrga	Caenorhabditis elegans	II	1950	2009	+	60	GenBank	2009
D02795	atcat	Caenorhabditis elegans	II	2795	2854	+	59	GenBank	2854
U02010	aatg	Caenorhabditis elegans	II	2010	2069	+	60	GenBank	2069
D02855	acnct	Caenorhabditis elegans	II	2855	2914	+	59	GenBank	2914
U02070	aacta	Caenorhabditis elegans	II	2070	2129	+	60	GenBank	2129
D02915	aactc	Caenorhabditis elegans	II	2915	2974	+	59	GenBank	2974
U02130	gcctt	Caenorhabditis elegans	II	2130	2189	+	60	GenBank	2189
D02975	tcctt	Caenorhabditis elegans	II	2975	3034	+	59	GenBank	3034
U02190	gctg	Caenorhabditis elegans	II	2190	2249	+	60	GenBank	2249
D03035	gccat	Caenorhabditis elegans	II	3035	3094	+	59	GenBank	3094
U02250	atcc	Caenorhabditis elegans	II	2250	2289	+	40	GenBank	2289
D03095	atcc	Caenorhabditis elegans	II	3095	3134	+	39	GenBank	3134
RESULT 4									
U0261382	T61382 standard; cDNA to mRNA; 3809 BP.	Caenorhabditis elegans	II	261382	261382	+	1	GenBank	261382
AC	T61382;								
DT	22-APR-1997 (first entry)								
DE	Parathyroid calcium receptor coding sequence clone pRucAR4.0.								
KW	Calcium receptor; human parathyroid gland adenoma tumour; pRucAR4.0.								
KW	primary hyperparathyroidism; Xenopus oocyte; alternative splicing;								
KW	calcium-activated chloride current; agonist; NPS R-467; NPS R-568;								
KW	variant; untranslated region; alternative polyadenylation; probe;								
KW	human Car gene; isoform; ss.								
OS	Homo sapiens.								
EH	Key	Location/Qualifiers							
FT	cds	375..3609							
FT	/*tag= a	/product= Calcium receptor							
FT	/note= "Pages 94-95 are missing from the specification,								
FT	sequence information was obtained from the Epo"								
PN	M09612697-A2.								
PD	02-MAY-1996.								
PE	23-OCT-1995; U13704.								
PR	21-OCT-1994; WO-U12117.								
PR	08-DEC-1994; US-353784.								
PA	(NPSR-) NPS PHARM INC.								
PI	Balandrin MF, Delmar EG, Moe ST, Nemeth EF, Van Wagenen BC;								
DR	WPI; 96-230520/23.								
DR	P-PSDB; W11889.								
PT	New di:arylalkyl amine cpds. useful for modulating inorganic ion								
PT	receptor activities - esp. for modulating effect of extracellular								
PT	calcium on cell surface calcium receptors, useful for treating e.g.								
PT	hyperparathyroidism, Paget's disease or osteoporosis								
PS	Example 1; Page 93-100; 231pp. English.								
CC	The sequences given in T61381-82 encode functional calcium receptors.								
CC	These sequences were isolated from human parathyroid gland adenoma								
CC	tumour using pRucAR4 as a hybridisation probe. mRNA was isolated from								

Query Match	5.98	Score 138.4	DB.1	Length 3809
Best Local Similarity	47.08	Pred. No. 3.6e-25		
Matches 498	Conservative 0	Mismatches 556	Indels 6	Gaps 2
OY 1233	ctaaacataatgagaccacaaatcagctgagcagcggaaagaacacaggtgtcctaagct	1292		
Db 1933	ctcttcatcacaacgaggaamaaactctgtgagagtgggttctccaggagagtgcccttgc	1992		
OY 1293	gtgtgtccagcgacgtgtcttgaaggagcagcagcag--tggtacgggtttccataac	1349		
Db 1993	aaactcacaccagactgcctggcagggacacagaaagcagatcattgagggagacccac	2052		
OY 1350	tgctgcttgggtgtgtgtccctgttgggcttggagacctccccaagaagcagagctcac	1409		
Db 2053	tgctgcttgggt	2112		
OY 1410	agatgcagccttggagacagaagatggtgacaccttggaggagagcagacgtgtcccg	1469		
Db 2113	gccttatacagatgcccacagatgactttctgttcacatgaaacacacacctctgcattg	2172		
OY 1470	cgcactgtgtgtgttttggcttgcgtgagacacaccttgggtgtgtgtgtgtgtgtgt	1529		
Db 2173	aagcagatcagatttctgtctgtgacgagaccccttggagatgcacacacctcttggc	2232		
OY 1530	acgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt	1589		
Db 2233	gt	2292		
OY 1590	cctgt	1649		
Db 2293	cccatgt	2352		
OY 1650	ggtagt	1709		
Db 2353	tgctgt	2412		
OY 1710	cagcgtcctcctgtcctgt	1769		
Db 2413	cagcgtcctcctgtcctgt	2472		
OY 1770	caacatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcat	1829		
Db 2473	cgt	2529		
OY 1830	caaaacacaggt	1889		
Db 2530	ggcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag	2589		
OY 1890	ctaactgt	1949		



Db	2590	GTGATCTGGCTCTACACCGGGCCCCCTCAAGTACCAGCAACAGAGAGCTGAGAGATACG	2649
Qy	1950	ctgtagatgcttgaagtcacagagagacaaactccctggcttatactagccttcctac	2009
Db	2650	ATCATCTTCATCAGCTGCTCCACGAGAGGCTCCCTCATGGCCCTGGGCTTCCTGATCGAGTAC	2709
Qy	2010	aatggctcctctcctacacagtgcttgccttgctgagcttacctggtgaagacttgcgaag	2065
Db	2710	ACCTGCTGGCTGGCTGCCATCTGCTCTCTTGTGCTTCAATGCCGGAAGCTGCCGAG	2769
Qy	2070	aactacacagagagcaaatgtgcacttcagcttccttcaactcgtgtcccgagtc	2129
Db	2770	AACCTCAATGAAGCAGAGTTCATCACCCTTGAGATGCTATCTTCTATGCTGATC	2829
Qy	2130	gccttcttcaaccagcgacgctcacaagcaatgcactgcctcgtcgagcaacatgag	2189
Db	2830	TCCCTCATTCACGAGCTATGCCACACCTATGCAAGATTGTCTGCGCTAGAGGTGAT	2889
Qy	2190	gctgagctgagcaagcctgcagcagcagccttcgtgggtatllctgcctaaagctcagtg	2249
Db	2890	GCAATCCCTGGCAGCCAGCTTTGGCTTGCTGCGTGATCTTCTTAACAAAGATCTACATC	2949
Qy	2250	atccctcgcgcgccagaccccaacagacagacagacacttcc	2289
Db	2950	ATTCTTTCAAGCCATCTCCCGCAACACCATGAGAGAGCTGC	2989
RESULT	5		
TS	195859	standard: cDNA to mRNA; 3809 BP.	
ID	TS5859		
AC	TS5859:		
DT	08-MAY-1998	(first entry)	
DE	Human parathyroid cell calcium receptor 4.0 (hUPCAR 4.0) cDNA.		
DE	Human parathyroid cell calcium receptor 4.0; hUPCAR 4.0;		
KW	calcium homeostasis; hyperparathyroidism; osteoporosis; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	373..3609	
FT		/*tag-a	
FT		/product= parathyroid-cell calcium_receptor_4.0	
PN	US5688938-A.		
PD	18-NOV-1997.		
PF	07-JUN-1995: 485588.		
PR	07-JUN-1995: US-485588.		
PR	23-AUG-1991: US-749451.		
PR	11-FEB-1992: US-834044.		
PR	21-AUG-1992: US-934161.		
PR	12-FEB-1993: US-017127.		
PR	23-FEB-1993: US-009389.		
PR	22-OCT-1993: US-141248.		
PR	19-AUG-1994: US-292827.		
PR	21-OCT-1994: WO-012117.		
PR	08-DEC-1994: US-353784.		
PA	(BGM ) BRIGHAM & WOMENS HOSPITAL.		
PA	(NPSP-) NPS PHARM INC.		
PI	Brown EM, Fuller FH, Garrett JE, Hebert SC;		
DR	WPI; 98-008040/01.		
DR	P-PDSID: W38274.		
PT	DNA encoding calcium receptor polypeptide(s) - useful for		
PT	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis		
PT	Claim 15: Columns 125-134; 174pp; English.		
CC	The present sequence encodes human parathyroid cell calcium		
CC	receptor 4.0 (hUPCAR 4.0).		
CC	The specification includes details of molecules that can modulate		
CC	one or more inorganic ion receptor activities, and antibodies and		
CC	antibody fragments targeted to inorganic ion receptor proteins. The		
CC	proteins, nucleic acids and antibodies may be used to treat		
CC	disorders by modulating one or more inorganic ion receptor		
CC	activities, preferably disorders of calcium homeostasis, e.g.		
CC	hyperparathyroidism and osteoporosis.		
Sequence	3809 BP: 910 A; 1071 C; 979 G; 849 T;		

[illegible]















Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

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QY 10 agcttcaatgagcagctgtaccacacctctccaggctatgagcgttgaggagata 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 AGGTATATTTCCGTGGTTTCGCTGTTACAGGCTATGATATTGCCATAGAGAGATA 283
QY 70 aacaactccagcagcgtctgtcccaacatacccccgtggtatccagctgtatgctgt 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 284 AACGACAGCCAGCCCTTCTCCCACTTGACGCTGGATACAGATATTGGACACTTGC 343
QY 130 tctgactctgccaatg---tgtatgcacgctgagagtgctctccc-----tgcca 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 AACACCGTTTCTTAAGGCTTGAAGCCACCTCGATTGTTGTGCTCAAAACAAATTGAT 403
QY 178 gggcaaacacacataagagctccaagagacctctccactctccctccagctgtgca 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 404 TCTTTGAACCTTGATGATGATTGTGCACTGCTCAAGACCATTCCTCTACGATTGCTGTG 463
QY 238 gtgattgagcctgacagacacacacccgtgtgtccacacagccgctgtgacctctc 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 GTGGAGCAACTGGCTCAGGCGCTCTCCACGCGCATGGCAATTCGCTGGGCTCTTCTAC 523
QY 298 ctgtgcatatagctatgtgcgcacagagcagagcgtcaagcgtgaagcggcagatccc 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 524 ATTCCCAAGCTCAGTTATGCTCTCTCCACAGACACTCTCTCAACCAACAAATTCATAG 583
QY 358 tcttctctgacacatccccaatgacacagatgacagagtgagagacatgtgtctgtc 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 584 TCTTTCTCCAAACCACTCCCAATGATGAGCAACAGGCGCACTGCATGACATATATC 643
QY 418 cagaagttcgggtgtgacctgacctctctgtgtgtgcacagcattgacagactatgscagta 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 GAGTATTTCCCTCGAAGCTGGGTGGGCAATTCACCTGATGAGACATATGGGCGCGG 703
QY 478 ggggtgtcagagcactgtgagaaacagccctgtgtcaggggcatctgcatgtcttaaggac 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 704 GGGATTGAGAAATTCAGAGAGAAAGCTGAGGAAAGGAGATATCTCATGACTTACGTGAA 763
QY 538 atcatgacctctctgtcccaagtggtgcgatagagagatgacgtctcatatcgcacctg 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 764 CTCATCTCCAGTACTGTATGAGGAAGA-----GATCCAGCATGTGTGAGAGTGAT 817
QY 598 gcccaagcggcggcaccacgtgtgtgtgttcttccacgcgcaggttgccagggctgt 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 818 CAATATTTCCAGGCGCAAGTATGTTGTTTCTTCATGAGCCAGATCTGAGCCCTC 877
QY 658 ttcgagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 878 ATCAAGGAGATTGTCCGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGGAGGCTGG 937
QY 718 gccctctcccaagcacaatcacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 777
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 938 GCCAGCTCTCCTCGATCGCATCGCTCAGTACTTCACGCTGTGGGGGAGCAATTTGA 997
QY 778 gtggccatcccaagagagggctgtccctgtgctgaagcgtt 818
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 998 TTCGCTCTGAAGGCTGGGCAATCTCCAGGCTTCCGGGCAATT 1038

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PD 18-NOV-1997.
PF 07-JUN-1995; 485588.
PR 07-JUN-1995; US-485588.
PR 23-AUG-1991; US-749451.
PR 11-FEB-1992; US-834044.
PR 21-AUG-1992; US-934161.
PR 12-FEB-1993; US-017127.
PR 23-FEB-1993; US-009389.
PR 22-OCT-1993; US-141248.
PR 19-AUG-1994; US-292827.
PR 21-OCT-1994; WO-012117.
PR 08-DEC-1994; US-353784.
PA (BGHM ) BRIGHAM & MOYENS HOSPITAL.
PA (NPSF-) NPS PHARM INC.
PI 3-oxo-EM, Fuller FH, Garrett JE, Hebert SC.
D3 WPI; 98-008040/01.
D3 P-PSDB; W82873.
PT DNA encoding calcium receptor polypeptide(s) - useful for
PT therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS Claim 15: Columns 117-126, 174pp: English.
CC The present sequence encodes human parathyroid cell calcium
CC receptor 5.2 (HupCar 5.2).
CC The specification includes details of molecules that can modulate
CC one or more inorganic ion receptor activities, and antibodies and
CC antibody fragments targeted to inorganic ion receptor proteins. The
CC proteins, nucleic acids and antibodies may be used to treat
CC disorders by modulating one or more inorganic ion receptor
CC activities, preferably disorders of calcium homeostasis, e.g.
CC hyperparathyroidism and osteoporosis.
SQ Sequence 5006 Bp; 1227 A; 1378 C; 1219 G; 1182 T;

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Query Match 5.7%; Score 132.6; DB 1; Length 5006;

Best Local Similarity 50.4%; Pred. No. 1,1e-23;

Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

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QY 10 agcttcaatgagcagctgtaccacacctctccaggctatgagcgttgaggagata 69
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 AGGTATATTTCCGTGGTTTCGCTGTTACAGGCTATGATATTGCCATAGAGAGATA 678
QY 70 aacaactccagcagcgtctgtcccaacatacccccgtggtatccagctgtatgctgt 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 AACGACAGCCAGCCCTTCTCCCACTTGACGCTGGATACAGATATTGGACACTTGC 738
QY 130 tctgactctgccaatg---tgtatgcacgctgagagtgctctccc-----tgcca 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 AACACCGTTTCTTAAGGCTTGAAGCCACCTCGATTGTTGTGCTCAAAACAAATTGAT 798
QY 178 gggcaaacacacataagagctccaagagacctctccactatccctccagtgctgca 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 TCTTTGAACCTTGATGATGATTGTGCACTGCTCAAGCAATATCTCTTACGATTGCTGTG 858
QY 238 gtgattgagcctgacagacacacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 GTGGAGCAACTGGCTCAGGCGCTCTCCACGCGCATGGCAATTCGCTGGGCTCTTCTAC 918
QY 298 ctgtgcatatagctatgtgcgcacagagcgtgtcaagcgtgaagcggcagatccc 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 ATTCCCAAGCTCAGTTATGCTCTCTCCACAGACACTCTCTCAACCAACAAATTCATAG 978
QY 358 tcttctctgacacatccccaatgacacagatgacagagtgagagacatgtgtctgtc 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 979 TCTTTCTCCGAAACCACTCCCAATGATGAGCAACAGGCGCATGCGCATGAGACATATC 1038
QY 418 cagaagttcgggtgtgacctgacctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1039 GAGTATTTCCCTCGAAGCTGGGTGGGCAATTCACCTGATGAGACTATGGGCGCGG 1098
QY 478 ggggtgtcagagcactgtgagaaacagccctgtgtcaggggcatctgcatgtcttaaggac 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1099 GGGATTGAGAAATTCAGAGAGAAAGCTGAGGAAAGGAGATATCTCATGACTTACGTGAA 1158
QY 538 atcatgacctctctgtcccaagtggtgcgatagagagatgacgtctcatatcgcacctg 597

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Db      1159  CTCATCTCCCACTACTCTCATATAGAGAGA-----GATCAGAGATGTGTAGAGTGATTT 1212
Oy      598  gccacgacggcgagcgcaacgcgtcgctggtgttttcttcacgcgcgcagttgcccagtggtt 657
Db      1213  CAAATTTCCACGCCGCAAAATCATCTGCTGTTTCTCCAGTGGGCCCAATCTTGAGCCCCTC 1272
Oy      658  ttcgcgtccgctggtgtctgtgcacacccgactgtgcgaagtggtgtgcccacaagaacttg 717
Db      1273  ATCAAGGAGATTTGTCCTCCGCCCAATATCAGGGCGCAAAATCTGGCTGGCCAGCGAGGCTCG 1332
Oy      718  gccctctccagcgacatcactctggtgtgcccgcgagatccagcgcattgtgagtgtcctggc 777
Db      1333  GCCAGCTCTCCTCCTGATGCCCATGCTTCAGTACTTCCAGCTGGTTTGCGGCAACATTGGA 1392
Oy      778  gtgcgcattccagaagaagagtgcttccctgtgcctgaagcgtt 818
Db      1393  TTCGCTCTGAAAGCTGGGCGAGATCCGAGGCTTCCGGGAATT 1433

RESULT  11
ID      V26963
AC      V26963 standard; cDNA to mRNA; 5006 BP.
AD      V26963;
DT      01-SEP-1998 (first entry)
DE      Human parathyroid calcium receptor 5.2 gene 5kb fragment.
KW      ss, calcium ion concentration; parathyroid hormone; homeostasis;
KW      kidney; calcium receptor; detection.
OS      Homo sapiens.
FT      FT
FT      FT key
FT      CDS
FT      Location/Qualifiers
          436..3702
          /tag= a
          /product= "pHUPCar 5.2 5kb fragment"

PR      US5763369-A.
PR      PD 09-JUN-1998.
PR      PE 07-JUN-1995; 484565.
PR      07-JUN-1995; US-7484565.
PR      23-AUG-1991; US-749451.
PR      11-FEB-1992; US-834044.
PR      21-AUG-1992; US-934161.
PR      12-FEB-1993; US-017127.
PR      23-FEB-1993; US-009389.
PR      22-OCT-1993; US-141248.
PR      19-AUG-1994; US-292827.
PR      21-OCT-1994; WO-012117.
PR      08-DEC-1994; US-533784.
PR      (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PR      PA (NPSM ) NPS PHARM INC.
PR      PI Brown EM, Garrett JE, Hebert SC;
PR      WPI: 98-347412/30.
PR      P-PSDB: WS4845.
DR      P-PSDB: WS4845.
PT      Calcium receptor poly:peptide(s) - useful for drug screening or
PT      antibody production
PS      Example 27; Fig 48; 174pp; English.
SS      The Human parathyroid calcium receptor gene encodes a 1088 amino acid
      protein. The tissue from which this receptor and receptors from bovine
      parathyroid and rat kidney are derived, respond to changes, and control
      changes, in calcium ion concentration, e.g. parathyroid hormone regulates
      Ca2+ homeostasis in blood and extracellular fluid, and kidney function
      alters through changes in Ca2+ levels in juxtaglomerular and proximal
      tubule cells in the kidney. The purified receptors (produced
      recombinantly) can be used to screen for compounds that modulate calcium
      receptor activity, especially those that can be used to treat diseases
      associated with the receptors in these tissues. They can also be used
      to raise antibodies for use in detection assays.
CC      Sequence 5006 BP; 1228 A; 1376 C; 1220 G; 1182 T;

Query Match 5.7%; Score 132.6; DB 1; Length 5006;
Best Local Similarity 50.4%; Pred. No. 1,1e-23;
Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3

10 agctcaatgagcatggtctaccacacctcttcacgagctatgcggttggttgaagagata 69

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Db	619	AGGATATATTTCCGTGGGTTTCCCTGGTTACAGAGCATATATTTTGGCATAGAGAGATA	678
Oy	70	aacaactccaaagccctctgcgcccaacatcacccctgggtacaaactcgtatgatgtgtgt	129
Db	679	AACAGCAGCCAGCCGCTCTTCTCCCACTTGAGAGCTGGATACAGGATATTGGACACTGCG	738
Oy	130	ctctgacctgcgaatg---tgatgcgcagcctggagatgctctcc-----tgcga	177
Db	739	AACACCGTTTCTAAGGCGCTTGGAGAGCCACCCCTGAGTTTGTGTGCTCAAAACAAATTCAT	798
Oy	178	gggcaacaaccaatagatagatccccaagaagaagacctctccactatctccctcagcgtgtgca	237
Db	799	TCTTTGAACCTTGAATAGATGTTCTGCACACTGCTCAGAGCAATTCCTCTACGATTGCTGTG	858
Oy	238	gtgatctggccctgcagacaccaaactcgtctgcacacaagaacccgcctctgagcccttc	297
Db	859	GTGGAGAGCAACTGGCTCAGGCGTCTCCACAGCGCAGTGGCAATCTGCTGGGCGCTTCTAC	918
Oy	298	ctgtgatattatgtcctatgctgctggcccaacagcagcagaagctcagctgtagaagcggcagatccc	357
Db	919	ATTCCCAAGGCTGAGTTATGCTCTCTCCACAGCACTCTCTAGCAACAAATCAATTCAG	978
Oy	358	tccttctctgcacccatccccaatgacaagatcccaagctgtagaacatgtgtctgtctgtg	417
Db	979	TCTTTCTCCGAACCATCCCAATGATAGAGCAACAGCCACAGCCATGGCAGACATCATC	1038
Oy	418	cagaagctcgggtggnaccttgatctctctgtgtgtgcagcagatgacgactatgtagcagcta	477
Db	1039	GAGTATTTCCGCTGGAACCTGGTGGGACCAATTCGACGTGATGACGATATAGGGGCGCG	1098
Oy	478	ggggtgcagagcactcgtgagaaacccagccctggctcagcggcgatctgattgcttcaaggac	537
Db	1099	GGGATTAGAAGATTCGACAGAGGAAGCTGAGGAAGGAGATATCTGATCTAGCTTACGTAA	1158
Oy	538	atactgcccctctctctgcgcagcgtggtgcagatgagagatgacatgctcatgctgcacactg	597
Db	1159	CTCATCTCCAGTACTCTGATAGAGAAAG-----GATCCACATCTGTGTAGAGTGATT	1212
Oy	598	gcccaagccggggccacacgctcgtgtgtgttttctccagccggcagcttgcgaaggatgttt	657
Db	1213	CAAAATTCACAGCGGCCAAGATCATCTGATTTCTCCAGTGGCCCGACATCTTGAAGCCCTC	1272
Oy	658	cttgagctcgtgtgtctgcacaaacccgactgcgcaagatgtgtgtctgcctcagaagccctgg	717
Db	1273	ATCAGAAGAGATGTGCGGCCCAATATCACGGCCAAATCTGGCTGGCCAGCGAGGCTTGG	1332
Oy	718	gcccctcccaagcaccatcaactatgggtggcccgagatccacagcagatgtggatgtgtctggc	777
Db	1333	GCCAGCTCTCTCCGATCGACATGCTCATGACTTCCAGTGTGTTGGCGGACCATTTGGA	1392
Oy	778	gtggccatcagaagaaggcctgtccctctgcctcgtgaaggcgtt	818
Db	1393	TTCGCTCTGAAGGCTGGCGAGATCCCGAGGCTTCCGGGAATT	1433
RESULT 12			
ID	V82484	standard; cDNA to mRNA; 5006 BP.	
AC	V82484		
DT	19-MAR-1999	(first entry)	
DE	Human parathyroid calcium receptor pHPuPar 5.2 encoding cDNA.		
KW	Parathyroid calcium receptor; inorganic ion receptor; osteoporosis;		
KW	calcium homeostasis; hyperparathyroidism; seizure; stroke; epilepsy;		
KW	spinal cord injury; hypoxia-induced nerve cell damage; cardiac arrest;		
KW	neonatal distress; neurodegenerative disease; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; dementia; muscle tension;		
OS	depression; anxiety; ss.		
FS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	436..3702	
FT	ET	/*tag- a	
FN	US5836684-A		



PD 12-JAN-1999.  
 PF 07-JUN-1995: 480751.  
 PR 07-JUN-1995: US-480751.  
 PR 23-AUG-1991: US-749451.  
 PR 11-FEB-1992: US-834044.  
 PR 21-AUG-1992: US-934161.  
 PR 12-FEB-1993: US-017127.  
 PR 23-FEB-1993: US-009389.  
 PR 22-OCT-1993: US-141248.  
 PR 19-AUG-1994: US-292827.  
 PR 21-OCT-1994: WO-012117.  
 PR 08-DEC-1994: US-353784.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 PA (NPSF-) NPS PHARM INC.  
 PI Balandrin MF, Brown EM, Del Mar EG, Garrett JE,  
 PI Hebert SC, Nemeth EF, Van Wagenen BC;  
 PI WPI: 99-119871/10.  
 DR P-PSDB; W89564.  
 PT Screening for calcium receptor-active compounds - by recombinant  
 PT expression of nucleic acid encoding calcium receptor and determining  
 PT the effect of compounds on calcium receptor activity  
 PS Claim 1: Fig 48; 176p; English.  
 CC A method has been developed of screening for a compound able to affect  
 CC one or more activities of a calcium receptor (CR) comprises: (A)  
 CC contacting a recombinant cell with a test compound, where the  
 CC recombinant cell comprises a recombinant nucleic acid expressing the CR,  
 CC provided that the cell does not have functional CR expression from  
 CC endogenous nucleic acid; (B) determining the ability of the test  
 CC compound to affect one or more activities of the calcium receptor; and  
 CC (C) comparing the ability with the ability of the test compound to  
 CC affect the one or more CR activities in a cell not comprising the  
 CC recombinant nucleic acid. The present sequence encodes human  
 CC parathyroid CR, designated a phnPCAR 5.2. The nucleic acid sequence of  
 CC phnPCAR 5.2 can be used as part of the recombinant nucleic acid in the  
 CC method described above. The compounds identified can be used to treat  
 CC diseases or disorders characterised by abnormal calcium homeostasis, e.g.,  
 CC hyperparathyroidism, osteoporosis and other bone and mineral-related  
 CC disorders. They can also be used for the treatment of diseases and  
 CC disorders associated with disrupted Ca<sup>2+</sup> responses, e.g., seizures,  
 CC stroke, spinal cord injury, hypoxia-induced nerve cell damage such as in  
 CC cardiac arrest or neonatal distress, epilepsy, neurodegenerative  
 CC diseases such as Alzheimer's disease, Huntington's disease and  
 CC Parkinson's disease, dementia, muscle tension, depression, and anxiety.  
 SQ Sequence 5006 BP: 1228 A: 1376 C: 1220 G: 1182 T:

Query Match 5.7%; Score 132.6; DB 1; Length 5006;  
 Best Local Similarity 50.4%; Pired. No. 1,1e-23;  
 Matches 414; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

QY 10 agcttcaatagcatgctaccacaccttccagagctatgcggcttgaggatgaata 69  
 DB 619 AGGATATATTTCGTTGGTTCGTTGCTACAGGCTATGATATTTCGCAAGAGAAATA 678  
 QY 70 aacaactccagggccctgcctcccaacatcacccctgggtggtacagcgtgatgtgt 129  
 DB 679 AACAGCAGCCAGCCCTTCTTCCCACTTGACGCTGGGATACAGATATTGACACTTC 738  
 QY 130 tctgactctgcacatg--tgatgcaagctgagagtgctctcc-----tgcca 177  
 DB 739 AACACGCTTTCTTGAAGCCTTGAAGCCACCCCTGAGTTTGTGTCTAAACAAATATGAT 798  
 QY 178 gggcaaacacacatagagctcccaagagaccttccacattcccttaaggtgtgtgca 237  
 DB 799 TCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGACACATTCCTCTACGATTGCTGTG 858  
 QY 238 gtgattggcctgacagacacacacgctgcctcccaagcccgccgctgagcccttc 297  
 DB 859 GTGGAGACAACTGGCTAGAGCGTCTCCACGGCACTGGCAATATGCTGGGGCTTTCTAC 918  
 QY 298 ctggtgcatattagctatgcggcagcagcagcagcgtcagcgtgaaagcgagctatccc 357  
 DB 919 ATTCCCAAGTCAGTTATGCTCTCTCCAGAGACTCTCTCAGCAACAAGAAATCAATTCAG 978

QY 358 tctttctgcgcacccatccccaatgacaaagttagagacatgtgtcgtgtgt 417  
 DB 979 TCTTTCCTCCGAACCATCCCAATGATGAGCACACAGCCACTCCGACGACATATATC 1038  
 QY 418 cagaagttcgggtgagactgtgacccctcctgtgttgcagcagctagacactatggcagct 477  
 DB 1039 GAGTATTCTCGCTGGAACCTGGTGGGACAAATTGCAGCTATATGACGACTATGGGGCCGG 1098  
 QY 478 ggggtgcagcgacatggaacccagccctgctcaggcgacatctgcatcttccaaggc 537  
 DB 1099 GGGATTGAGAAATTCGACGAGCAAGCTGAGAGAAAGGATATCTGCACTTCAGTGA 1158  
 QY 538 atatgacctctcctgcgcccggtggcgatgagaagatgtagtgccctcagcccaactgt 597  
 DB 1159 CTATCTCCAGTACTCTGTATGAGGAAGA-----GATCCGATGATGGTAGAGTGATTT 1212  
 QY 598 gcccaaggccggcgacacccgctggtgtgtttttccagcccgagttgscagaggtgtt 657  
 DB 1213 CAAAATTCACAGGCGCAAAAGTATCATGTGTCTTCAGTGGCCCAATCTTAGCCCTC 1272  
 QY 658 ttcgagtcctgtgtgtgtacaaacctgactgcgaaggtgtgtgtcgcctcagaagcctgtg 717  
 DB 1273 ATCAAGGAGATGTGTCCGGCCCAATATCACGCGCAAGATCTGCTGGCCAGGAGCCTGG 1332  
 QY 718 gccctccagcgacatcactgtgggtggtcccgagatccagcattggggtgtgtgtgtg 777  
 DB 1333 GCCAGCTCTCCCTGATGGCATGCTCCTAGTACTTCCACGTGGTGTGGCGCACCATTTGA 1392  
 QY 778 gtggcattccagaagaggtgtccctggtcgtgaagtcgt 818  
 DB 1393 TTGCGTCTGAAGGCTGGGCAATCCAGGCTTCCGGGAATT 1433

RESULT 13  
 ID T89290 standard: cDNA; 4131 BP.  
 AC T89290:  
 DT 27-MAR-1998 (first entry)  
 DE Dogfish shark kidney calcium receptor related protein cDNA.  
 KW Calcium receptor related protein; Car-RP; dogfish shark; SKCAR-RP;  
 KM Polyclonal-sensing receptor; aquaculture; fish farming;  
 OS salinity tolerance; ss.  
 NS Squalus acanthias.  
 FH Key Location/Qualifiers  
 FT CDS 439..3519  
 FT /\*tag= a  
 FT polyA\_site 4076..4113  
 FT /\*tag= b  
 PN W09735977-A1.  
 PD 02-OCT-1997.  
 PF 27-MAR-1997: U05031.  
 PR 27-MAR-1996: US-622738.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 PI Brown E, Harris HW, Hebert S;  
 PI WPI: 97-489640/45.  
 DR P-PSDB; W32059.  
 PT New isolated Aquatic polyvalent cation-sensing receptor - used to  
 PT develop products for increasing or decreasing the salinity tolerance  
 PT of fish for use in aquaculture  
 PS Claim 2: Fig 4A-F; 57p; English.  
 CC This cDNA clone codes for dogfish shark kidney calcium receptor  
 CC related protein (SKCAR-RP, see W32059), an aquatic polyvalent  
 CC cation-sensing receptor (PVCAR). It was isolated from a shark  
 CC kidney cDNA library using a rat kidney calcium receptor cDNA as  
 CC probe. Also claimed are: a probe comprising the 4131 bp SKCAR-RP  
 CC sequence; an isolated PVCAR present in the plasma membrane of  
 CC aquatic species, especially on the apical membrane of epithelial  
 CC cells of elasmobranch fish, particularly from cells found in the  
 CC collecting duct or late distal tubule in the kidney, intestine,  
 CC gill, rectal gland, gonad or brain; an antibody that specifically  
 CC binds to a PVCAR; and a method of screening for aquatic PVCAR  
 CC agonists and antagonists. Modulation of the expression of the



CC aquaculture PVCr activators or inhibits aquaculture PVCr mediated ion  
CC transport and endocrine changes that permit fish to adapt to free  
CC or salt water. The method facilitates the aquaculture of marine  
CC fish and can provide for the development of marine fish that are  
CC easily adaptable to fresh water aquaculture.

S0 Sequence 4131 Bp; 1028 A; 1161 C; 1019 G; 923 T;

Query Match	5.5%	Score 129;	DB 1;	Length 4131;
Best Local Similarity	46.1%;	Pred	No.8.2e-23;	
Matches 509;	Conservative	0;	Mismatches 590;	Indels 6;
				Gaps 2

QY	1210	cctccacatgctcccaagttccagctcaacataatgagccaaatccagttccagcgaa	1269
Db	1997	CCTACGCTAAAGCCAGAGGACCGACTCAACATCAACGAAAGAAATTCCTCTGGAGTGGCT	2056
QY	1270	agaaaccaccagctgctcaagtctgtgtgtccagcgactgtcttgaaggcac---cagc	1326
Db	2057	TCTCCAAAGTGTGTTCTTCTCCAACTGCAGTGGAGACTGTGTGGCCGGGACCAAGAGAGG	2116
QY	1327	gagtggttaagggtttccatcactgtctgtttgagtgtgtccctgtgtggactgtggact	1386
Db	2117	GGATCATCGAGGGGGAGCCACCCTGCTGCTTTGAATGATGACATGCAATGTCAGAGGAGAGT	2176
QY	1387	tcctccacaagagcgagcctctacaagttccagcctgtgtgtgaacagaagatgtggacgtg	1446
Db	2177	TCACTATGTAAGAAAGATGCAAGTGCCTGTACAAAGTGCCTCCGCAATGTTTCTGTGTGAATG	2236
QY	1447	agggaaaccagacactgtcttcccgcgacagtgtgtgtttttgtgctttgtcgtagcacact	1506
Db	2237	AGAACCAACAGTGTGTGATGCGCAAGAGATGAGTACACTGTGTGTGAAGGGAGGCGCTTCG	2286
QY	1507	cttggtgtcgtcgtcgcaagtaaacgctgcgtctgtctgtctgtctgtgtggactgtgccc	1566
Db	2297	GGATGCTCTGACCACTTCTTCGCGCTAGTGGGCACTCTGTATCACTCTTTCGTGTGGGGG	2356
QY	1567	tgattgtcgtagaacctatgaaccccgtgtgtgtgtgtgagtcagcaagggtccgcgcgtgttc	1626
Db	2357	TCTTCATCAAGTTTCAAGAAACATCTCCCATGTGAAGGCCAACCAACGGGAGTGTCTTACAC	2416
QY	1627	ttaatgtcggagctccctgtgcagcagtagtgcagcgctctatgctctcttgttggaaacca	1686
Db	2417	TGCGCTCTTCTCCCTATGTGCTGTCTCCAGCTCGCTATCTTCAATCGGCAAGCCCA	2476
QY	1687	caaggcctgcgtctgtctagcagcgagccctcttgcctgtgtttcacacatctcctgt	1746
Db	2477	GGGACTGGACCTGTGGGCTCCGGCCAAACGGGCTTTGGCATGAGCTTGCCTGTGTCATCT	2536
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QY	1807	ctacattctacaagcctgtgtgtccaaacaacagcgtctgtcctgttgtgtatgatacgt	1866
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QY	1867	caagcgccacgctgtatctgttactaactgtcgtgtgtgtgtgtgagcccaatgtcctgta	1926
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QY	1927	gggaataccagcgtctcccccacatctgtgtatgtctgtgtgtgcagaagaacaaactccctg	1986
Db	2714	GGAACTCTAGCTGAGAGAGAGAGTATCTTCATCACTGCACAGAGGGCTCTGCTCATAGG	2773
QY	1987	gcttcatacagcgtccctctctacaatgagcctctctccataagtgactgttgcctgtcagct	2046
Db	2774	CGCTGGGCTTCTCATATGGCTATCACTGCTCTCTCGCCGCCATCTGCTTCTTCTTGCTCT	2833
QY	2047	acctgtgttaaggactgtccagagactcaacaagcagcacaatgtgttcaactcaagctgc	2106
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QY	2107	tcttcaaatctcgttctgtatgcgtccttctccacaagcgagcgtctataagcgtcaagt	2166

Db 2894 TGATCTTCTTCATCGTCTGGATATCCTTATGCCGCCCATCTCAGCACTTAAGGCAAGT 2953  
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 Db 2954 TTGTGTGGGCGGTGGAGGTATTTGCCATCTCTGCGCTTCACGCTTCGGGCTGCTGGGCTCA 3013  
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 QY 2287 tccagcctccattccaggaactaac 2311  
 Db 3074 TGGCGTGCAGCAGCGCGGCCCAAGC 3098

RESULT	14
ID	T95860
AC	T95860 standard; cDNA to mRNA. 4131 BP.
DT	08-MAY-1998 (first entry)
DE	Rat kidney cell calcium receptor 3A (RakCar 3A) cDNA.
KW	Rat kidney cell calcium receptor 3A; RakCar 3A;
KW	calcium homeostasis; hyperparathyroidism; osteoporosis; ss.
OS	Rattus sp.
FH	key
FT	Location/Qualifiers
FT	CDS
FT	574..3813
FT	/tag= a
FT	/product= kidney_cell_calcium_receptor_3A
PX	US5688938-A.
PN	18-NOV-1997.
PP	07-JUN-1995.
PR	07-JUN-1995; US-485588.
PR	23-AUG-1991; US-749451.
PR	11-FEB-1992; US-834044.
PR	21-AUG-1992; US-934161.
PR	12-FEB-1993; US-017127.
PR	23-FEB-1993; US-009389.
PR	22-OCT-1993; US-141248.
PR	19-AUG-1994; US-292827.
PR	21-OCT-1994; WO-012117.
PR	08-DEC-1994; US-353784.
PA	(BGM ) BRIGHAM & WOMENS HOSPITAL.
PI	(NSP-) NPS PHARM INC.
PI	Brown EM, Fuller FH, Garrett JE, Hebert SC;
DR	WPI; 98-008040/01.
DN	P-PSTD; W38275.
PT	DNA encoding calcium receptor polypeptide(s) - useful for
PT	therapeutic purposes, e.g. hyperparathyroidism and osteoporosis
PS	Claim 15; Columns 133-142; 174pp; English.
CC	The present sequence encodes rat kidney cell calcium
CC	receptor 3A (RakCar 3A).
CC	The specification includes details of molecules that can modulate
CC	one or more inorganic ion receptor activities, and antibodies and
CC	antibody fragments targeted to inorganic ion receptor proteins. The
CC	proteins, nucleic acids and antibodies may be used to treat
CC	disorders by modulating one or more inorganic ion receptor
CC	activities, preferably disorders of calcium homeostasis, e.g.
CC	hyperparathyroidism and osteoporosis.
SQ	Sequence 4131 BP; 987 A; 1170 C; 1053 G; 921 T;

Query Match                      5.3%    Score 123.4; DB 1; Length 4131;  
 Best Local Similarity    46.0%; Pred. No. 2,le-21;  
 Matches    492; Conservative    0; Mismatches    571; Indels         6; Gaps         2.

QY	1233	ctaacataaatgagaccaaaatccaggtgcacggaaagaacacccagtgcttaagtct	1292
DB	2134	CTCCTCATCAATGAGAGAAGATCTTGTGGAGTGCGTTCTCCAGAGAGGTGCCTTCCTCC	2193
OY	1293	gtgtgttccagcgaactgtccttcgaaggagc---cacgcaagtgttaagtggtttcatcac	1349
DB	2194	AATTGACACCAGGAGATGTCACGACAGGACACGAAGAGGGGATCATCAGAGAGGCCAAC	2253







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QY 1650 gtagtggcagccctctatggtctcttggggaaccacaagcgtgctgtctacgc 1709
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Db 2554 TGCTTCTCCAGCTCCTTGTCTTCAATGGGGAGCCCGAGACTGGAGCTGCCGCTGGCA 2613
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Db 2614 CAGCTGCTTTCGGCTCAGCTTGTGTCTGTATCTGTGATCTTGTGTAGAACCAAT 2673
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QY 1770 caactaatcatcatcttcaaglttccacaagctaacatctacacagcctgggtc 1829
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QY 2190 gctgggtgagcagcgtgagcagcggcttgggtatcttctgctaaagtgtacgtg 2249
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